[Graduate Research Symposium]

HEALTHCARE ASSOCIATED INFECTIONS - COMPUTATIONAL MODELING AND INFERENCE

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University of Iowa
comp|epi
computational epidemiology research

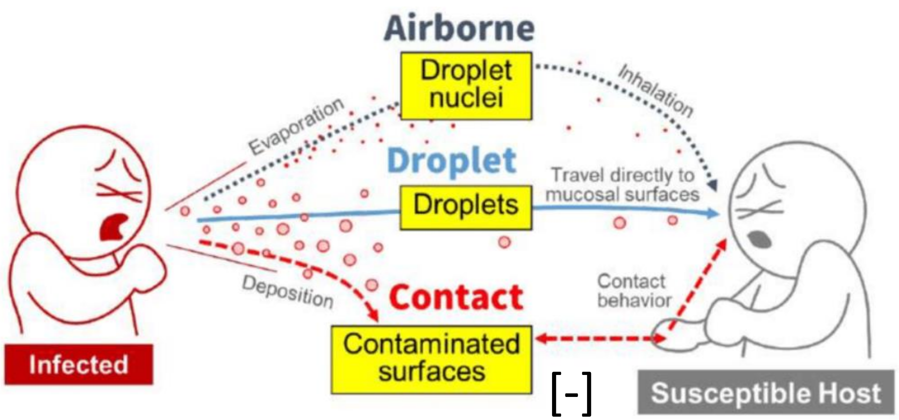
THE UNIVERSITY OF IOWA®

HAIs are threat to patients

- *Healthcare-associated infections* (HAIs): infections that occur during care
- Each year, roughly 4% of patients in the US are diagnosed with infection during their care in the hospital [*]
- Healthcare facilities are interested in preventing HAIs
- However, there are challenges in designing effective interventions

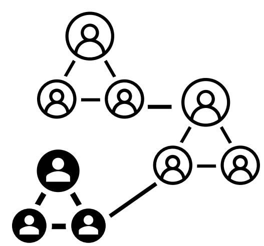
Challenge in realistic disease modeling and simulation due to

(i) complex nature of disease



[-]

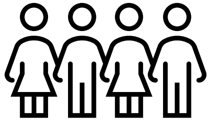
(ii) heterogeneity in contacts



Challenge due to missing infections

Symptomatic (not recorded)

Asymptomatic (Latent spreaders)



[*] CDC, "Healthcare-associated infections (hais),“ https://www.cdc.gov/winnablebattles/report/HAIs.html.
[-] Gameiro Silva, M. An analysis of the transmission modes of COVID-19 in light of the concepts of Indoor Air Quality. 2020

Outline

HAI

Part 1: Computational Modeling

Designing NPIs

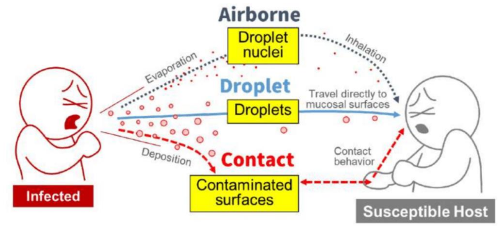
Part 2: Optimization Algorithms

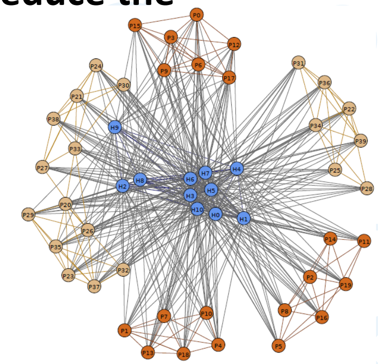
Missing Infections

Part 3: Machine Learning

Patient Embedding

Q: How to design interventions to reduce the spread of disease?





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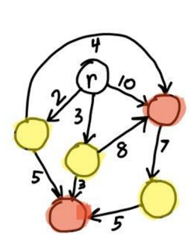

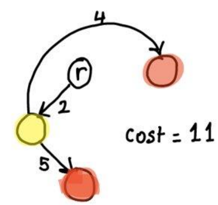

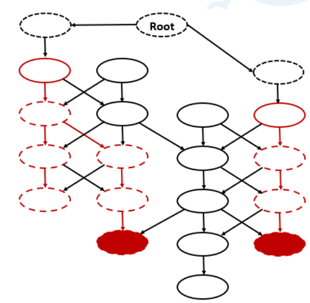

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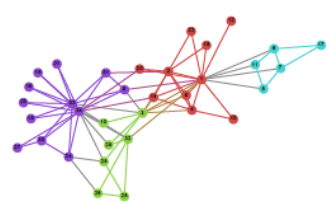

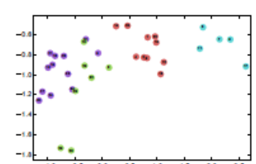

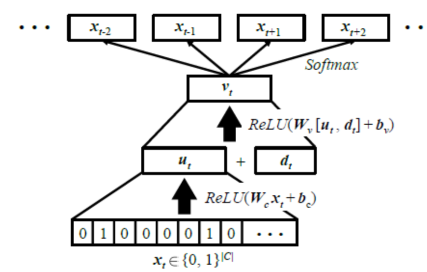

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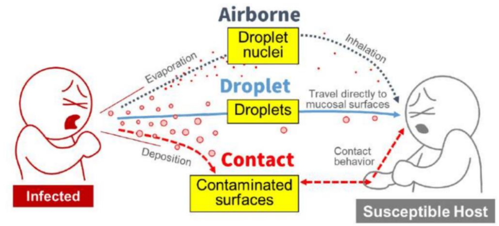

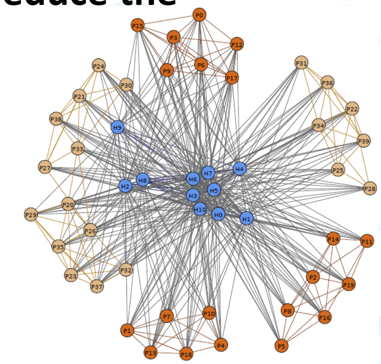

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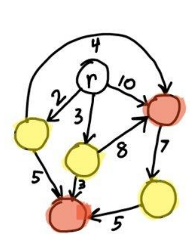

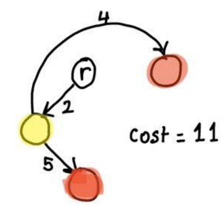

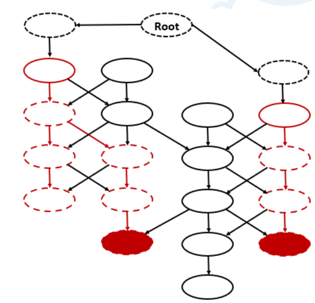

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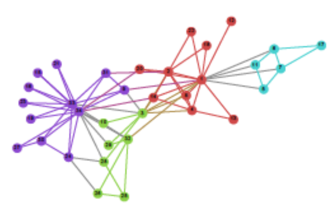
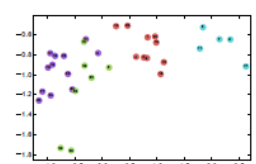
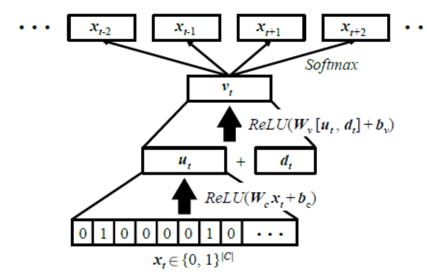
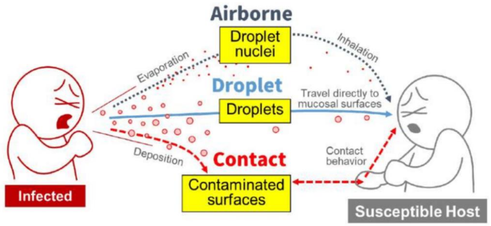






Compartmental models



- Designed to model the dynamics of infectious diseases under the assumption of ***homogeneous mixing*** in mathematical epidemiology [*]

Common cold

$$\boxed{S} \rightleftarrows \boxed{I}$$

Measles, Mumps, and Rubella (MMR)

$$\boxed{S} \rightarrow \boxed{I} \rightarrow \boxed{R}$$

COVID-19

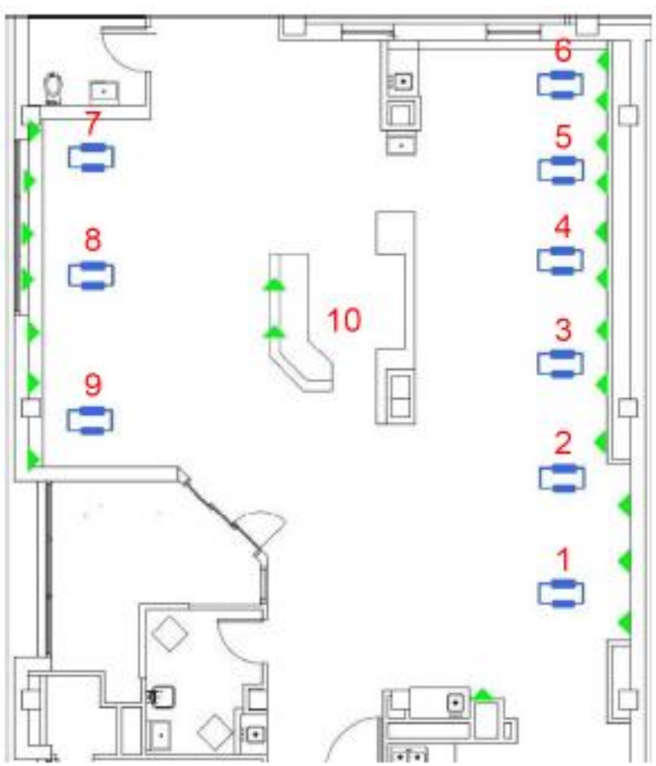
$$\boxed{S} \rightarrow \boxed{E} \rightarrow \boxed{I} \rightarrow \boxed{R}$$

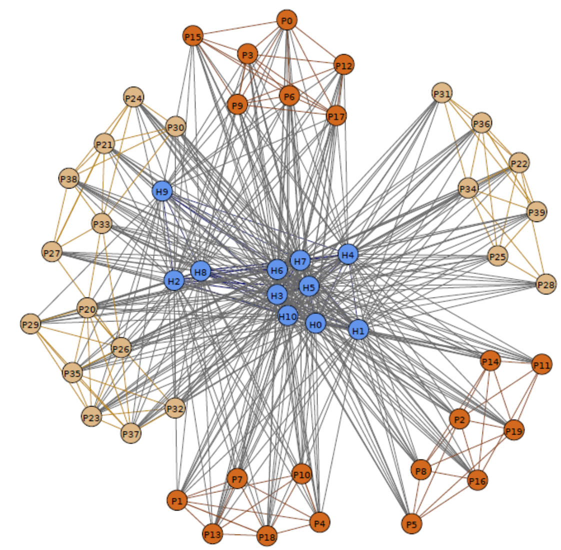
Limitation: Ignores heterogeneity at the individual level
-> Difficult to design individual-level intervention strategies

[*] N. B. Dimitrov and L. A. Meyers, "Mathematical Approaches to Infectious Disease Prediction and Control," in Risk and Optimization in an Uncertain World, INFORMS 2010
[-] S. Li et al., "Dynamics and Control of Infections Transmitted From Person to Person Through the Environment," AJ of Epidemiology, 2009

Contact networks

- We use *motes* to capture fine-grained contacts between people
  - Contacts btw. HCPs were captured at the dialysis unit and MICU at UIHC [+]



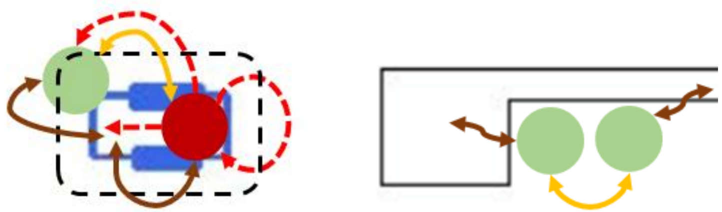


Agent-based simulations
Infection flows through edges in the ***contact network*** and the infection state of nodes follow the ***compartmental model***

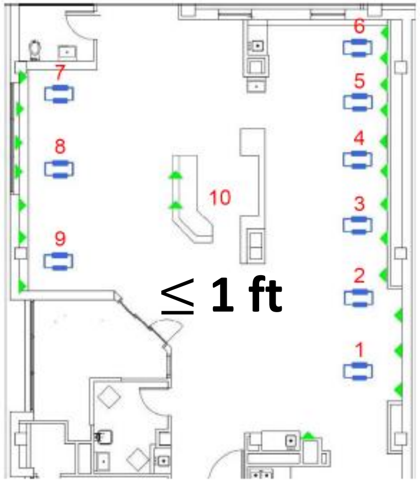
[+] **H. Jang**, S. Justice, P. M. Polgreen, **A. M. Segre**, D. K. Sewell, and **S. V. Pemmaraju**, "Evaluating Architectural Changes to Alter Pathogen Dynamics in a Dialysis Unit," ASONAM 2019

Effect of architectural changes on MRSA spread

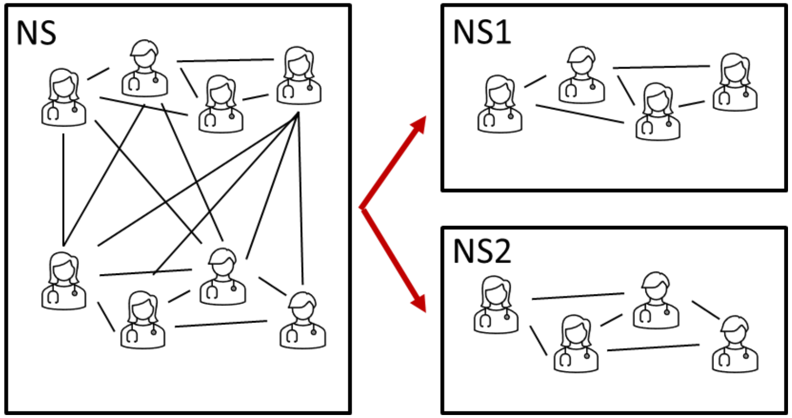
Disease model



Contact network



Interventions & results



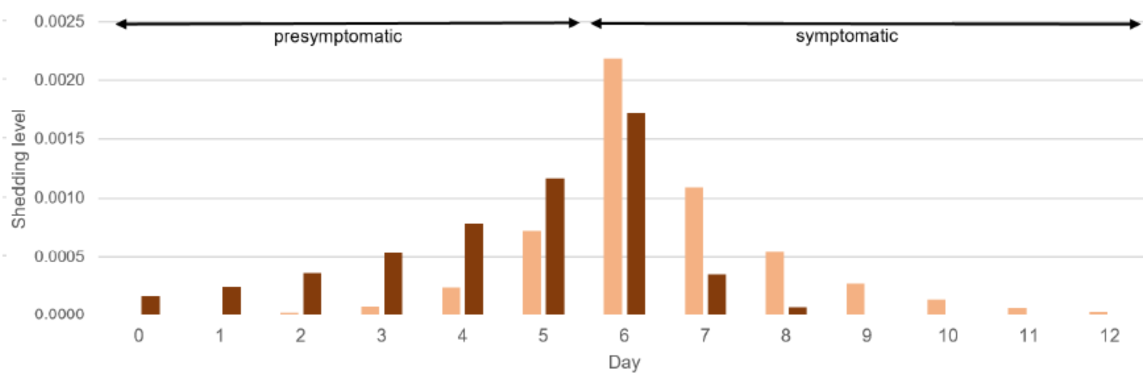
What we expected
Contacts↓
→ Pathogen spread less
→ infection count ↓

What we observed
Infection count ↑
Dilution effect: pathogen on locations reduces risk

[+] **H. Jang**, S. Justice, P. M. Polgreen, **A. M. Segre**, D. K. Sewell, and **S. V. Pemmaraju**, "Evaluating Architectural Changes to Alter Pathogen Dynamics in a Dialysis Unit," **ASONAM 2019 [Best Paper Award]**

Effect of NPIs on COVID-19 shedding model

Disease model



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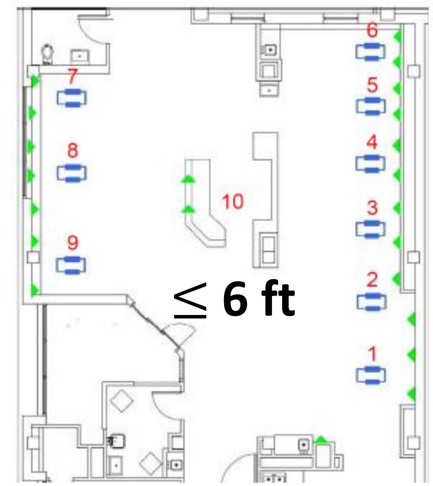

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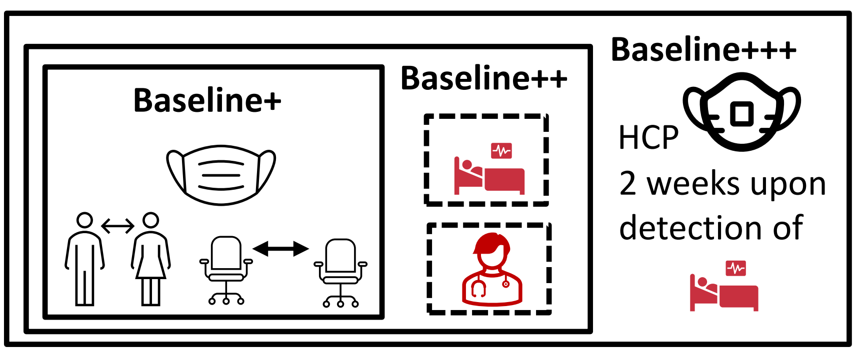

Attack rate
88% -> **35%**

No additional infection rate
6% -> **32%**

[+] **H. Jang**, P. M. Polgreen, **A. M. Segre**, and **S. V. Pemmaraju**, "Covid-19 modeling and non-pharmaceutical interventions in an outpatient dialysis unit," **PLOS Computational Biology 2021**

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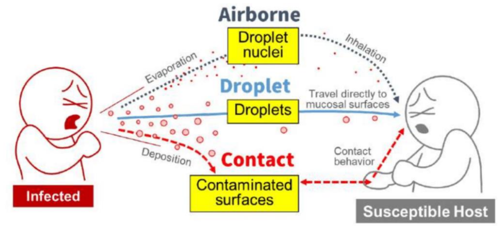

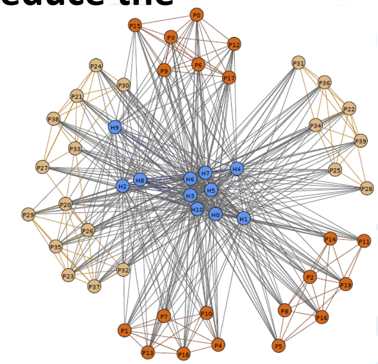

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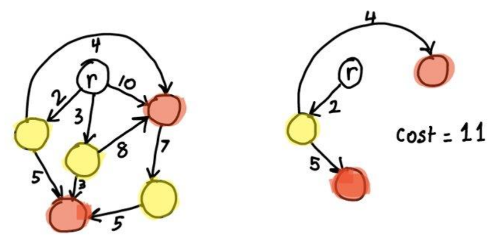

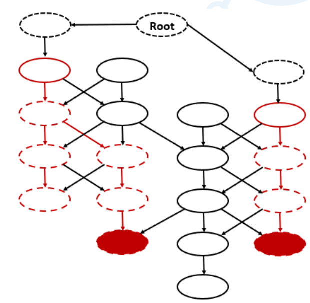

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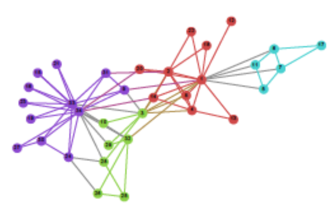
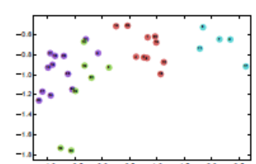
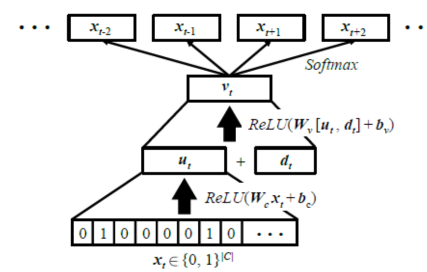


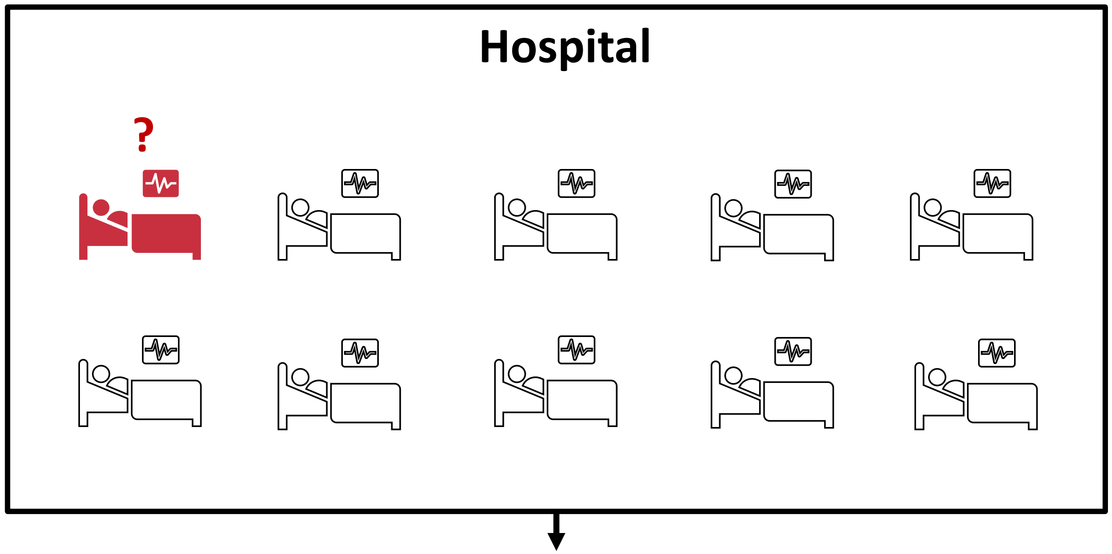




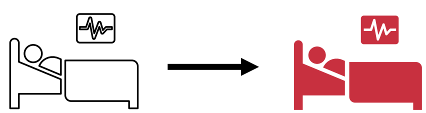
Asymptomatic cases make interventions challenging

~ 10% are Asymptomatic CDI

[-, +]



Need to detect asymptomatic cases

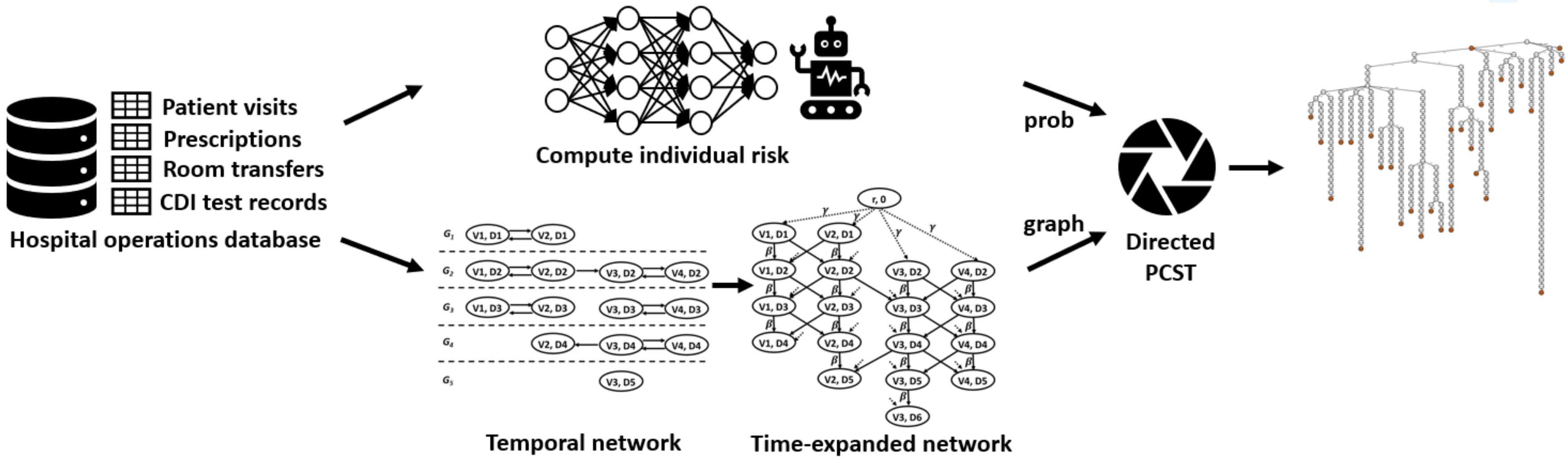


(i) exposed to the pathogen
(ii) susceptible

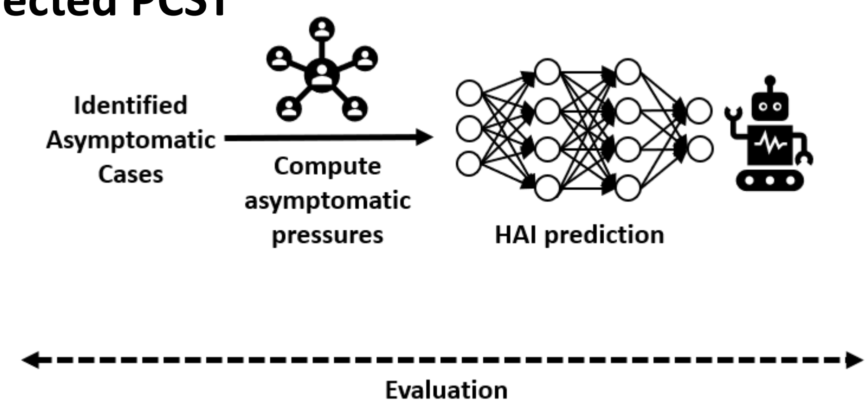
[-] S. Leekha et al., "Asymptomatic Clostridium difficile colonization in a tertiary care hospital: Admission prevalence and risk factors," American Journal of Infection Control, 2013
[+] L. Kyne et al., "Asymptomatic Carriage of Clostridium difficile and Serum Levels of IgG Antibody against Toxin A," New England Journal of Medicine, 2000

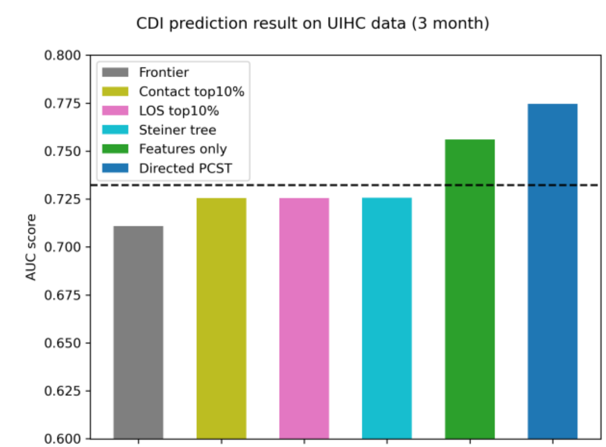
Asymptomatic CDI Detection via Directed PCST

(i) Detect asymptomatic cases



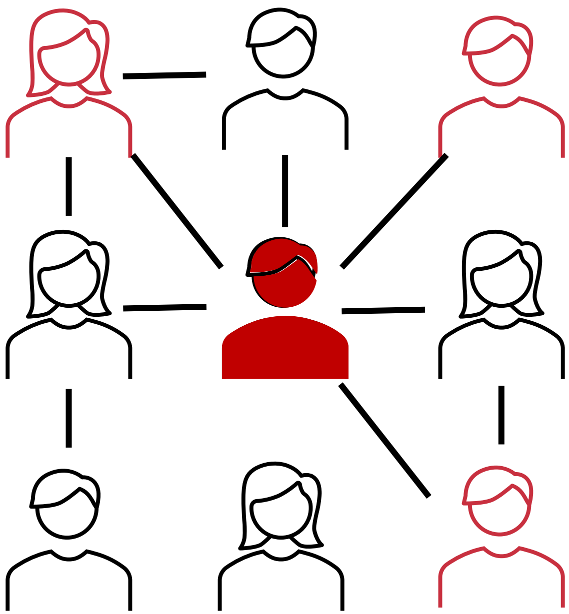
(ii) Evaluate asymptomatic cases detected by Directed PCST



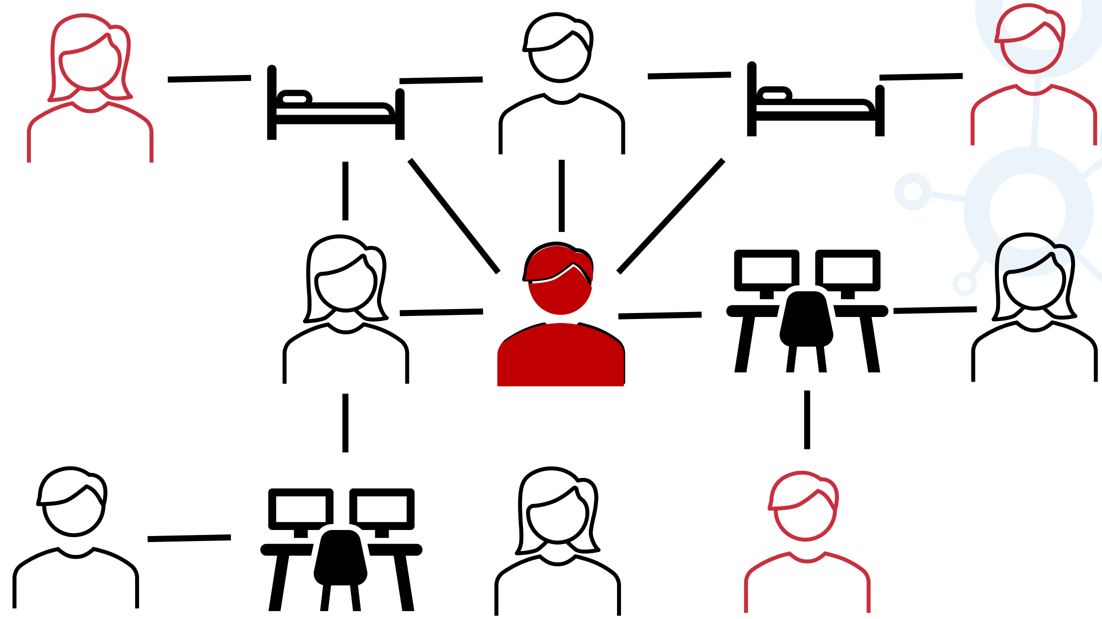


[+] **H. Jang**, S. Pai, **B. Adhikari**, and **S. V. Pemmaraju**, "Risk-aware temporal cascade reconstruction to detect asymptomatic cases," ***IEEE ICDM 2021 (one of the best ranked papers), KAIS 2022 (extended paper)***

Prior works in source detection



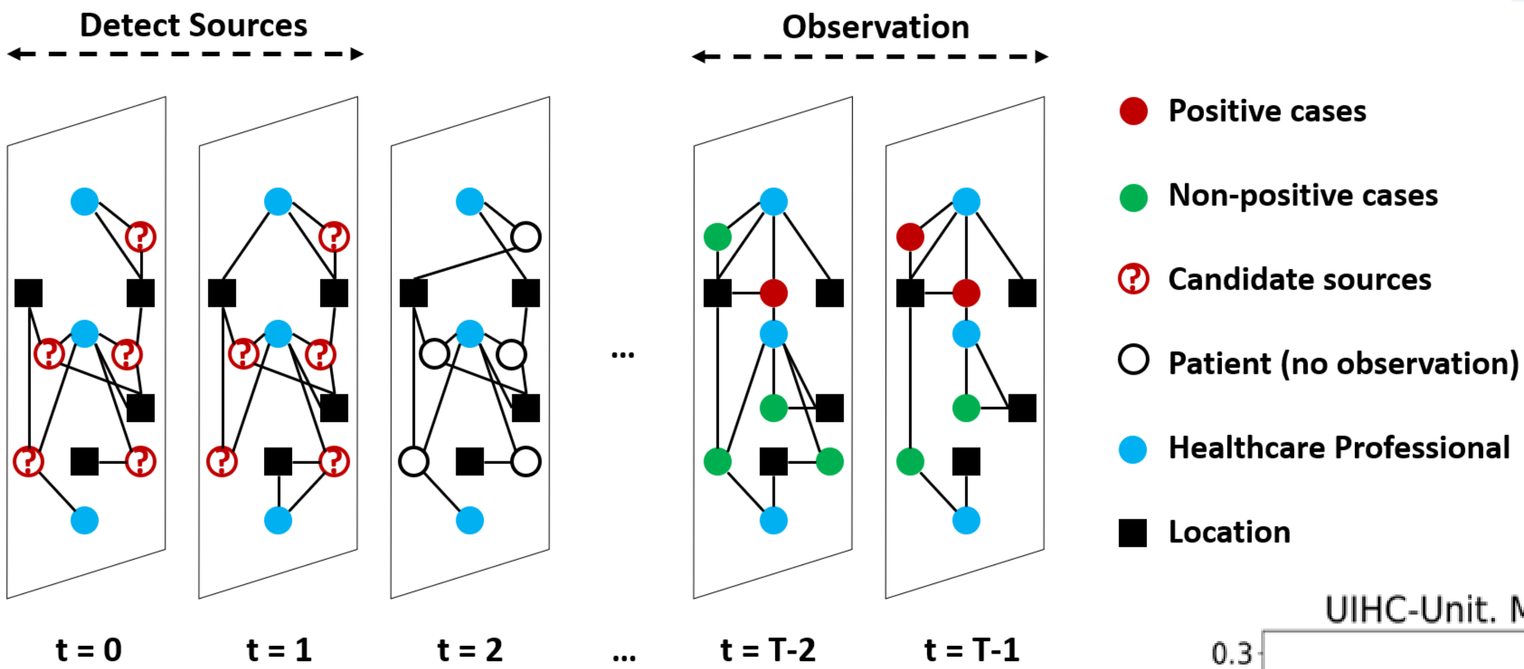
[+, - , =]

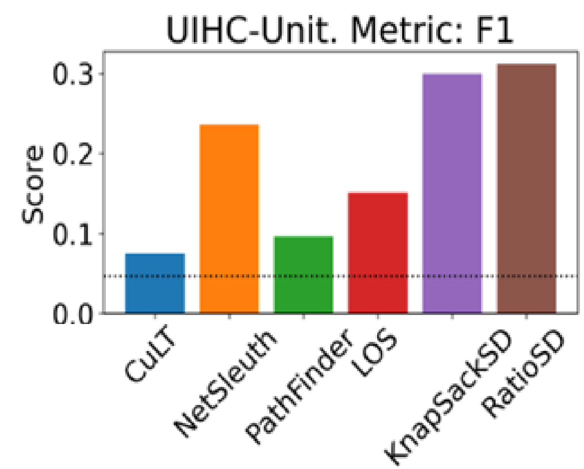


We show our work on source detection problem on the load sharing model

[+] Prakash, B. A. et al. Efficiently spotting the starting points of an epidemic in a large graph. KAIS 2014
[-] Shah, D. and Zaman, T. Detecting Sources of Computer Viruses in Networks: Theory and Experiment. SIGMETRICS Perform. Eval. Rev 2010
[=] Lappas, T.; Terzi, E.; Gunopulos, D.; and Mannila, H. Finding Effectors in Social Networks. KDD 2010

Detecting sources of HAI





[+] **H. Jang**, A. Fu, J. Cui, M. Kamruzzaman, A. B. Prakash, A. Vullikanti, **Adhikari, B.**, and **S. V. Pemmaraju.** Detecting sources of healthcare associated infections. ***In submission***

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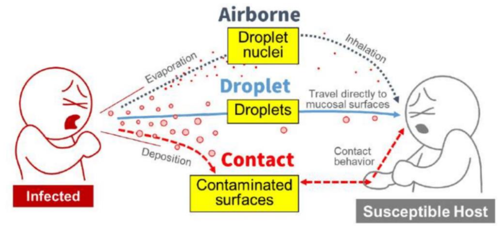

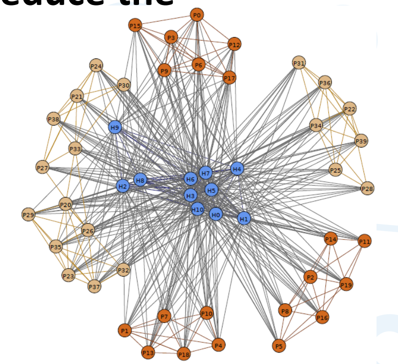

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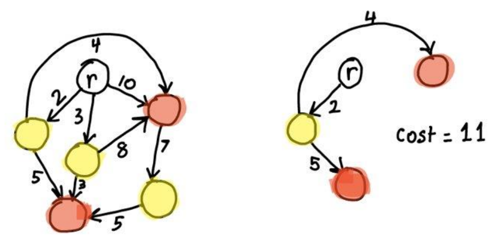

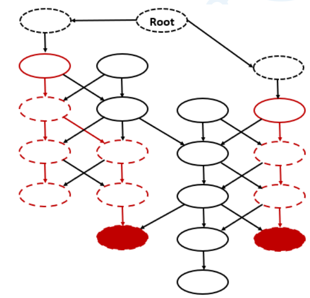

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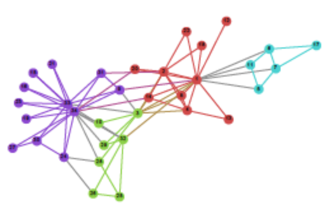
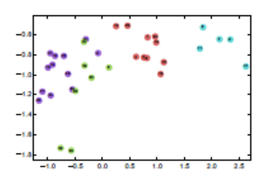
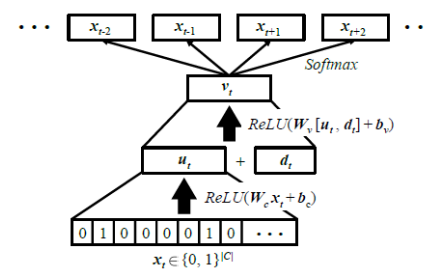
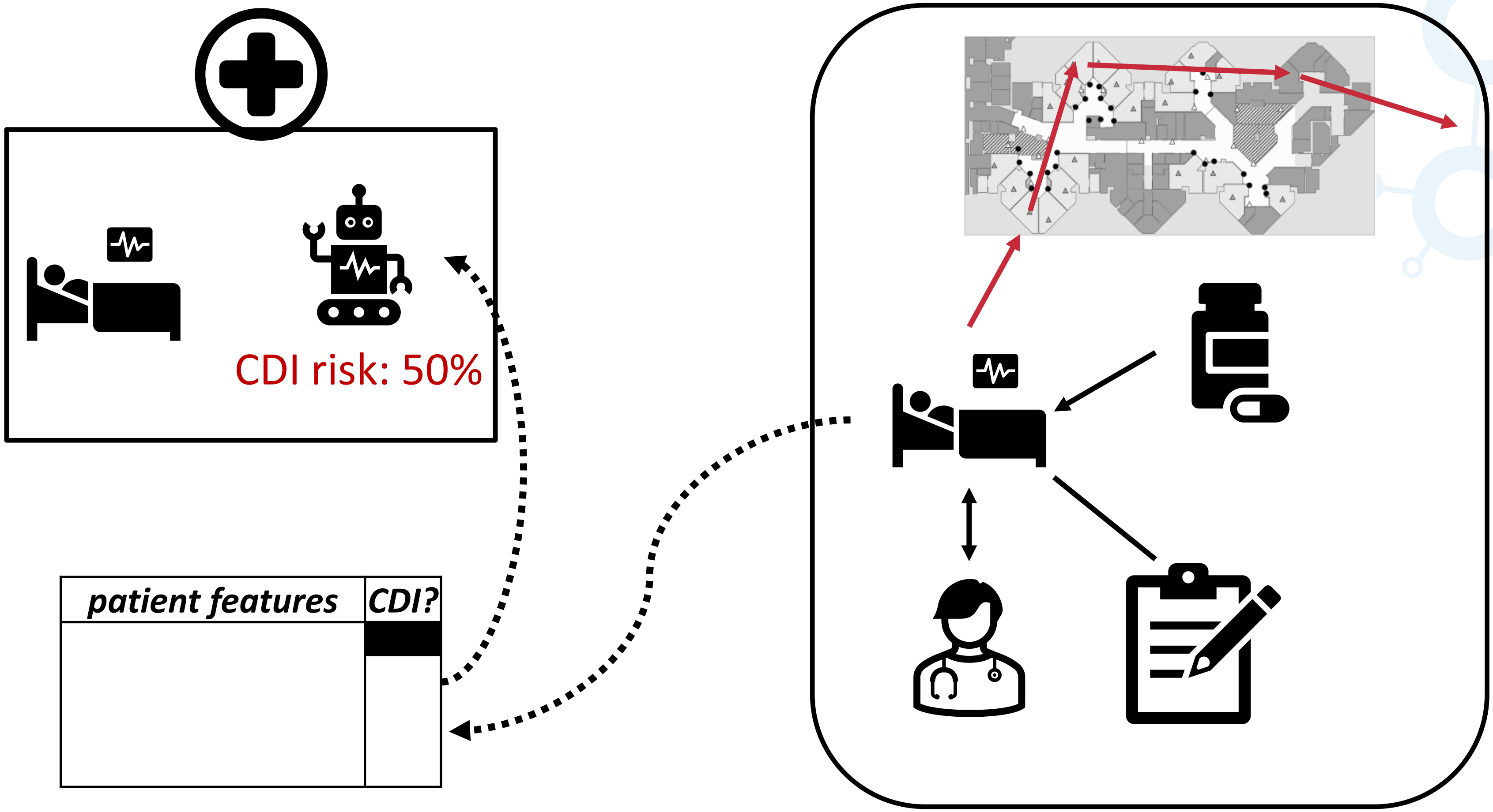


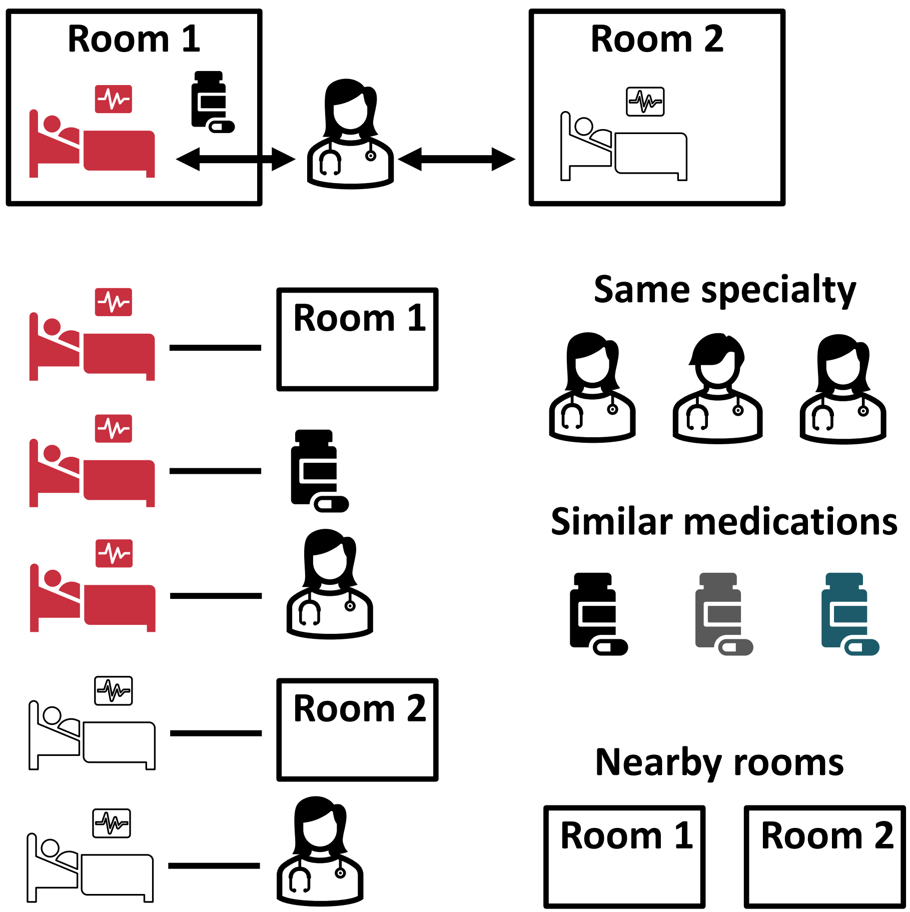




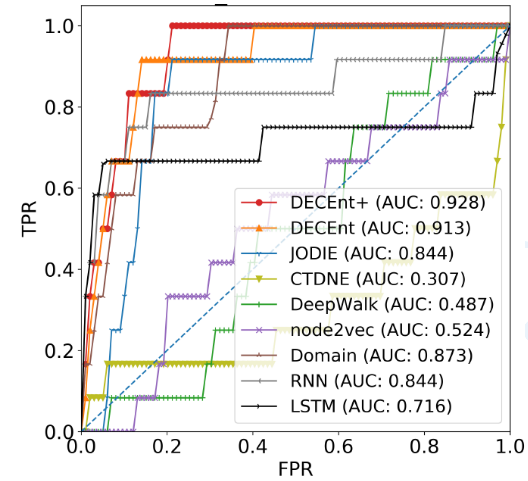
Need for the patient embedding



DECEnt: Dynamic Healthcare Embeddings for Improving Patient Care



Transfer into MICU



Early detection of CDI

Method	CDI
RNN	0.56 (0.119)
LSTM	0.585 (0.103)
Domain	0.655 (0.123)
DeepWalk	0.494 (0.087)
Node2Vec	0.453 (0.098)
CTDNE	0.463 (0.101)
JODIE	0.552 (0.192)
DECEnt	0.732 (0.069)
DECEnt +	**0.736 (0.064)**

[a]The value in bold denotes best performance

[+] **H. Jang**, S. Lee, H. Hasan, **S. Pemmaraju, B. Adhikari**, "Dynamic Healthcare Embeddings for Improving Patient Care", **IEEE/ACM ASONAM 2022**

Special thanks to

Alberto Segre

Sriram Pemmaraju

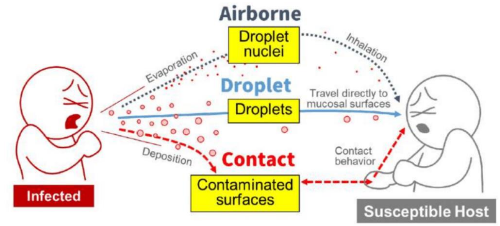
Bijaya Adhikari

- Collaborators
  - Prof. Philip M. Polgreen, Prof. Daniel K. Sewell
  - Samuel Justice, Shreyas Pai, Sulyun Lee, Hasib Hasan
- Collaborators (external)
  - Prof. Aditya Prakash, Prof. Anil Vullikanti
  - Andrew Fu, Jiaming Cui, Mehtun Kamruzzaman

NSF
CDC
Centers for Disease Control and Prevention
University of Iowa
comp|epi
computational epidemiology research
The University of Iowa

Back up slides

Compartmental models



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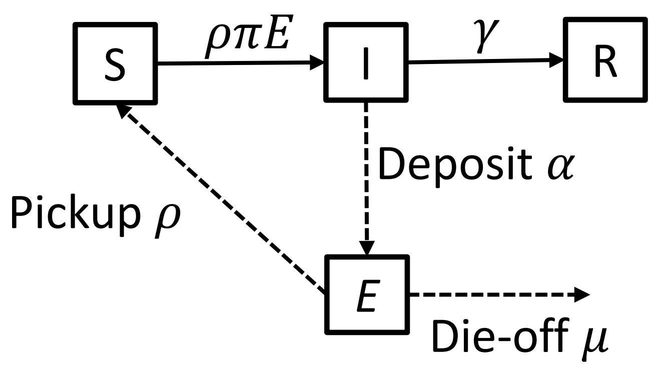
$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$

- Environmental contamination can be modeled using compartmental models [-]



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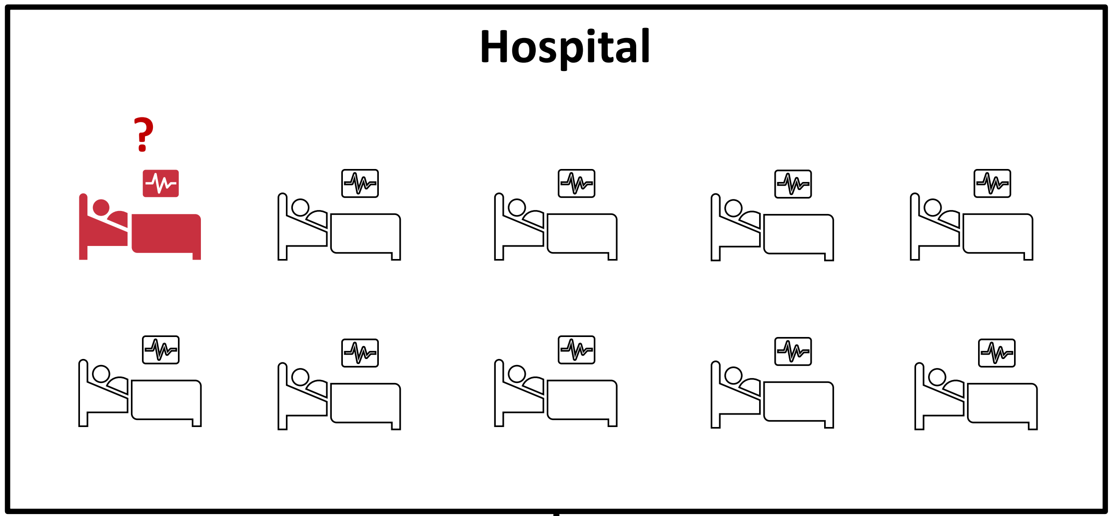
~ 10% are Asymptomatic CDI

[-, +]



Need to detect asymptomatic cases

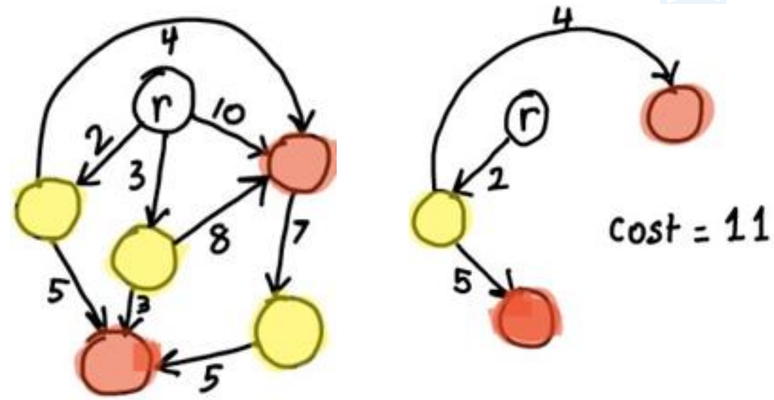
Directed Steiner tree problem

[-] S. Leekha et al., "Asymptomatic Clostridium difficile colonization in a tertiary care hospital: Admission prevalence and risk factors," American Journal of Infection Control, 2013
[+] L. Kyne et al., "Asymptomatic Carriage of Clostridium difficile and Serum Levels of IgG Antibody against Toxin A," New England Journal of Medicine, 2000

Directed Steiner tree problem

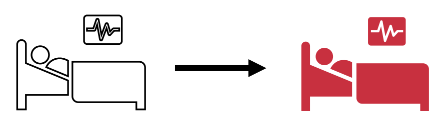
- The ***directed Steiner tree (DST)*** problem
  - INPUT: A directed graph $G = (V, E)$, an edge weight $w(e)$ for each edge e in E, a special vertex r (*root*) and a set S of special vertices (*terminals*).
  - OUTPUT: A directed tree T rooted at r, spanning all terminals S that minimizes

$$\sum_{e \in T} w(e)$$



$G = (V, E)$ $T = (V', E')$

- Connection to the ***missing infections*** problem
  - r: infection source
  - S: observed infections
  - $w(e)$: likelihood of transmission
  - T: infection cascade
  - Nodes in paths of T: Missing infections

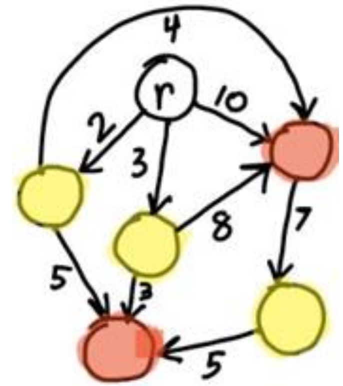


(i) exposed to the pathogen
(ii) **susceptible**

Directed *prize-collecting* Steiner tree problem

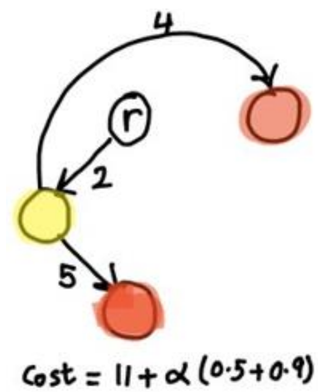
- The ***directed Steiner tree (DST)*** problem
  - INPUT: A directed graph $G = (V, E)$, an edge weight $w(e)$ for each edge e in E, a special vertex r (***root***) and a set S of special vertices (***terminals***) and a ***node weight*** $p(v)$ ***for*** $v \in V$.
  - OUTPUT: A directed tree T rooted at r, spanning all terminals S that minimizes

$$\sum_{e \in T} w(e) + \alpha \sum_{v \notin T} p(v)$$

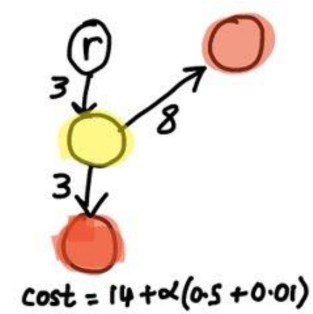


$G = (V, E)$

- Connection to the ***missing infections*** problem
  - $p(v)$: measure of susceptibility. ***the likelihood of*** node being an asymptomatic
  - α: controls relative importance of included $w(e)$ and excluded $p(v)$
  - Note: $\alpha = 0$ yields the DST problem

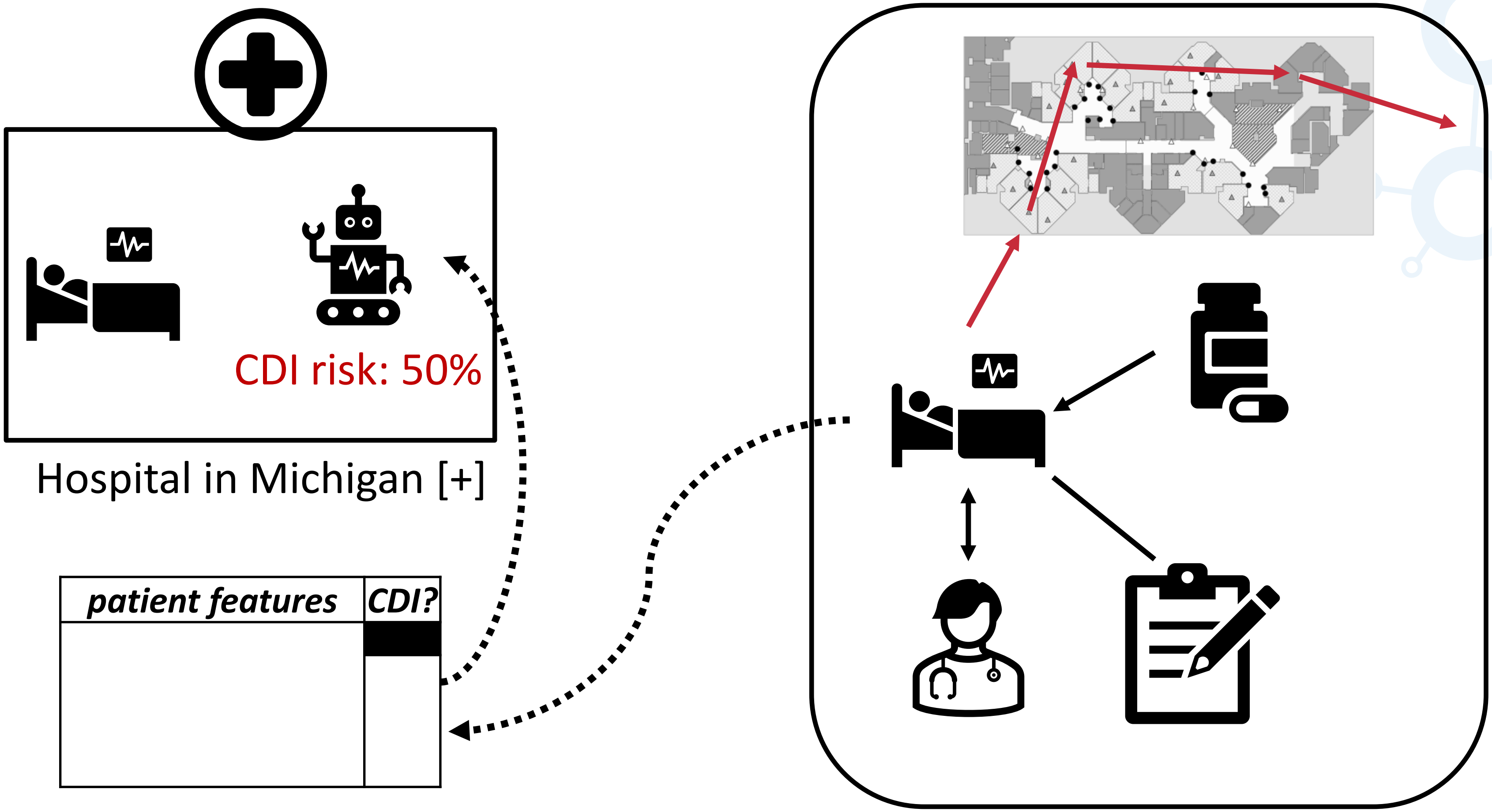


$T_1 = (V', E')$



$T_2 = (V', E')$

Need for the patient embedding



[+] Jenna Wien, “Realizing the Potential of AI in Clinical Care - Understanding and Overcoming Barriers,” Department of Biostatistics Seminar, University of Iowa, October 17, 2022