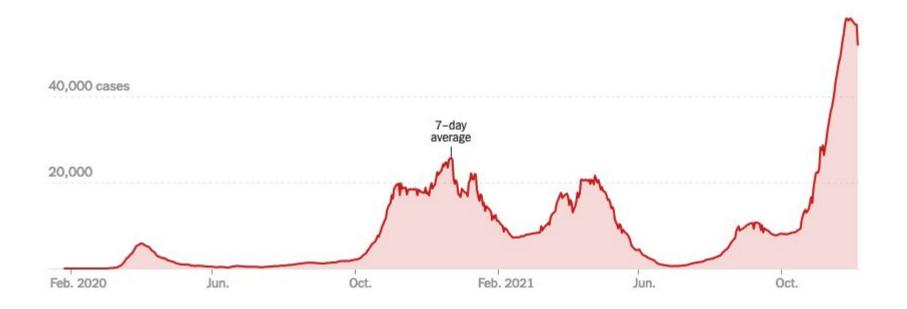
# Controlling Epidemic Diffusion with Temporal Graph and Graph Neural Network

**CS599 - Graph Analytics** 

### New reported cases

All time

Last 90 days



7 December 2021

Zora Che

### **Motivations for Epidemic Modeling**

How can we leverage graph information to test efficiently and accurately the most high impact nodes to control epidemic diffusion?

#### **Considering:**

- Hub nodes, or nodes with high degree may be a super-superspreader
- We have incomplete information of the full interaction graph in a real-life setting
- We may not know all initial infected nodes

### Graph G:

- V is the vertex set
- A is the adjacency matrix (assume binary)
- $X \in \mathbb{R}^{m \times |V|}$  is a matrix of node features

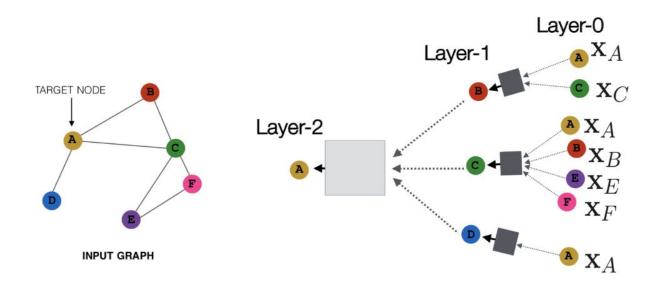
#### Main Tasks:

- Node classification
- Graph classification
- Graph generation

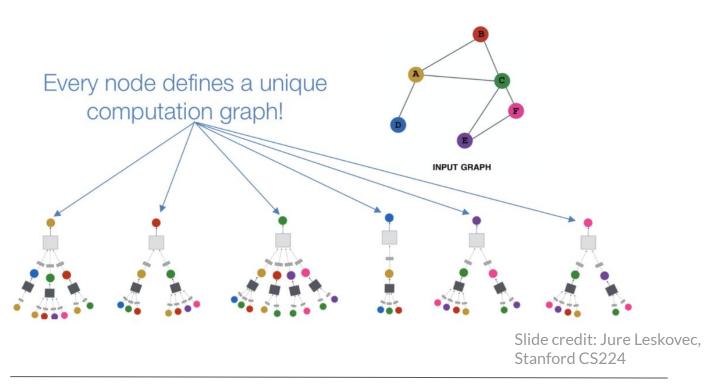
Based on Node embedding

Slide credit: Jure Leskovec, Stanford CS224

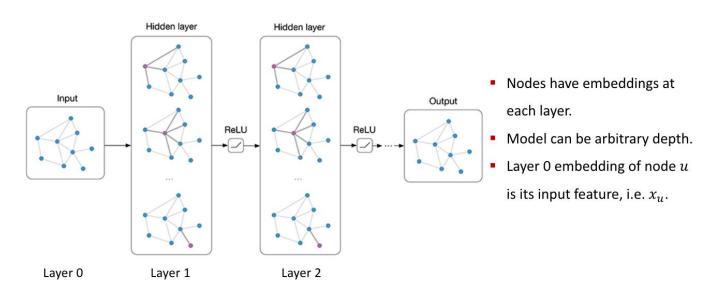
Generate node embeddings based on local neighborhoods



Slide credit: Jure Leskovec, Stanford CS224

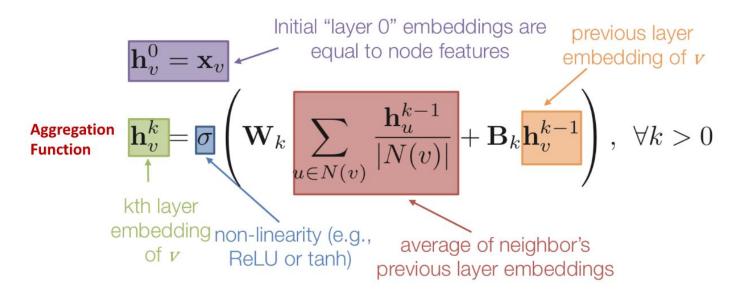


Basic approach: Average neighbor information and apply a neural network



Slide credit: Jure Leskovec, Stanford CS224

Basic approach: Average neighbor information and apply a neural network



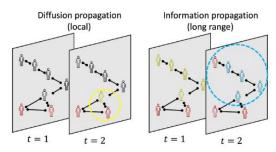
Slide credit: Jure Leskovec, Stanford CS224

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### **Using GNN for Epidemic Prediction and Control**

Controlling Graph Dynamics with Reinforcement Learning and Graph Neural Networks (Meirom et al, 2021)

- Set up a framework for epidemic prediction and control on temporal graph using RL with Graph Neural Network
- Provided baselines on a range of synthetic and real world datasets

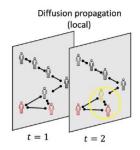


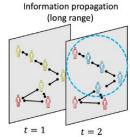
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### **Project Overview**

Github: https://github.com/zorache/Controlling-Graph-Dynamics/

- Provided an implementation of the epidemic spread framework, heuristic methods, and supervised learning with GNN
- Experimented on synthetic preferential attachment networks, and on the GR-QC collaboration network (Leskovec et al, 2007)





#### **Problem Definition**

#### **SEIR Epidemic Spread**

Every node (person) can be in one of the following states:

susceptible – a healthy, yet uninfected person (S state)

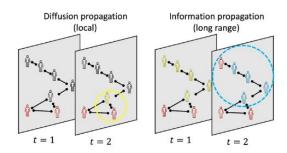
latent – infected but cannot infect others (L state)

infectious – may infect other nodes (I state)

removed - self-quarantined and isolated from the
graph (R state)

If a susceptible node interacts with an infectious node, the probability of it remaining healthy is  $\prod_{e \in E_v(t)} (1-p_e(t))$ 

Otherwise, it becomes latent and the latent node stays latent at time t if  $t < T_n + D_n$ 



 $p_e(t)$  Transmission prob of an given edge at time t

Incubation period

 $D_n$ 

Both are assigned randomly in experiments; transmission prob between 0.5 and 1, incubation is random in  $\{1,2,3,4,5\}$ 

### **Heuristic Methods**

#### Rank Nodes based on # of infected neighbors in 1-hop and 2-hop

Rationale: if you are in an epidemic hotspot, you are more likely to be infected at the next time step. Prioritize testing nodes that have high numbers of infected neighbors, and high number of total neighbors of neighbors who are infected

Con: in real life this calculation may be difficult to obtain

#### **Implementation**

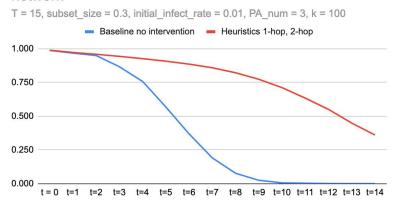
- Input: edge list of the graph
- Graph representation: doubly linked linked list, as implemented for assignment
- Fill a (#num nodes, 2) shaped array storing # of 1-hop infected neighbor, # of 2-hop infected neighbor
- Lexicological sort the array to get the top k index of nodes to be tested

Why is this a good graph representation?

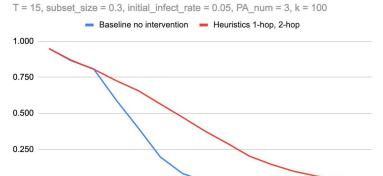
- For large graphs, isolated nodes and their edges can be removed from the graph easily

### **Heuristic Method (hop) Experiments**

### % of healthy nodes on a temporal sampling of PA network



#### % of healthy nodes on a temporal sampling of PA network

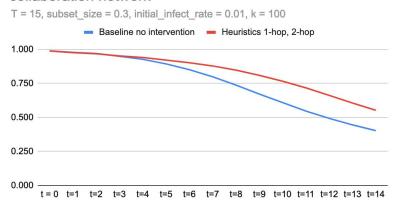


t = 0 t=1 t=2 t=3 t=4 t=5 t=6 t=7 t=8 t=9 t=10 t=11 t=12 t=13 t=14

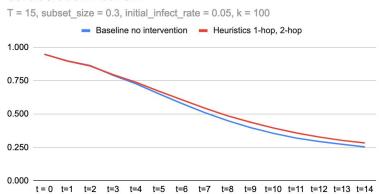
5 Trials for each experiment setting, variance is less than 0.02 for all no intervention baselines Average percent of healthy nodes across all trials is graphed here for each time step for each setting

### **Heuristic Methods Experiments**

### % of healthy nodes on a temporal sampling of GR-QC collaboration network



### % of healthy nodes on a temporal sampling of GR-QC collaboration network



5 Trials for each experiment setting, variance is less than 0.02 for all no intervention baselines Average percent of healthy nodes across all trials is graphed here for each time step for each setting

#### **Heuristic Methods**

#### Testing nodes every half-incubation period (similar to University Testing)

Rationale: if the epidemic is controlled, testing nodes every half incubation period can efficiently control outbreak

Con: would not work well when epidemic is not controlled and rates of transmission is high in the population

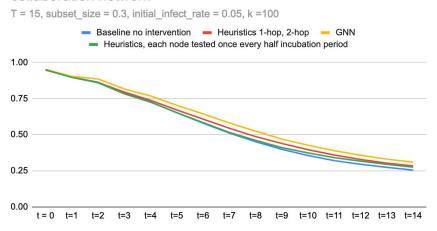
#### **Implementation**

- Each node has a testing schedule of every half incubation period, though only k randomly is chosen to test at each step
  - Keeping intervention numbers the same
  - Also may reflect real-life testing, where students may miss testing

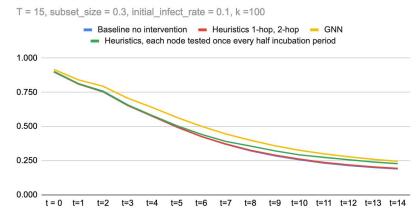
### **BU's Testing policy**

### Testing each node half of one incubation period appears to be another adequate heuristic

### % of healthy nodes on a temporal sampling of GR-QC collaboration network



### % of healthy nodes on a temporal sampling of GR-QC collaboration network



### **Data Processing for GNN**

Static node features  $\zeta_v^s(t)$ 

Dynamic node features  $\zeta_v^d(t)$ 

Dynamic edge features

#### Static node

topological graph centralities (betweenness, closeness, eigenvector, and degree centralities) and random node features.

#### Dynamic node

one-hot vector of dimension 4, corresponding to either untested, tested positive, tested negative, or tested positive in a step before the prior step.

#### Dynamic Edge

multi-graph view of temporal change, where the edges are all the interactions for a window period prior and including the current time step, and the feature is a vector of dimension 2 with the time step difference of the edge compared to current time, and the edge attribute of transmission probability

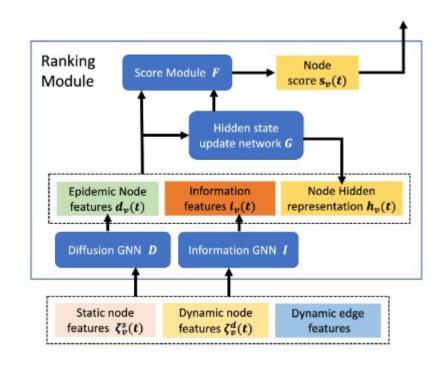
**D**: 1 layer graph convolution network to locally diffuse at time t

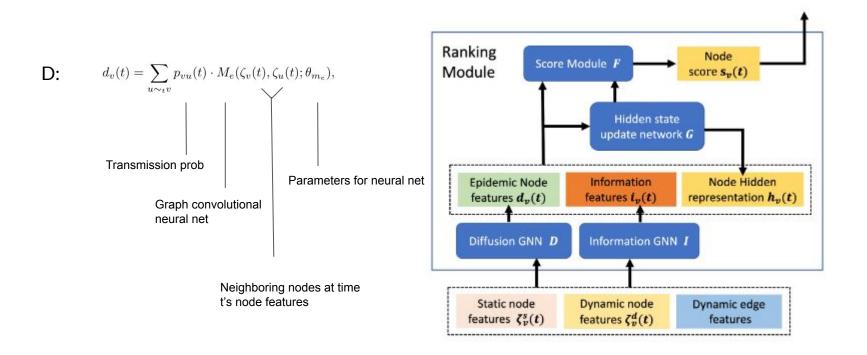
I: MLP on the multi-graph with all observed time edges

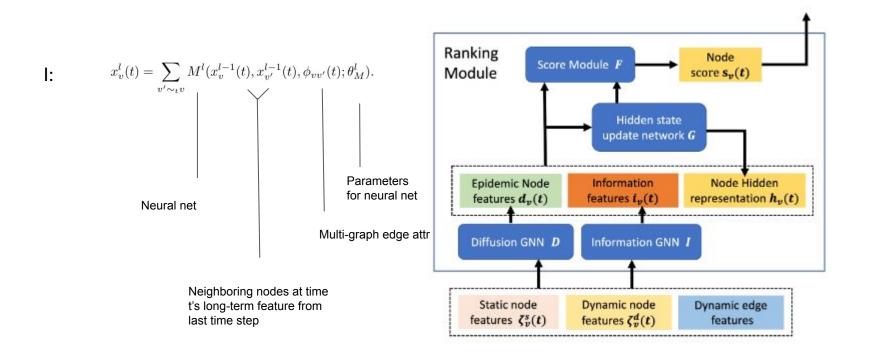
**G**: updates hidden node representation

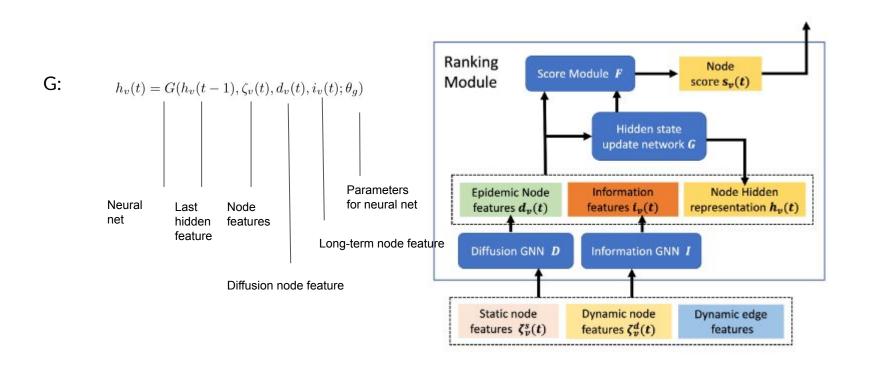
**F**: scores each node's probability of being infected

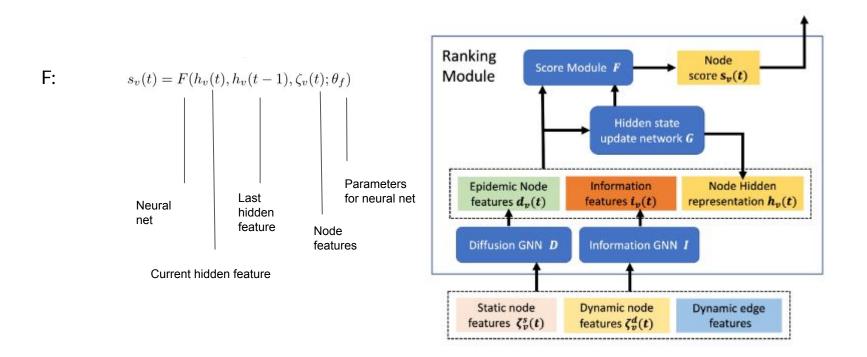
Loss: binary cross entropy of predicted scores and the ground truth of the node at that time
Goal: predict nodes that are not healthy with high scores











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### **Experiments**

Table 1: Dataset Summary

Method \Graph	$avg_{deg}$	nodes	edges
$PA_2(Generated)$	2	1000	
PA <sub>5</sub> (Generated)	5	1000	_
GR-QC	_	5242	28980

Table 2: Percentage of healthy nodes at t=14, initial infection rate =0.01

Method \Graph	$PA_3$	$PA_5$	GR-QC
No intervention	0	0	0.403
Heuristic-hop	0.36	0.186	0.553
Heuristic-half-incubation	0.008	0.009	0.42
GNN	0.271	0.253	0.496

Table 3: Percentage of healthy nodes at t=14, initial infection rate =0.05

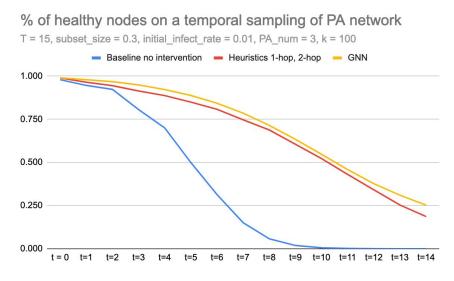
Method \Graph	$PA_3$	$PA_5$	GR-QC
No intervention	0	0	0.255
Heuristic-hop	0.031	0.023	0.284
Heuristic-half-incubation	0.01	0.009	0.275
GNN	0.195	0.146	0.310
GNN, no init given	0.092	0.13	0.287

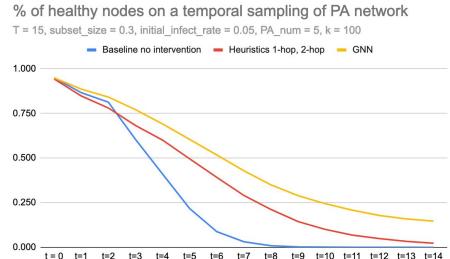
Table 4: Percentage of healthy nodes at t=14, initial infection rate =0.1

Method \Graph	$PA_3$	$PA_5$	GR-QC
No intervention	0	0	0.190
Heuristic-hop	0.005	0.011	0.194
Heuristic-half-incubation	0.006	0.005	0.228
GNN	0.141	0.113	0.282
GNN, no init given	0.078	0.103	0.228

### **GNN Experiments**

#### GNN outperforms heuristics for initial infect=0.05, 0.1

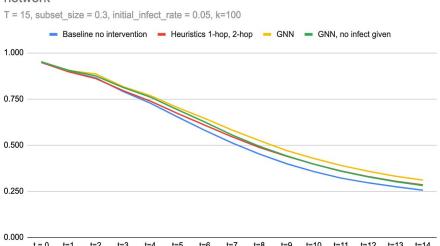




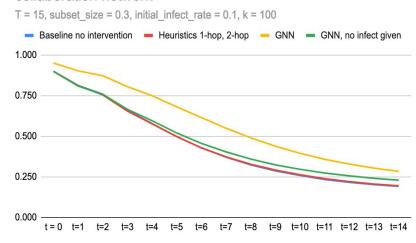
### **GNN Experiments**

#### GNN outperforms heuristics even when no initial infect is given

% of healthy nodes on a temporal sampling of GR-QC collaboration network



% of healthy nodes on a temporal sampling of GR-QC collaboration network



### **Open Questions and Directions**

This project has shown GNN outperforms heuristic methods at infect rates=0.05 and 0.1. GNN may also handle the case with no initial infect information.

#### How can we generalize for graphs we have yet to see?

- More compute and training on more graphs for more epochs
  - Ideally we also have parameters of the graph to generate synthetic networks that mimics the graph

## Gap of current model lies in epochs trained, and complexity of ranking module, esp the recurrent module

- Though the experiments outperform the heuristics, it has not matched accuracy from the paper due to possible model differences (simpler model layers were chosen for consideration of GPU memory), and epochs and number of graphs trained on (~30 epoch for this model architecture is the bottleneck for my compute capacity)
  - Smaller batching would solve the issue at the cost of time

#### References

Jure Leskovec, Stanford CS224W: Machine Learning with Graphs, <a href="http://cs224w.stanford.ed">http://cs224w.stanford.ed</a>

Meirom, Eli, et al. "Controlling Graph Dynamics with Reinforcement Learning and Graph Neural Networks." *International Conference on Machine Learning*. PMLR, 2021.