Vaccination Strategies by Probabilistic Node-level SIR Model over Dynamic Network

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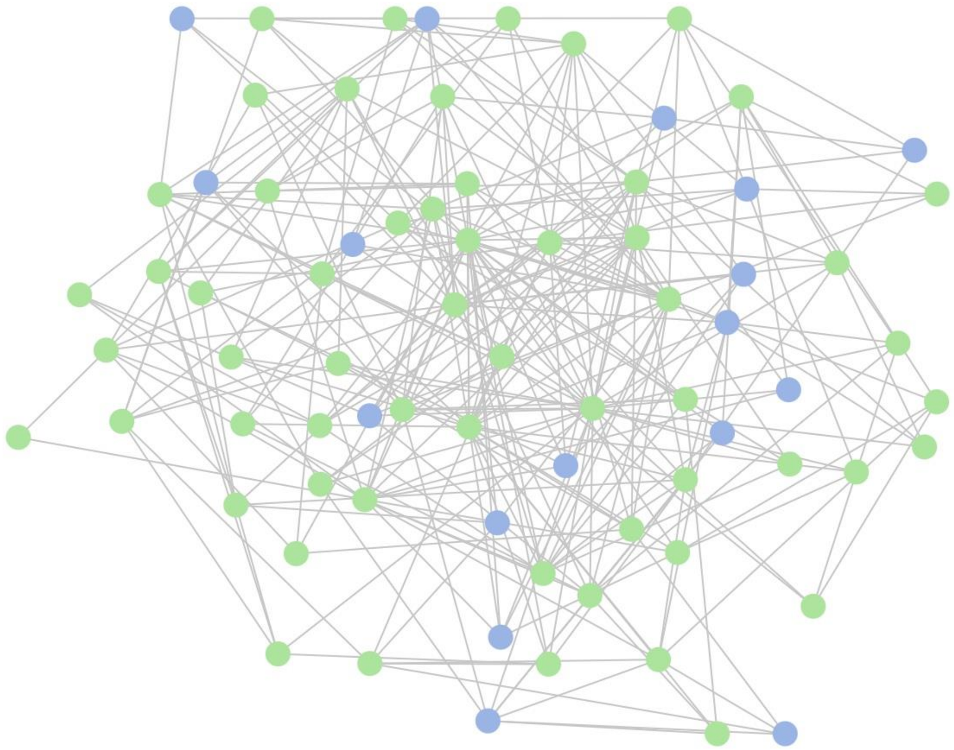
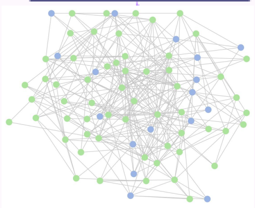
Content



Introduction

- Statistical physics of vaccination
  - mean-field model (*assume fully mixing*)
    - Non-behavioral epidemiological vaccination
      - SIR
      - SEIR
      - extension
        - mean-field metapopulation
        - social and age-group
    - Behavior-vaccination dynamics
      - Phenomenological models
      - Game theoretical models
      - Psychological models
  - network model (*individual based*)
    - Non-behavioral epidemiological vaccination
      - vaccination strategies (*site percolation*)
        - Random immunization
        - Targeted immunization
          - Degree-based targeted vaccination
          - Centrality-based targeted vaccination
        - Vaccination without global knowledge
          - Acquaintance vaccination
          - Other strategies
        - Vaccination on other types of networks
          - Vaccination on community networks
          - Vaccination on adaptive networks
          - Vaccination on multiplex networks
    - Behavior-vaccination dynamics
      - static networks
      - empirical networks
      - adaptive networks
      - multilayer networks



Assume perfect vaccination

consider opinion clusters

SIR Model: Deterministic & Network

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

$$\frac{ds}{dt} = -\beta s i$$

$$\frac{di}{dt} = \beta s i - \gamma i$$

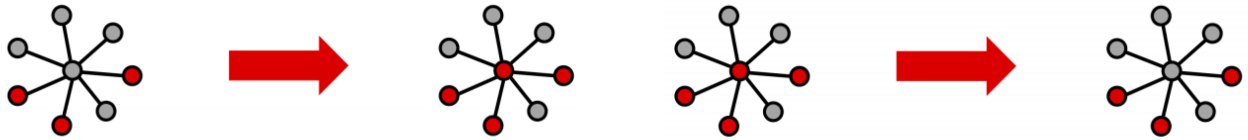
$$\frac{dr}{dt} = \gamma i$$

$$s = s_0 e^{-\frac{\beta}{\gamma} r}$$

$$\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\frac{\beta}{\gamma} r})$$

$$t = \frac{1}{\gamma} \int_0^r \frac{du}{1 - u - s_0 e^{-\frac{\beta}{\gamma} u}}$$

Node infection Node recovery



Pictures from http://www.leonidzhukov.net/hse/2020/networks/lectures/lecture10.pdf

$$P_{get\ infected} \approx \beta s_k(t) \sum_{j \in N(k)} i_j(t) \delta(t) \qquad P_{get\ recovered} = \gamma i_k(t) \delta(t)$$

$$\frac{ds_k}{dt} = -\beta s_k \sum_j A_{kj} s_j$$

$$\frac{di_k}{dt} = \beta s_k \sum_j A_{kj} s_j - \gamma i_k$$

$$\frac{dr_k}{dt} = \gamma i_k$$

$$then\ \frac{di_k}{dt} = \beta(1 - i_k - r_k) \sum_j A_{kj} i_j - \gamma i_k$$

Probabilistic Node-level Model: SIR

$s_k(t)$: *probability that at t node k is susceptible*
$i_k(t)$: *probability that at t node k is infected*
$r_k(t)$: *probability that at t node k is recovered*
β : *individual transmission/infection rate*
(probability to get infected on a contact in time δt)
γ : *recovery rate*
(probability to recover in a unit time δt).

Consider the network of potential contacts using adjacency matrix A.
The network is undirected -> matrix A is symmetric
The diagonal elements are zeros.
Aij represents whether node i has contact with node j. If node i and node j are connected, Aij=1; otherwise, Aij=0.

For example:
$$\begin{bmatrix} 0 & 1 & 0 & \dots & 1 & \\ 1 & 0 & & & & \\ 0 & & 0 & & & \\ \dots & & & \dots & & \\ 1 & & & & 0 & \\ & & & & & 0 \end{bmatrix}$$

We could use certain degree distribution to get matrix A by python package networkx.

$$\frac{ds_k}{dt} = -\beta s_k \sum_j A_{kj} s_j$$

$$\frac{di_k}{dt} = \beta s_k \sum_j A_{kj} s_j - \gamma i_k$$

$$\frac{dr_k}{dt} = \gamma i_k$$

$$then \ \frac{di_k}{dt} = \beta(1 - i_k - r_k) \sum_j A_{kj} i_j - \gamma i_k$$

Comparison: Deterministic & Network

	Deterministic model	Network model
network assumption	assmue people get fully mixed	consider network of potential contacts. use matrix A to represent the connection
meaning of s, i, r	ratio of susceptible, infected and recovered people	state of a node, or the probability of a node to get susceptible, infected or recovered
β, γ	β is the rate of transmission, γ is the rate of recovery	β is the rate of transmission on a contact, γ is the rate of recovery
connection	all nodes reachable	matrix A is $\begin{bmatrix} 0 & 1 & 1 & \dots & 1 & \\ 1 & 0 & & & & \\ 1 & & 0 & & & \\ \dots & & & \dots & & \\ 1 & & & & 0 & \\ & & & & & 0 \end{bmatrix}$

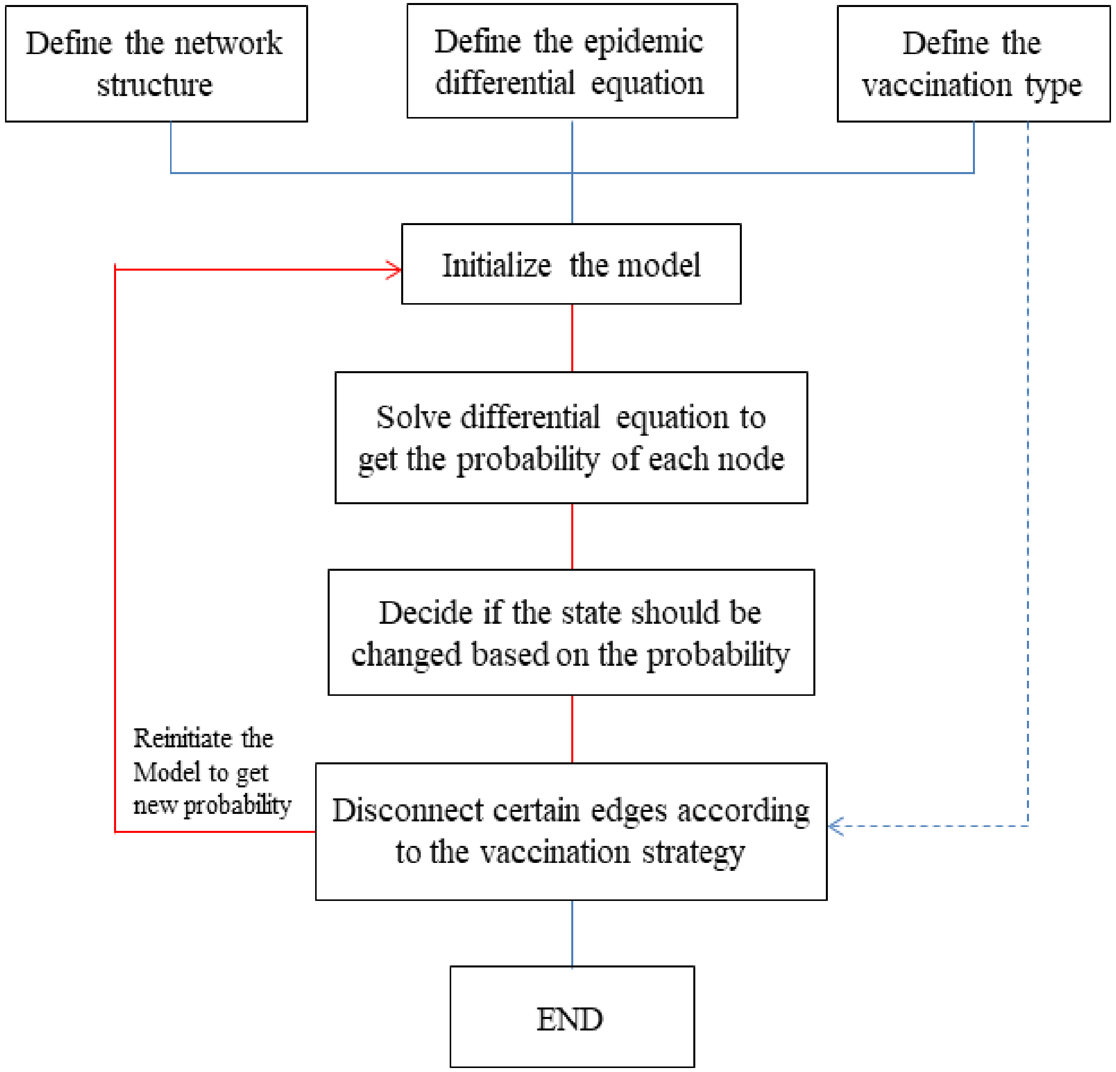
Probabilistic Node-level Model: SIR

$$\frac{ds_k}{dt} = -\beta s_k \sum_j A_{kj} s_j$$

$$\frac{di_k}{dt} = \beta s_k \sum_j A_{kj} s_j - \gamma i_k$$

$$\frac{dr_k}{dt} = \gamma i_k$$

$$then\ \frac{di_k}{dt} = \beta(1 - i_k - r_k) \sum_j A_{kj} i_j - \gamma i_k$$



Vaccinations over Networks

- The goal of the vaccination process:
  - to reduce the transmissibility
  - pass the **percolation threshold** (leads to minimization of the number of infected individuals in the network)

$$prob\ of\ being\ reached\ is\ \frac{kP(k)}{N<k>}$$

$$N: the\ number\ of\ nodes$$

$$P(k): the\ fraction\ of\ nodes\ having\ degree\ (number\ of\ links)\ k$$

$$<k> = \sum_k kP(k): the\ average\ degree\ of\ nodes\ in\ the\ network.$$

$$<n_i> = \beta_I \sum_k \frac{P(k)k(k-1)}{<k>} > 1$$

$$\left(\frac{<k^2>}{<k>} - 1\right) > \frac{1}{\beta_I} = \frac{1}{T}$$

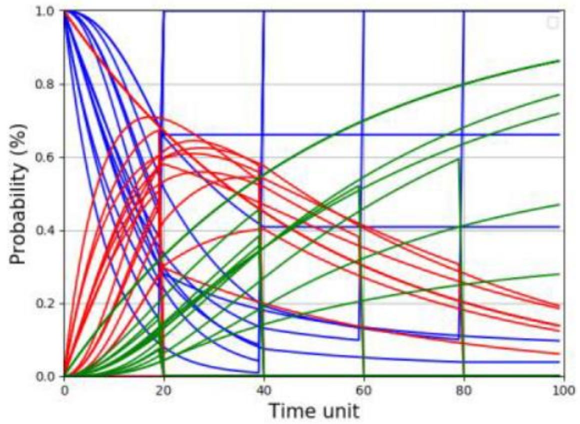


Figure 2

Probabilistic Node-level SIR Model under vaccination

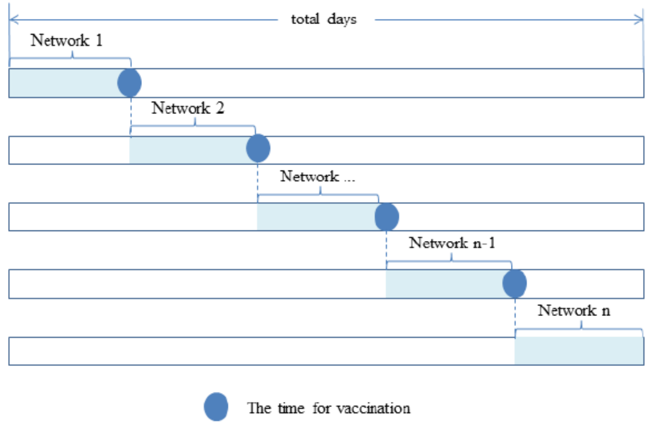


Figure 3

Dynamic network under vaccination

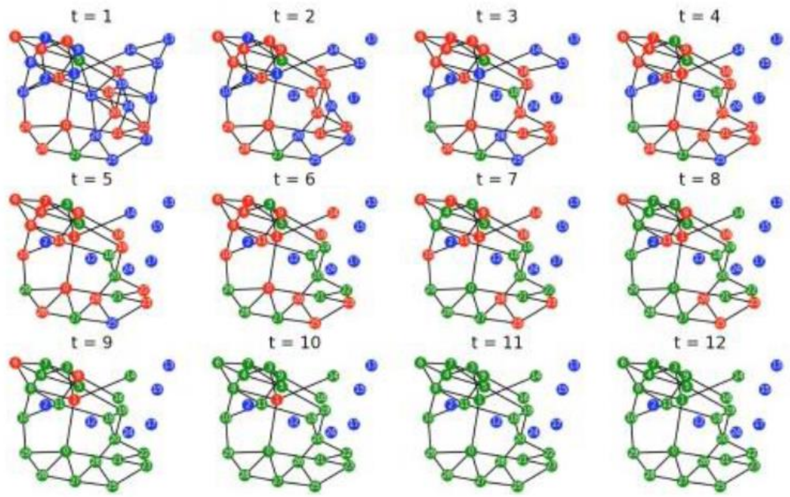


Figure 4 Example for Dynamic Network under vaccination

Random Immunization

β_I :*infection rate*

γ :*recovery rate*

x :*immunization rate, the fraction of vaccinated node in a*

x_c :*minimal value of x, vaccination threshold*

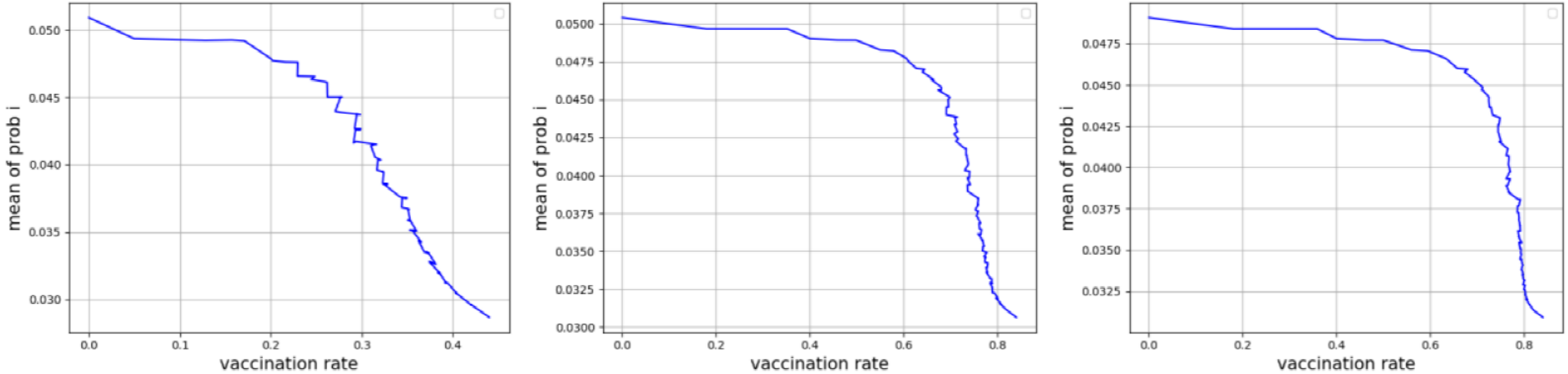
β_{I_c} :*infection rate under* x_c

Recall **percolation threshold**

$$\left(\frac{<k^2>}{<k>} - 1\right) > \frac{1}{\beta_I(1-x)} \rightarrow 0$$

$$x_c = 1 - \frac{1}{\beta_I}\frac{<k>}{<k^2> - <k>}$$

The epidemic will only be arrested if xc → 1.



Random network Small world network Scale-free network

Figure 5 Numerical Simulation Result for Random Immunization

Targeted Immunization

Targeted immunization of the **HUBs** (the most highly connected nodes in the network)

$$\beta_{I_c} = \beta_I(1 - x_c)$$
$$= \frac{< k' >}{< k'^2 > - < k' >}$$
$$= \frac{(1-f) < k >_c}{(1-f)^2 < k^2 >_c + f(1-f) < k >_c - (1-f) < k >}$$
$$= \frac{< k >_c}{(1-f)(< k^2 >_c - < k >_c)}$$

$$x_c = 1 - \frac{1}{\beta_I} \frac{< k >_c}{(1-f)(< k^2 >_c - < k >_c)}$$

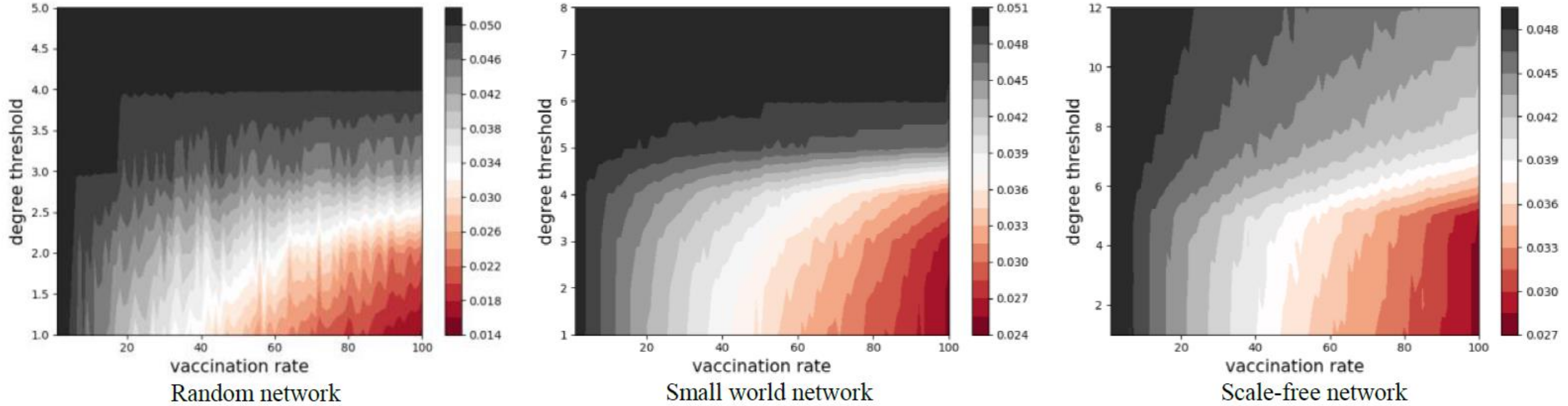


Figure 6 Numerical Simulation Contour for Parameter test

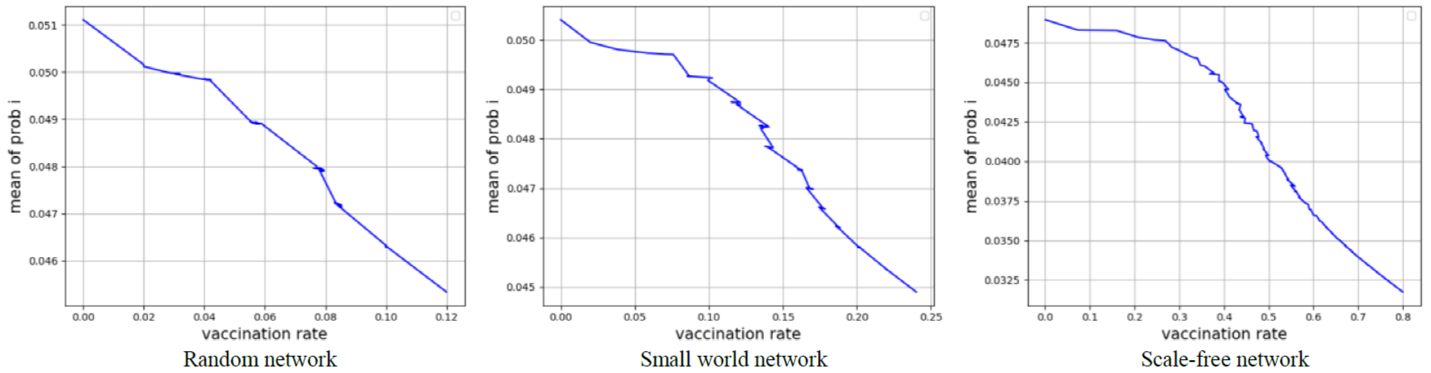
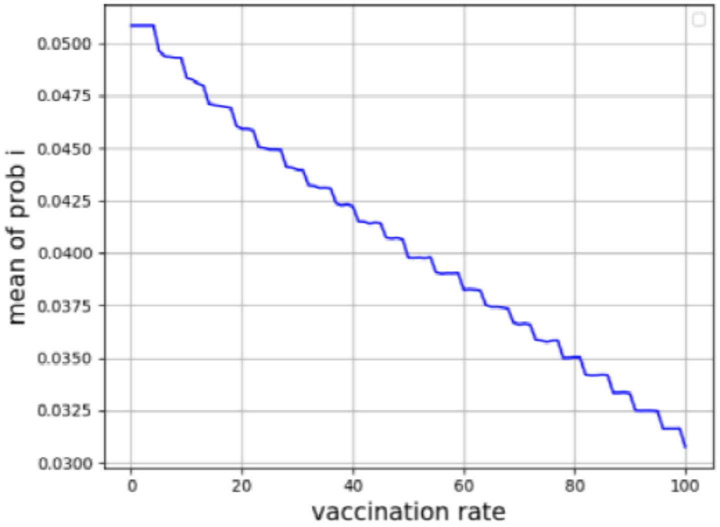


Figure 7 Numerical Simulation Result for Targeted Immunization

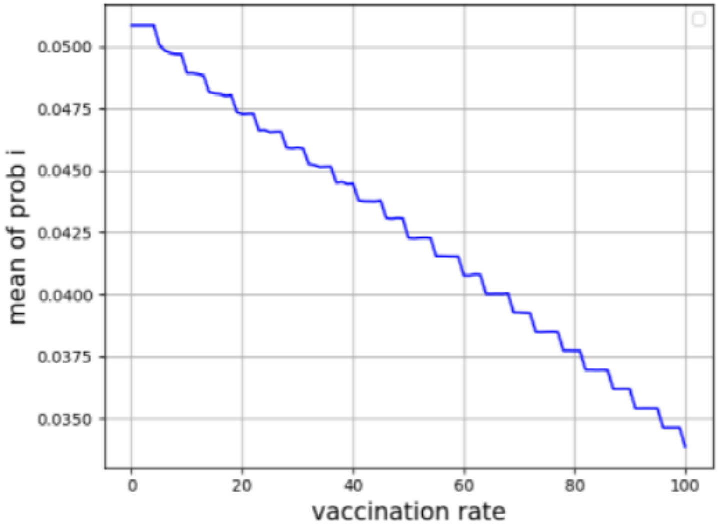
(k_c=2 for random, k_c=4 for small world, kc=8 for scale free)

Acquaintance Immunization

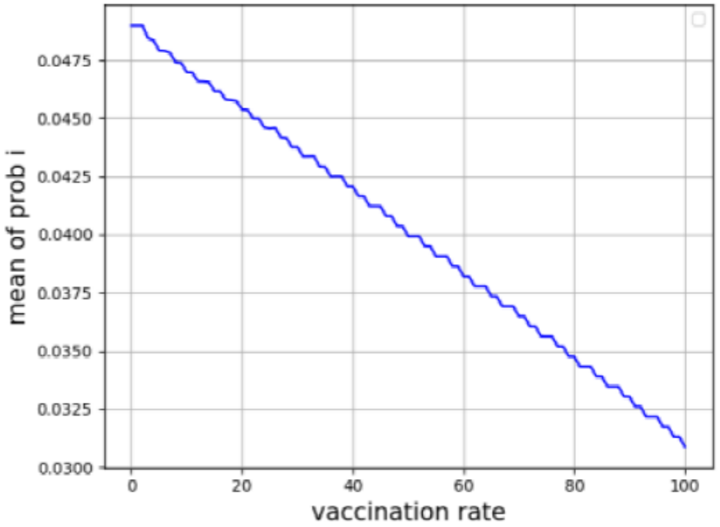
- Only requires knowledge of local information.
- Selection of a fraction p of nodes with at least one connection at random and vaccine his or her neighbors



Random network



Small world network

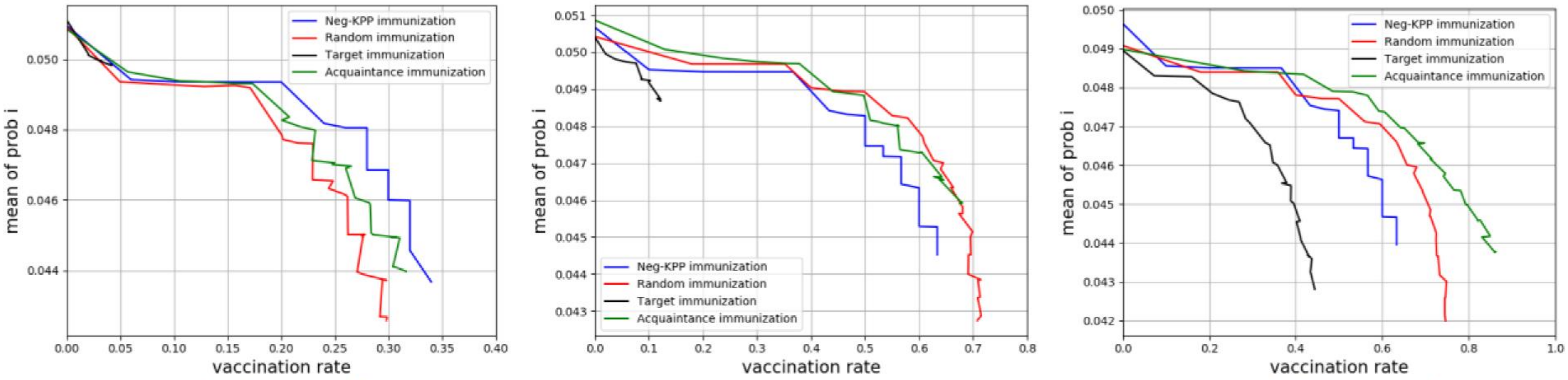


Scale-free network

KPP Immunization

- Negative Key Player Problem
- S_k: the size of each component in the fragment of the network
- Hirschman-Herfindahl index(HHI)
- To find a ratio of nodes to vaccine with the ratio get the minimum of HHI

$$H = 1 - \sum_k \left(\frac{S_k}{n}\right)^2$$



Random network

Small world network

Scale-free network

Figure 9 Numerical Simulation Result for Neg-KPP Immunization based on HHI

Conclusions

Contribution:

- updated network corresponded to the vaccination study based on percolation problem

- Random immunization, degree-based target immunization, and acquaintance immunization are verified under this dynamic network

- A new vaccination strategy based on Negative Key Player Problem applying Hirschman-Herfindahl index (HHI)

Future work:

- Imperfect information about the network
- Behavior-vaccination loop

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