ETH zürich

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:

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

- 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 state”

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 $[t, t+dt)$:

$$total\_rate(t)dt = \big(total\_infection\_rate(t) + total\_recovery\_rate(t)\big)dt$$

$$total\_infection\_rate(t) = \sum_{\{u \in at\_risk\_nodes(t)\}} \beta \times number\_of\_infected\_neighbours[u]\,(t)$$

$$total\_recovery\_rate(t) = \delta \times number\_of\_infected\_nodes(t)$$

- Naive implementation: Create a random number at each time step and check whether an event will happen ⇒ 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
- $f(total\_rate(t), s)ds \equiv$ Probability that the next event will happen during $[t + s, t + s + ds)$
- It can be shown that

$$f(total\_rate(t), s)ds = total\_rate(t) \times \exp[-total\_rate(t)s]\, ds$$

- $\Rightarrow \tau$ is exponentially distributed with rate parameter $total\_rate(t)$

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.

```
function Gillespie_network_epidemic(G, τ, γ, initial_infections, t_max)
    times, S, I, R ← [0], [|G|-len(initial_infections)], [len(initial_infections)], [0]
    infected_nodes ← initial_infections
    at_risk_nodes ← uninfected nodes with infected neighbours
    for each node u in at_risk_nodes do
        infection_rate[u] = τ × number of infected neighbours
    total_infection_rate ← ∑_{u∈at_risk_nodes} infection_rate[u],
    total_recovery_rate ← γ × len(infected_nodes)
    total_rate ← total_transmission_rate + total_recovery_rate
    time ← exponential_variate(total_rate)
    while time< t_max and total_rate> 0 do
        r = uniform_random(0,total_rate)
        if r <total_recovery_rate then
            u = random.choice(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 infection_rate[u] / 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 ← time + 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

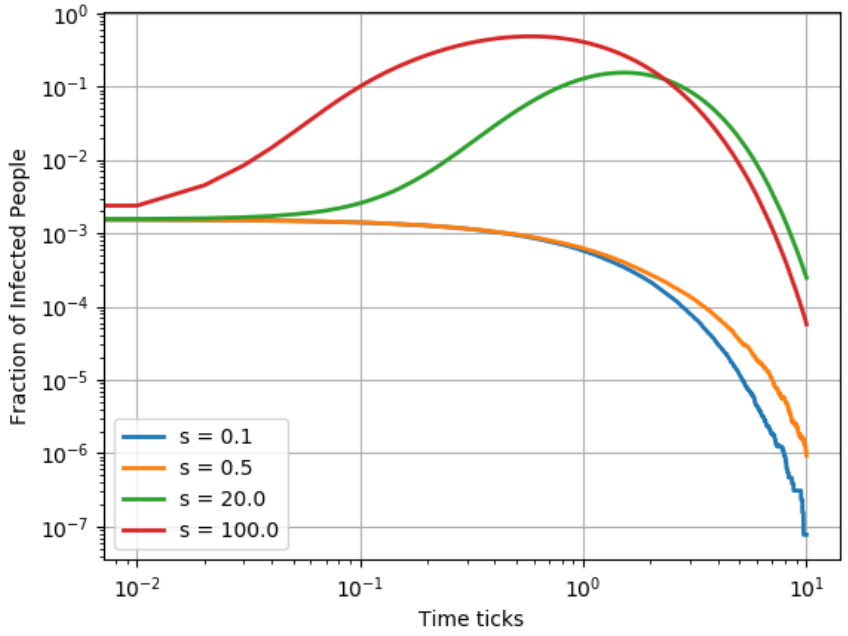
3. Update the status of all nodes and all rates. Compute the time when the next event will happen and go to 2.

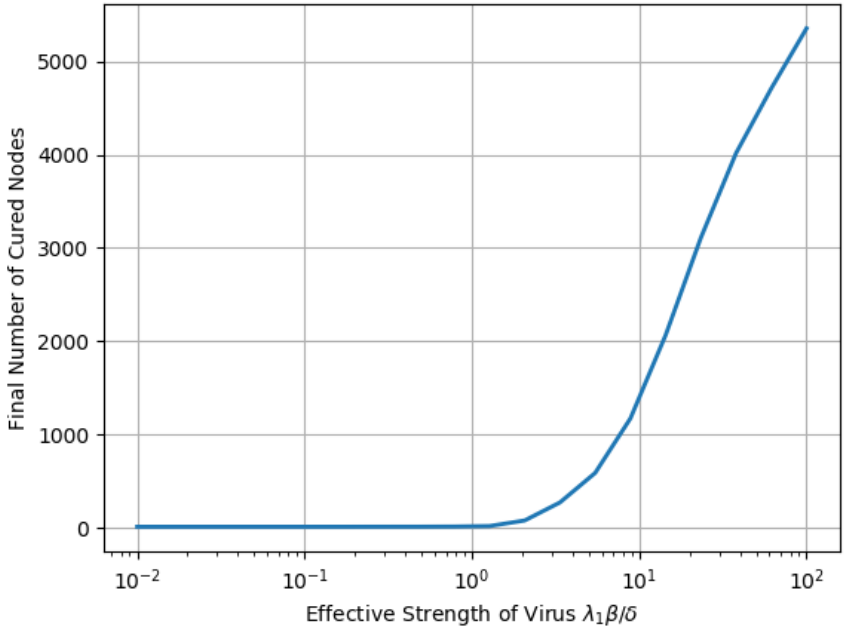
Taken from “Mathematics of Epidemics on Networks”

Simulation Results I

Reproduction of previous work

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

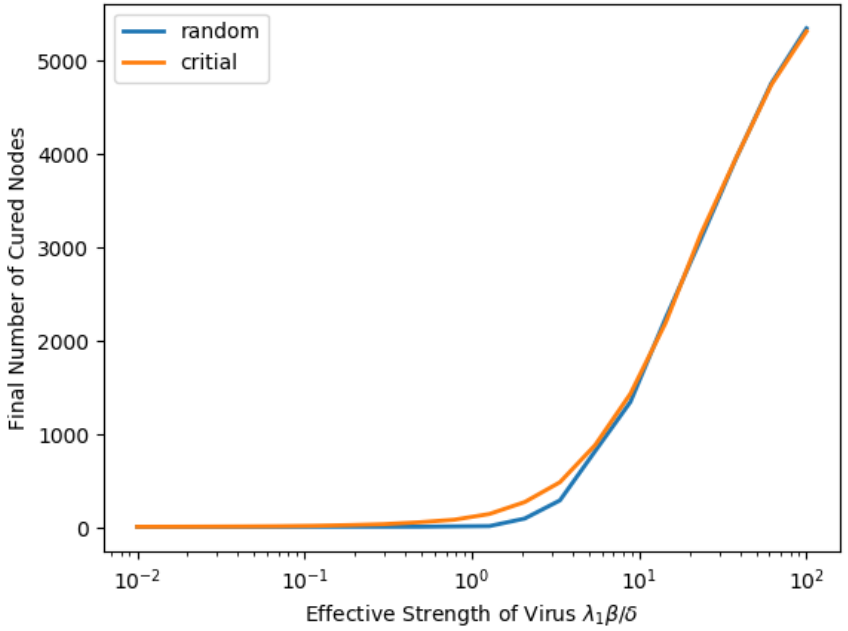


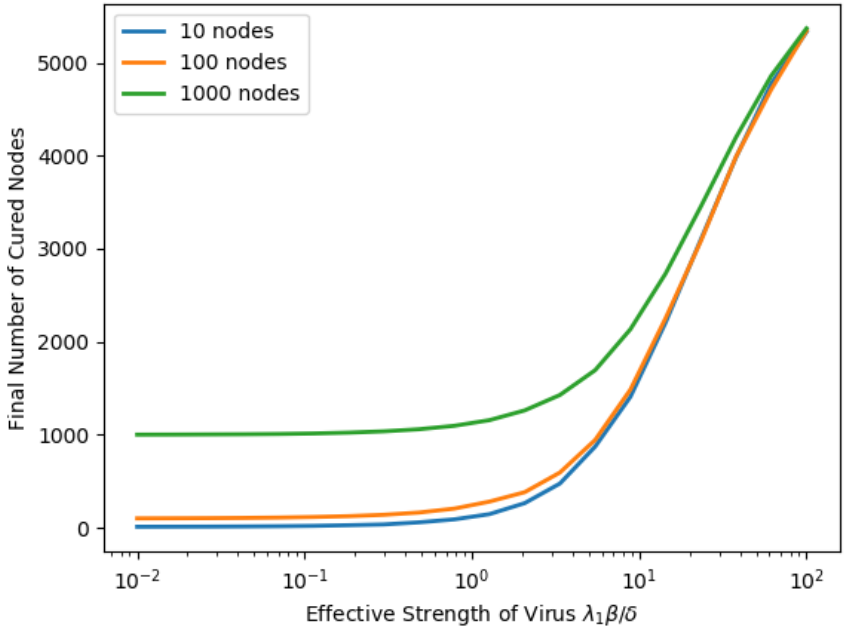


Simulation Results II

Challenging the model with different initial infections

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

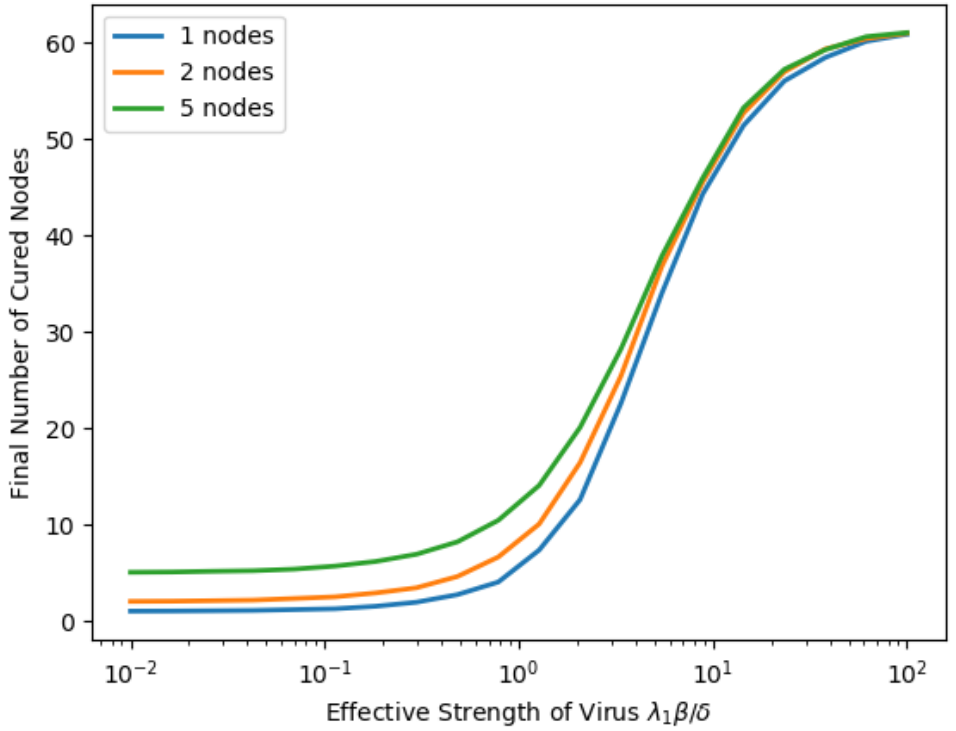




Simulation Results III

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

- B. A. Prakash, D. Chakrabarti, N. Valler, M. Faloutsos, C. Faloutsos. Threshold conditions for arbitrary cascade models on arbitrary networks. Knowledge and Information Systems manuscript No. KAIS-12-3483R1, 2012.
- Istvan Z. Kiss, Joel C. Miller, Peter L. Simon. Mathematics of Epidemics on Networks, Volume 46, Page 382. Springer, Cham, 2017.
- Hirsch MW. Differential Equations, Dynamical Systems and Linear Algebra. Morris W. Hirsch, Stephen Smale Robert L. Devaney, Stephen Smale, 1974.
- Radek Erban, S. Jonathan Chapman, Philip K. MAINI. A practical guide to stochastic simulations of reaction-diffusion processes. https://arxiv.org/pdf/0704.1908.pdf.