

Acquaintance immunization in SIR scale free graph

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Introduction 1/2

The question we are going to answer today:

If a vaccine against CO-VID is found tomorrow, which vaccination strategy leads to the suppression of the endemic state for a lowest immunization rate ?

What we know already

- ▶ Random immunisation is not an efficient strategy (cf. presentation of Ronald & Chunxue).
- ▶ Targeted the hubs of the networks are super efficient strategy (cf. presentation of Ronald & Chunxue), but implies that we know the graph (which is not true).

Introduction 2/2

What we are going to do:

- ▶ Use the SIR (Susceptible Infectious-Removed) epidemiological model with scale free graph model.
- ▶ Reduce the problem as a static site bond percolation model (cf. Chunxue presentation).
- ▶ Recall the condition for the threshold bound percolation (= condition of the eendemic state).
- ▶ Propose and analysis an acquaintance immunization strategy.
- ▶ Give simulation results for random / targeted / acquaintance immunization strategy for coronavirus parameters.

Outlines

1. Position of the problem: (45min)
 - 1.1 SIR model definition and Hypothesis
 - 1.2 Quick demo
 - 1.3 SIR-Immunisation model as bond percolation
 2. The Acquaintance strategy: (1hour)
 - 2.1 Formulation
 - 2.2 Demo and comparison
- Appendix: Analysis

SIR model definition and Hypothesis 1/3

- ▶ Undirected Scale free graph network $P(k) = k^{-\gamma}$, for $2 < \gamma \leq 3$
- ▶ Assume that the network is static: every day is the same day (vs dynamics).
- ▶ Every node can be either Susceptible of being infected, Infected or Removed of the network.
- ▶ All node can be infected (no natural immunisation)
- ▶ Initialisation: a fraction f of a population is infected (I)

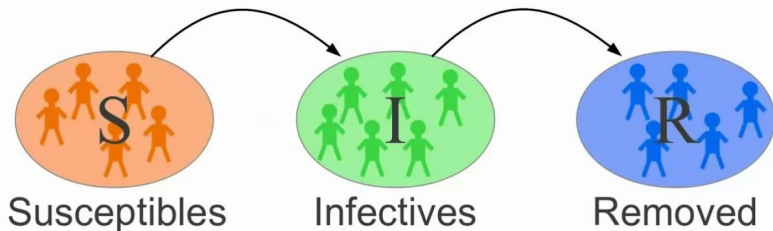


Figure 1: Illustration SIR model

SIR model definition and Hypothesis 2/3

- ▶ An Infectious node (I) remains infectious for an exponential time with mean τ . When they recovered, they are removed (R) . They can no longer be infected by the disease.
- ▶ During it infectious period, the infected individual (I) has infection contact randomly in time according a homogeneous Poisson process with rate r .

Let's establish the probability for each neighbor of (I) of not being infected (exercise)

- ▶ Indications 1 : Let N the number neighbor of infected people over a period of time: $N \sim \text{Poisson}(r)$
- ▶ Indications 2 : It can be shown (not asked) that the number of infectious neighbor over a time τ is $N_\tau \sim \text{Poisson}(r\tau)$

SIR model definition and Hypothesis 3/3

Let's establish the probability for each neighbor of (I) of not being infected (Solution)

- ▶ $P(N_\tau = 0) = e^{-r\tau}$, the probability that the number of infected neighbor over a period of time τ is zero
- ▶ So the probability for neighbor of infected people being infected is:

$$\boxed{p_b = 1 - e^{-r\tau}} \quad (1)$$

over a period of time τ

- ▶ Limits conditions: If $r \rightarrow \infty$, $p_b \rightarrow 1$ OK. If $\tau \rightarrow \infty$, $p_b \rightarrow 1$ OK.

Demo: SIR model in the case of coronavirus 1/3

Experimental conditions

- ▶ $\gamma = 2.9$
- ▶ Number of node = 10^6
- ▶ Number of edges = 878087
- ▶ Percentage of nodes infected a time 0 = 0.05
- ▶ Rate $r = 0.27$ and Recovery time $\tau = 10$ days (AN: $p_b = 0.97$)

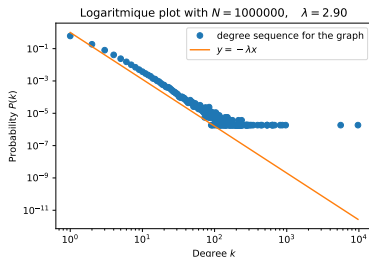


Figure 2: Log plot of probability of node degree with degree

Demo: SIR model in the case of coronavirus 2/3

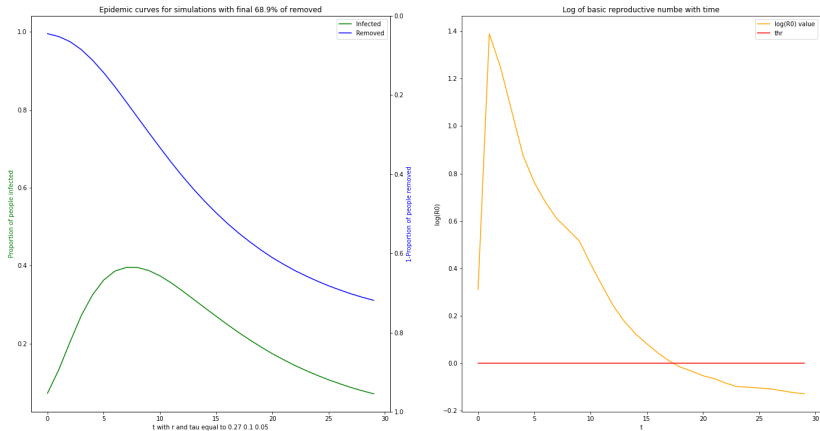


Figure 3: Epidemic simulation over time, worst case scenario

Demo: SIR model in the case of coronavirus 3/3

Comments on results : on left part

- ▶ We finish with 69% of the population removed.
- ▶ **That's perfectly match with the worst case scenario proposed by the NYT:** 224 millions Americans can be infected by the virus vs 226 millions with this estimation.
- ▶ There is a pic very fast in the beginning: hubs are infected very soon. We will come back to this later but any guess ?

Comments on results : on right part

- ▶ Plot of the value that matter in order to define an endemic state. Any guess ?

SIR-Immunisation model as bond percolation 1/6

Recall: Percolation (cf. Chunxue presentation)

- ▶ A typical percolation system consist of a d-dimensional grid of length L in which some nodes are removed with some probability p .
- ▶ Starting from a spanning cluster (idem a large cluster that extend from 1 edge of the lattice to the other), above some critical probability p_c , the system become disconnected into small clusters (idem as impossible to cross from 1 side of the grid to the other by following the conducting lines). And below this critical probability p_c , the spanning cluster still exists.

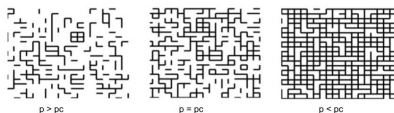


Figure 4: Illustration Percolation in 2D grid

SIR-Immunisation model as bond percolation 2/6

General immunization can be seen as a site percolation problem

- ▶ Each immunized / vaccinated individual can be regarded as a site which is removed from the network
- ▶ The goal of the immunisation process is to pass (or at least approach) the percolation threshold, leading to minimization of the number of infected people with the minimal proportion of (S) population to immunized / vaccinated

Hypothesis

- ▶ No consideration dynamics anymore
- ▶ We consider the situation in the endemic state = when the spanning component exists
- ▶ Only considering the critical threshold
- ▶ Like before, direct link with the condition of the destruction of the giant component

SIR-Immunisation model as bond percolation 3/6

Recall: condition of the destruction of the giant component (cf. Chunxue & Junjie presentation), the condition used to be:

$$\frac{\langle k^2 \rangle}{\langle k \rangle} = 2 \quad (2)$$

And this express that, in the giant component, the neighbor of every node as exactly 2 neighbors. As it was explained by Prof. Duzhin, that's the limit condition where, whatever node you delete, you will destroy the giant component.

Condition in our case: idea

If an infected individual infects, on average, at least one other individuals, then the epidemic can reach en endemic state.

SIR-Immunisation model as bond percolation 4/6

Let find the condition of the destruction of the endemic state
(with no immunization strategy)

Let's call n_k the number of neighbors infected knowing that the infection has just attain a node of degree k . We have:

$$n_k = p_b(k-1)P_{\text{following an edge brings us to a vertex of degree } k}$$

First, let determine what is the probability that, following an edge, brings us to a vertex of degree k (exercise)

Hypothesis and indications

1. Number of node of degree k : $Np(k)$ with N the number of node in the graph and $p(k)$ the fraction of vertices in the network with degree k ,
2. Number of edges = $\frac{N\langle k \rangle}{2}$
3. Let suppose that edges are a random matching conditioned on the vertex's degrees.

SIR-Immunisation model as bond percolation 5/6

- ▶ To arrive at a vertex with degree k , we must have followed an edge attached to one of the $Np(k)$ vertices of degree k in the network.
- ▶ And because of the random matching, the end point of every edge in the network has the same probability: $\frac{k}{2\frac{N\langle k \rangle}{2}}$.

So:

$$P_{\text{following an edge brings us to a vertex of degree } k} = \frac{kp(k)}{\langle k \rangle} \quad (3)$$

And so, we get

$$n_k = p_b(k-1) \frac{kp(k)}{\langle k \rangle} \quad (4)$$

SIR-Immunisation model as bond percolation 6/6

Condition of the destruction of the endemic state (with no immunization strategy)

$$\langle n_k \rangle < 1 \quad (5)$$

$$\langle n_k \rangle = \frac{p_b}{\langle k \rangle} \sum_k p(k) k(k-1) < 1 \quad (6)$$

$$\boxed{\frac{\langle k^2 \rangle}{\langle k \rangle} - 1 < \frac{1}{p_b}} \quad (7)$$

And this express that, in average an infected node (I) should not infected more than 1 other person.

Consequence

Because $\gamma \leq 3$, $\langle k^2 \rangle \rightarrow \infty$, and so, in our modelisation, an endemic state can spread in this network regardless of how small the infection rate r is or how quick the time recovery τ is.

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Formulation 1/4

What we know already

- ▶ Random immunisation is not an efficient strategy (cf. presentation of Ronald & Chunxue).
- ▶ Targeted the hubs of the networks are super efficient strategy (cf. presentation of Ronald & Chunxue), but implies that we know the graph (which is not true).

The main idea

- ▶ How to reach the hub without knowing the exact topology of the graph
- ▶ Thank to the super useful property graph : "In average, your friend has more friend than you."
- ▶ Exercise : show this property

Formulation 2/4

Proof of "In average, your friend has more friend than you."

- ▶ This means that the average degree of neighbors is higher than the average degree of a node, which is $\langle k \rangle$
- ▶ We know $P_{\text{following an edge brings us to a vertex of degree } k} = \frac{k p(k)}{\langle k \rangle}$
- ▶ So, average degree of neighbors = $\frac{\langle k^2 \rangle}{\langle k \rangle}$
- ▶ Finally, $\frac{\langle k^2 \rangle}{\langle k \rangle} \geq \langle k \rangle$

OK

Formulation 3/4

The strategy

1. Pick K nodes at random in the (S) population
2. Look at their direct neighbors who are also (S). They will be the ones who will be immunized/ vaccinated

The advantages

- ▶ The strategy is purely local, requiring minimal information about randomly selected nodes and their immediate environment.
- ▶ Because, in average, your friend has more friend than you, the neighbors of the node that you pick have, in average, a higher degree than the node.

Formulation 4/4

Illustration on example

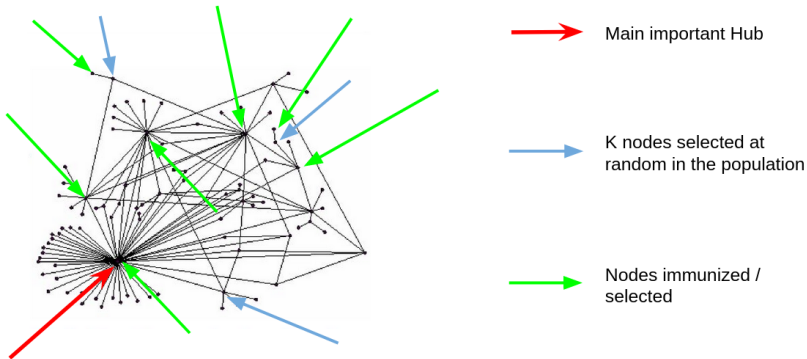


Figure 5: Illustration of the idea

Demo and comparison 1/4

Let's compare the random method, the targeted method and the acquaintance strategies in the case of coronavirus

Experimental conditions

- ▶ $\gamma = 2.9$
- ▶ Number of node = 10^5
- ▶ Number of edges = 88644
- ▶ Percentage of nodes infected a time 0 = 0.05
- ▶ Rate $r = 0.27$ and Recovery time $\tau = 10$ days (AN: $p_b = 0.97$)
- ▶ $K = 20\%$
- ▶ Experience repeated 10 times

Demo and comparison 2/4

Results

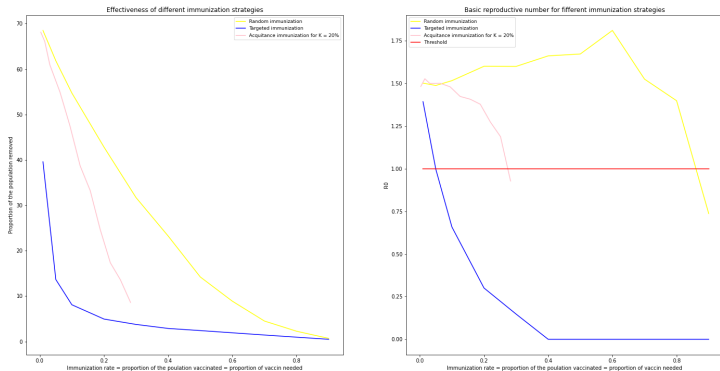


Figure 6: Comparison between the different strategies

Demo and comparison 3/4

Comments on results : on left part

- ▶ Why I don't finish at 100% immunization rate for the case Acquaintance ? Any guess ?
It is because, in the case of 100% immunization, I immunized all the neighbors of the 20% I pick in the beginning, but not all the population. Here, the final rate immunization is 28%.
- ▶ Random strategy is in fact a very bad one whereas the targeted strategy is super efficient.
- ▶ Acquaintance is just in the middle of the 2, starting from the results of random to the strategy of targeted

Demo and comparison 4/4

	Random	Targeted	Acquittance $K = 20\%$
Percentage of the population vaccinate in order to pass the threshold condition	85%'	5%	30%

Table 1: Final results

Comments on results : on right part

- ▶ What is surprising is the increase of the R_0 value
- ▶ The Acquittance immunisation gives very well results.

Conclusion

What we have done:

- ▶ Use the SIR (Susceptible Infectious-Removed) epidemiological model with scale free graph model.
- ▶ Reduce the problem as a static site bond percolation model.
- ▶ Recall the condition for the threshold bound percolation (= condition of the endemic state).
- ▶ Propose and analysis an acquaintance immunization strategy.
- ▶ Give simulation results for random / targeted / acquaintance immunization strategy for coronavirus parameters.

References

Madar et al., "Immunization and epidemic dynamics in complex networks"

Cohen, Havlin, and Ben-Avraham, "Structural properties of scale free networks"

Cohen, Havlin, and Ben-Avraham, "Efficient immunization strategies for computer networks and populations"

Cohen et al., "Resilience of the internet to random breakdowns"

Simulate an epidemic - 3Blue1Brown

A conceptual model for the coronavirus disease 2019 (COVID-19) outbreak in Wuhan, China with individual reaction and governmental action

Github repo

Analysis 1/6

Notations

- ▶ l : hop distance from the starting point (suppose unique here)
- ▶ $n_l(k)$: number of node of degree k in layer l that are Suceptible and reached by the disease
- ▶ s_k : the event that a node of degree k is susceptible to the disease (not immunized, and therefore maybe infected through the course of epidemic spreading)
- ▶ $p(k|k', s_{k'})$: the probability of reaching a node of degree k through following a link from a susceptible node of degree k' .
- ▶ $p(s_k|k', s_{k'}, k)$: the probability that a node of degree k is also susceptible given both the node and the neighbor's degrees (k'), and the fact that the neighbor is also susceptible.
- ▶ $v_p(k)$: the probability that the acquaintance (coming from neigbord of degree k) is not selected in all vaccine attempt
- ▶ p is the random fractionp of the N nodes and look for a random acquaintance with whom they are in contact.

Analysis 2/6

Equation

To find out the number of nodes, $n_{l+1}(k)$, of degree k that are susceptible and are reached in the course of the epidemic, we multiply the number of links going out of the l^{th} layer by the probability of reaching a node of degree k through following a link from a susceptible node, $p(k|k', s_{k'})$. Then, we multiply by the probability that this node is also susceptible given both the node and the neighbor's degrees, and the fact that the neighbor is also susceptible, $p(s_k|k, k', s_{k'})$.

$$\blacktriangleright n_{l+1}(k) = p_b \sum_{k'} n_l(k') (k' - 1) p(k|k', s_{k'}) p(s_k|k, k', s_{k'})$$

Analysis 3/6

Development 1/4

- ▶ $p(k|k', s_{k'}) = \frac{p(s_{k'}|k', k)p(K|k')}{p(s_{k'}|k')}$
- ▶ $p(k|k') = P_{\text{following an edge brings us to a vertex of degree } k} = \frac{kp(k)}{\langle k \rangle} = \Phi(k)$ (independent of k')
- ▶ A random site (of degree k') is selected in each step with probability $1/N$. The probability of being redirected to a specific acquaintance is $\frac{1}{k'}$. Thus, the probability that the acquaintance is not selected in one particular attempt, is $1 - \frac{1}{Nk'}$, and in all Np vaccination attempts, it is:
 $v_p(k') = (1 - \frac{1}{Nk'})^{Np} \sim e^{-p/k'}$. If the neighbor's degree is not known, the probability is $v_p = \langle v_p(k') \rangle = \langle e^{-p/k'} \rangle$

Analysis 4/6

Development 2/4

- ▶ In general, the probability that a node with degree k is susceptible is $p(s_k|k) = \prod_k v_p = v_p^k$
- ▶ If the degree of one neighbor (which is the one through which the epidemic propagated) is known to be k' :
$$p(s_k|k, k') = e^{\frac{-p}{k'}} v_p^{k-1}$$
- ▶ $p(s_k|k, k') = p(s_k|k, k', s_{k'})$

Development 3/4

- ▶
$$p(k|k', s_{k'}) = \frac{\Phi(k)e^{-p/k}}{\langle e^{\frac{-p}{k'}} \rangle}$$
- ▶ We substitute in $n_{l+1}(k)$, and we get:
- ▶
$$n_{l+1}(k) = p_b v_p^{k-2} \Phi(k) e^{-p/k} \sum_{k'} n_l(k') (k' - 1) e^{-p/k'}$$

Analysis 5/6

Development 4/4

- ▶ Since the sum on k' does not depend on k , it leads to the stable distribution of degree in a layer l :

$$n_l(k) = a_l v_p^{k-2} \Phi(k) e^{-p/k}, \text{ for some } a_l$$

Final results 1/2

- ▶ We substitute in $n_{l+1}(k)$, and we get:
- ▶ $n_{l+1}(k) = n_l(k) p_b \sum_{k'} \Phi(k') (k' - 1) v_p^{k'-2} e^{-2p/k'}$

Analysis 6/6

Final results 2/2

- Therefore, if the sum is smaller than 1 immunization is sub-critical and the epidemic is arrested. Thus, we obtain a relation for p_c :

$$\sum_k \Phi(k)(k-1)v_{p_c}^{k-2}e^{-2p_c/k} = p_c^{-1}$$

Remark

- The term $v_{p_c}^{k-2}$ in above equation induces an exponential cutoff on the degree distribution of susceptible nodes
- You can do that for double acquaintance