



Modeling and Simulating Disease Outbreaks for Arbitrary Topological Systems

Based on: B. A. Prakash, D. Chakrabarti, N. Valler, M. Faloutsos, C. Faloutsos. Threshold conditions for arbitrary cascade models on arbitrary networks.

Underlying Theory Behind Our Project

- We shall consider the effects of topology and virus propagation model (VPM) when analyzing virus outbreaks
- The topology shall be given by a connectivity matrix
- It turns out that the topological effects can be decoupled from the VPM
- We can define the effective strength:

$$s = \lambda_1 \cdot C_{\text{VPM}}$$

- No epidemic for $s < 1$

Proof Overview: Initial Conditions

- We start out with our general model: $S^*I^2V^*$
 1. Susceptible Class: Contains all of the susceptible states. All nodes that are elements of this class can be infected by neighbors.
 2. Infected Class: Contains two infected states (E,I). All nodes that are elements of this class are infected.
 3. Vigilant Class: Contains all of the vigilant states. All nodes that are elements of this class cannot be infected or cause infections.
- Two Assumptions:
 1. Infections can only be spread through neighboring nodes
 2. There exists a “starting infected class”

Proof Overview: Outline

- We can define a vector that completely describes our state at time t.
- We shall then analyze the fixed points where no node is an infected state
- If this fixed point is stable for small perturbations, we know that it shall not come to an epidemic

Goal of Our Project

- Reproduce the results of the paper (for the SIR model, $s = \lambda_1 * \frac{\beta}{\delta}$)
- Push the model towards its boundaries
 1. Is the model still applicable for many/important initially infected nodes?
 2. Is the model still applicable for small networks?

Simulating the Time Evolution of the SIR Model on Arbitrary Networks using the Gillespie Algorithm

- Two possible events of the SIR model:

- An infected node infects a susceptible neighbour (with probability βdt in $[t, t + dt)$)
 - An infected node gets recovered (with probability δdt in $[t, t + dt)$)

- Probability, that exactly one events happens in $[t, t + dt)$:

$$\text{total_rate}(t)dt = (\text{total_infection_rate}(t) + \text{total_recovery_rate}(t))dt$$

$$\text{total_infection_rate}(t) = \sum_{\{u \in \text{at_risk_nodes}(t)\}} \beta \times \text{number_of_infected_neighbours}[u](t)$$

$$\text{total_recovery_rate}(t) = \delta \times \text{number_of_infected_nodes}(t)$$

- Naive implementation: Create a random number at each time step and check whether an event will happen \Rightarrow Increasing computational intensity with decreasing Δt

Simulating the Time Evolution of the SIR Model on Arbitrary Networks using the Gillespie Algorithm

- Approach: Calculate time $t + \tau$ at which the next event will happen
- $f(\text{total_rate}(t), s)ds \equiv$ Probability that the next event will happen during $[t + s, t + s + ds)$
- It can be shown that

$$f(\text{total_rate}(t), s)ds = \text{total_rate}(t) \times \exp[-\text{total_rate}(t)s] ds$$

- $\Rightarrow \tau$ is exponentially distributed with rate parameter $\text{total_rate}(t)$

Pseudocode of the Gillespie Algorithm

Input: Network G , per-edge transmission rate τ , recovery rate γ , set of index node(s) initial_infecteds, maximum time t_{\max} .

Output: Lists times, S , I , and R giving number in each state at each time.

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function Gillespie_network_epidemic( $G, \tau, \gamma, \text{initial\_infections}, t_{\max}$ )
    times,  $S, I, R \leftarrow [0], [|G|-\text{len(initial\_infections)}, [\text{len(initial\_infections)}], [0]$ 
    infected_nodes  $\leftarrow \text{initial\_infections}$ 
    at_risk_nodes  $\leftarrow \text{uninfected nodes with infected neighbours}$ 
    for each node  $u$  in at_risk_nodes do
        infection_rate[ $u$ ]  $\leftarrow \tau \times \text{number of infected neighbours}$ 
    total_infection_rate  $\leftarrow \sum_{u \in \text{at\_risk\_nodes}} \text{infection\_rate}[u]$ ,
    total_recovery_rate  $\leftarrow \gamma \times \text{len}(\text{infected\_nodes})$ 
    total_rate  $\leftarrow \text{total\_transmission\_rate} + \text{total\_recovery\_rate}$ 
    time  $\leftarrow \text{exponential variate(total rate)}$ 
    while time  $< t_{\max}$  and total_rate  $> 0$  do
         $r = \text{uniform\_random}(0, \text{total\_rate})$ 
        if  $r < \text{total\_recovery\_rate}$  then
             $u = \text{random.choice}(\text{infected\_nodes})$ 
            remove  $u$  from infected_nodes
            reduce infection_rate[v] for  $u$ 's susceptible neighbours  $v$ 
        else
            choose  $u$  from at_risk_nodes with probability  $\frac{\text{infection\_rate}[u]}{\text{total\_infection\_rate}}$ .
            remove  $u$  from at_risk_nodes
            add  $u$  to infected_nodes
            for susceptible neighbours  $v$  of  $u$  do
                if  $v$  not in at_risk_nodes then
                    add  $v$  to at_risk_nodes
                    update infection_rate[v]
    update times,  $S, I$ , and  $R$ 
    update total_recovery_rate, total_infection_rate, and total_rate
    time  $\leftarrow \text{time} + \text{exponential\_variate(total\_rate)}$ 
return times,  $S, I, R$ 
```

1. Initialise the status of all nodes, compute all rates and the time at which the first event will happen

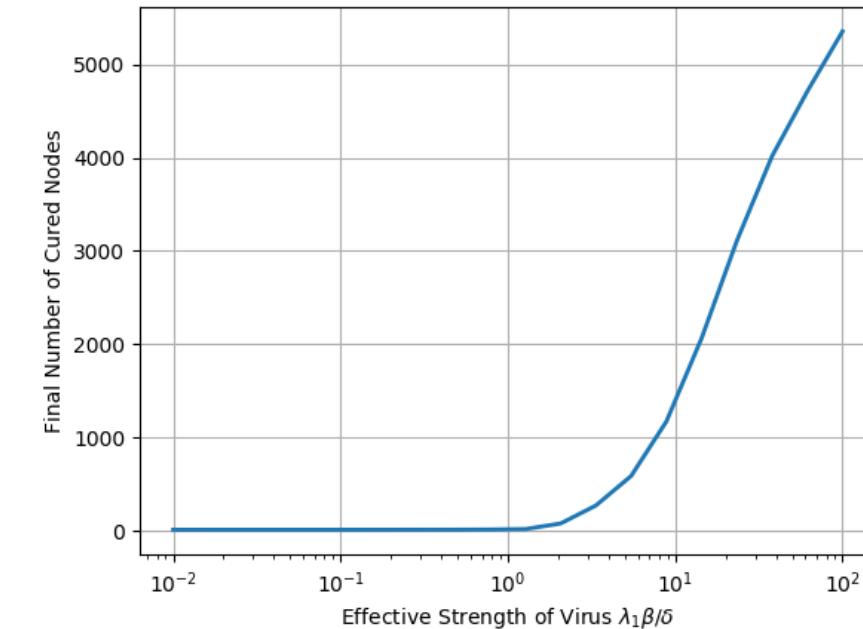
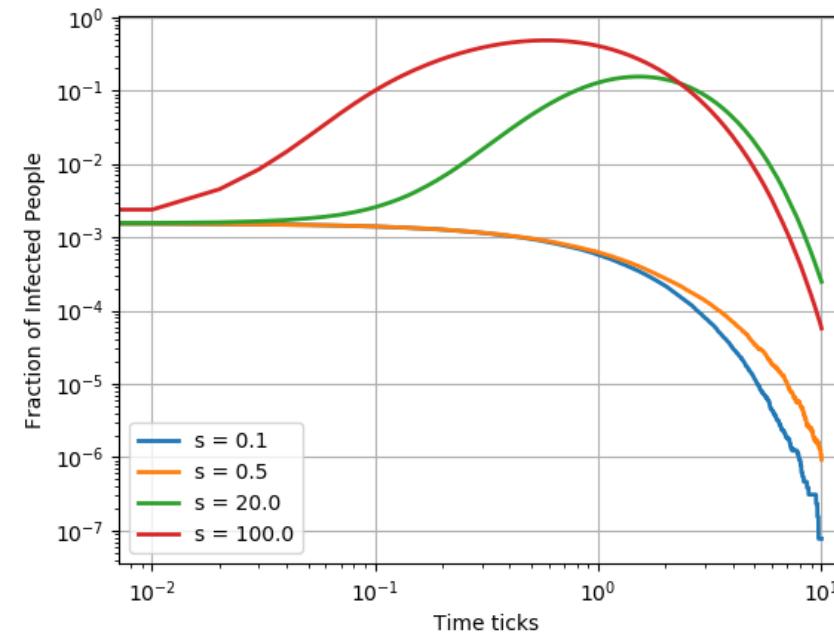
2. Compute which event will happen

3. Update the status of all nodes and all rates. Compute the time when the next event will happen and go to 2.

Simulation Results I

Reproduction of previous work

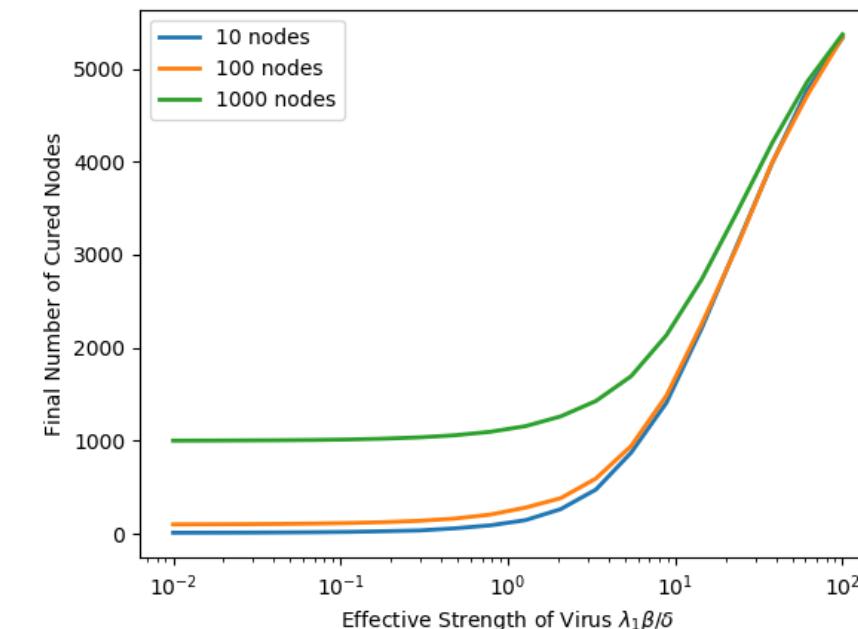
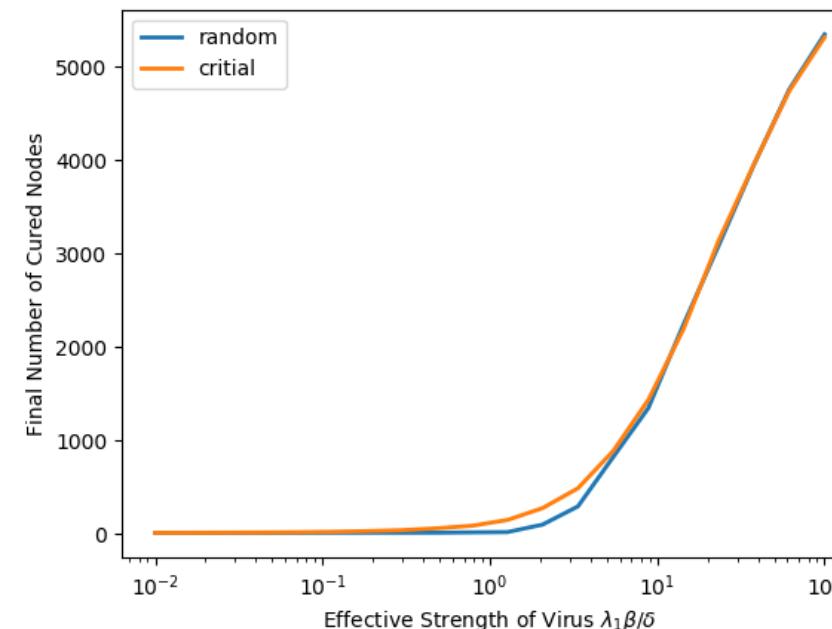
- Data set AS-OREGON (6474 nodes)
- 10 random nodes initially infected



Simulation Results II

Challenging the model with different initial infections

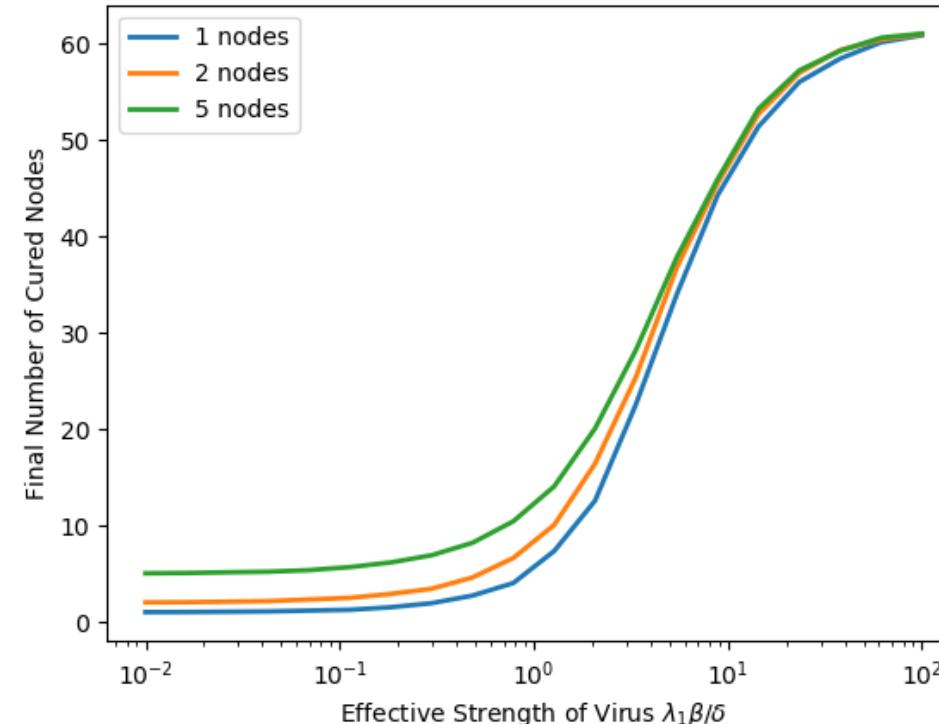
- Infection of nodes with highest eigenvector centrality (critical nodes)
- Infection of more nodes



Simulation Results III

Challenging the model with a small network

- Data set TERRORIST (62 nodes)
- Infection of critical nodes (highest centrality)



Summary & Outlook

Model generally very robust

- Valid for larger networks regardless of initial infection
- Small networks push it towards its boundaries

Further research necessary

- We only covered the SIR model
- Influence of averaging
 - Worst-case scenario more interesting for applications

Sources

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