Quality Criteria for Control of Epidemics.

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Abstract

Total number of infected and maximum number of infected are considered as criteria for control by delayed isolation of SIR-type epidemic on a temporal Barabasi-Albert graph. Simulations are run to estimate the optimal delays.

Key words: delayed isolation; control of epidemics; temporal Barabasi-Albert graph; total number of infected; maximum number of infected; flattening the curve

1 Introduction

How can we control the epidemics of type Susceptible → Infected → Recovered (SIR)?

In March 2020, the world reacts on the spread of COVID-19 with isolation in order to stop pandemic or minimize the damage. By isolation people understand voluntary and non-voluntary restrictions on social interactions. Simply speaking, in-person contacts are limited to the closest circles. These measures cause obvious economical problems. So, isolation has its own price. This economical criterion will be studied a lot in the future for sure. In this work, we analyze the effect of the isolation on the spread of the disease.

There were already some attempts to do it. One good animation of Brownian motion approach can be found in [1] and more theoretical work is in [2]. Classic differential approach referred so much recently is explained well in [3].

We apply graph approach. A problem of SIS (Susceptible → Infected → Susceptible) epidemic control on graphs was considered in [4]. SIS model isn't applicable to COVID-19 and influenza . We consider SIR model on a temporal graph. This graph is built by Barabasi–Albert preferential attachment mechanism [5], which is known to be one the best to reflect social connections. Then we run this SIR simulation with 2-,4-,6- week restriction on communication with "popular" nodes (ones with the degree equal or greater than 5), starting with different delays from the beginning of epidemic process. The result is presented as plots of the infected and recovered. The computer code can be found at [6].

2 Model and Parameters

2.1 Graph

Barabasi–Albert graph of size n is built by a consecutive augmenting process. After initiation of the graph G with m nodes and no edges, one connects a new node x to G with m edges in such a way that the probability that x is connected to $a \in G$ is equal to the degree of a. So, "popular" nodes grow faster (see fig. 1). The number m is a parameter, in this work $m = 3$. The building process stops when the size of G reaches n. We transform G to a temporal graph by assigning the times of availability to the edges. We assume time to be discrete, measured in days by natural numbers.

If two nodes $x, y \in G$ are connected by an edge with the assigned time moment t, we say x and y are *temporal neighbors* at t. The number of temporal neighbors of a node $x \in G$ at t is called *temporal degree* of x at t.

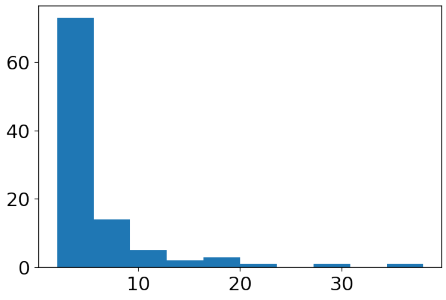

Figure 1: Histogram of the distribution of node degrees in Barabasi graph with $n = 100$, $m = 3$.

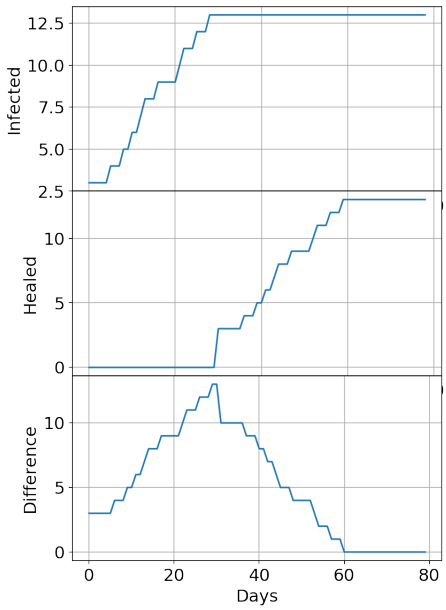

Figure 2: Number of infected, recovered nodes and their difference against time.

2.2 Epidemic process

When the Barabasi–Albert graph of n nodes is built we can simulate an epidemic as SIR process. All recovered assumed to be immune to secondary infection during the considered epidemic. Each node in G has a status: "susceptible", "infected" or "recovered". Nodes are contagious if and only if they have status "infected". Someone may ask why don't we have a status "dead". Despite how cruel it sounds, for the spread of the disease, dead and recovered play the same role because they can't get infected no more. After G is initiated with i infected nodes at the day zero (see fig. 3, 5), every day each contagious node infects with p probability each of its temporal neighbors with the status "susceptible", meaning changing the temporal neighbor's status to "infected". The duration of status "infected" is 30 days, after which the node becomes "recovered" (see fig. 4, 6). What should the value of parameter p be? The triple product of an average temporal degree, duration of "infected" status and p should be equal to the *reproductive number* of the infection, i.e. how many new people in average get infected from one infected. The reproductive number of COVID-19 is an open question. Different statistics methods give quite different results [7]. Here we assume that COVID-19 has reproductive number 3.6. The average temporal degree of 5000-node Barabasi-Graph is about 5.99. So, we set $p = 0.02 \approx 3.6/(5.99 \cdot 30)$. The Python code used for all simulations in this work is left in an open access [6]. Everyone is welcome to play with p and other parameters.

Since the random number generator is involved, the infection process may go differently even on the same graph and same initially infected nodes (see fig. 7, 8). We should take into account in the following experiments.

To observe the epidemic we plot the number of infected, recovered and difference of them against time (see fig. 2).

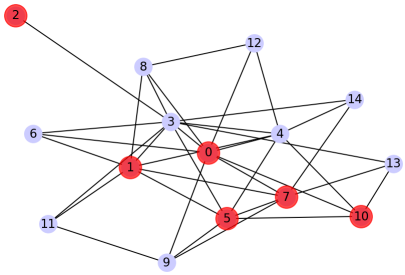

Figure 3: Barabasi 15-node graph with 6 infected nodes.

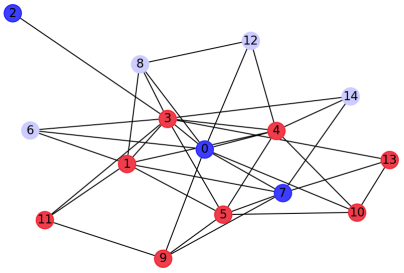

Figure 4: Infected 15-node graph after 32 days. Blue nodes are recovered or dead.

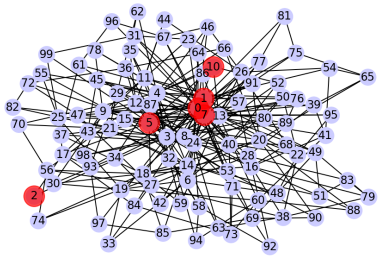

Figure 5: Barabasi 100-node graph with 6 initially infected.

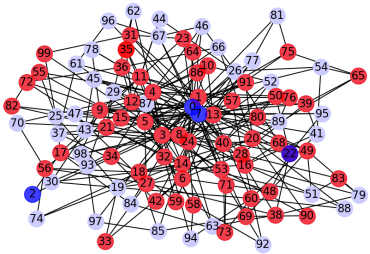

Figure 6: Barabasi 100-node graph after 32 days.

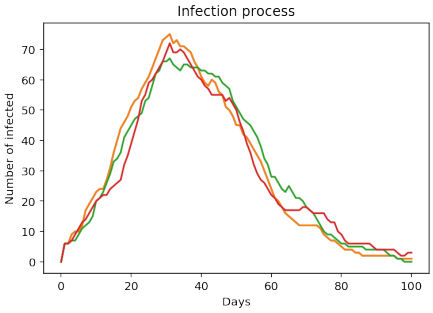

Figure 7: Variability of epidemic process on 100-node graph showed by three different random seeds.

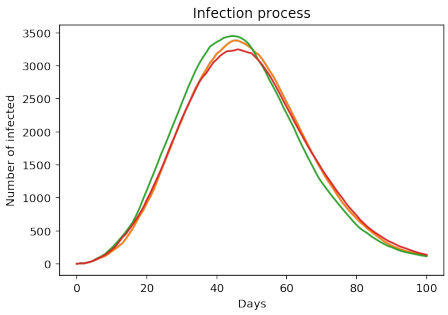

Figure 8: Variability of epidemic process on 5000-node graph showed by three different random seeds.

2.3 Isolation

One inconvenience of classic epidemic models based on differential equations or Brownian motion is that it is hard to conduct experiments with isolation. Temporal graphs allow us to do it relatively easy. First, for simplicity, we give one availability time moment per day to each edge of G during $[t_1, t_T]$. (In the future works, someone can try to model more complex distributions of schedules on the graph, for example, make some edges available on week days and others only on the weekends.) Then we enforce "No gathering 5 or more people" rule from day t_s to day t_f as following: every node $x \in G$ in the time interval $[t_s, t_f] \subset [t_1, t_T]$ disconnects from its neighbor which has temporal degree 5 or more. Since we do it in iterative manner for all nodes in G on each time step, at some point "popular" nodes stop being "popular" and keep some connections.

The time of the beginning of isolation t_s we call *isolation delay*.

Somebody could say that isolating "popular" nodes isn't the same that "no gathering". Well, we think it is equivalent because gathering in a group of k people at day t means that temporal degree of each person in this group greater or equal k. You may see a lecture in college as a gathering of k students or you may say that the professor has a temporal degree k or higher. If students don't come in their lecture because of "no gathering", they lower the temporal degree of them and of the professor.

3 Quality criteria

The epidemic brings complex damage to society. Individuals going through the illness work less and, in the severe cases, may die. So, it makes sense to consider measures against the infection and study the effectiveness of them.

The first quality criterion of the actions against the epidemic processes we choose to be F_{tot}, the total number of people getting sick during the epidemic.

Now let's think about dead. Their number depends on the total number of infected but also depends on the available spots in hospitals. If too many ill people in severe conditions simultaneously come for help, there may not be enough of it for them. Thus, another approach would be to minimize the maximum number of infected during the epidemic period (so-called "flattening"). So, the second quality criterion is $F_{max} = \max_t F^t$, where F^t is the number of currently infected at a day t of the epidemic.

We consider isolation as a single tool to reduce both F_{tot} and $F_{\max}$. The isolation has two control parameters: its duration l and the starting time of it t_s. It is reasonably to assume that the cost of isolation does not depend on t_s. This allows to perform optimization of F_{tot} and $F_{\max}$ over t_s ignoring the cost of the isolation for a fixed l.

However, the cost of isolation does depend on l. This dependency is not studied in this work, where we make experiments with a few fixed values of l. So, we remove l from arguments of objective functions to their upper indices and limit ourselves in considering two following mathematical

Problem 1: Minimize the objective function F^l_{tot} over t_s.

Problem 2: Minimize the objective function F^l_{max} over t_s.

The experiments conducted in the next section are meant in a view of these two problems above but, of course, may give some other food for thought.

4 Experiments and Observations

We conducted experiments on 5000-node temporal Barabasi-Albert graph with no isolation and the isolation of lengths $l = 14, 28, 42$ days starting at $t = 14, 21, 28$ day from beginning of epidemic. Each simulation is run with the same random seed. For the convenience of comparison the graphs of simulations for

Table 1: Total numbers of ever infected.

	No isol.	14-th	21-th	28-th	35-th	42-th
2 weeks	4450	4405	4342	4236	4230	4270
4 weeks	4450	4328	4181	4023	4006	4148
6 weeks	4450	4288	4070	3900	3888	4105

the same length of the delay are combined in one plot. Thus, we obtained three plots 11, 13 and 14 for $l = 14, 28, 42$, respectively.

The total numbers of ever infected over the epidemic time people are in tables 1 and 2 contains the maximum numbers of infected during the epidemic periods. Observe that min-max values of infected obtained with delay equal 28, 28 and 21, for 2-,4-,6-week isolation, respectively. The minimum total numbers of infected are obtained on 35-day delay of all 2-,4-,6-week isolation. Notice that the results may vary from one random seed to another (see fig. 12).

Giving a better estimate for the optimal delay meets some difficulties. First, we would have to average it over random seeds. Second, we don't observe unimodality of the objective function F_{tot}. For example, its values for 2-week isolation from 24- to 35-day delay can be seen on fig. 9. The function F_{max} seem to behave nicer 10. The unimodality of F_{max} is a direction for a future theoretical research.

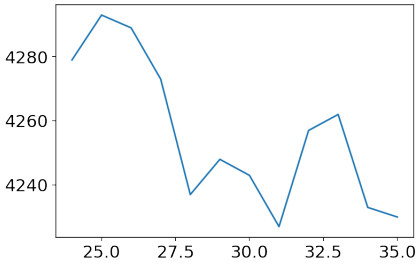

Figure 9: Non-convex behavior of F_{tot}^{14}.

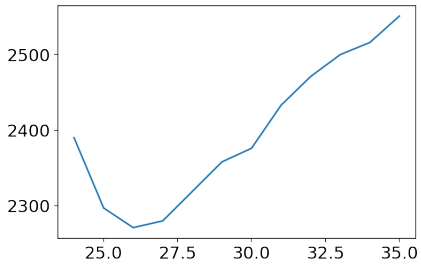

Figure 10: Nicer behavior of F_{max}^{14}.

For the same random seed, which was used to compute figures 11, 13, 14 and tables 1, 2, we compute the optimal delay for F_{max}. It is 26, 25, 23 for, respectively, for 2-,4-,6-week isolation.

Table 2: Maximum numbers of infected.

	No isol.	14-th	21-th	28-th	35-th	42-th
2 weeks	3208	3013	2700	2319	2551	2985
4 weeks	3208	2629	1925	1897	2547	2985
6 weeks	3208	2447	1497	1897	2547	2985

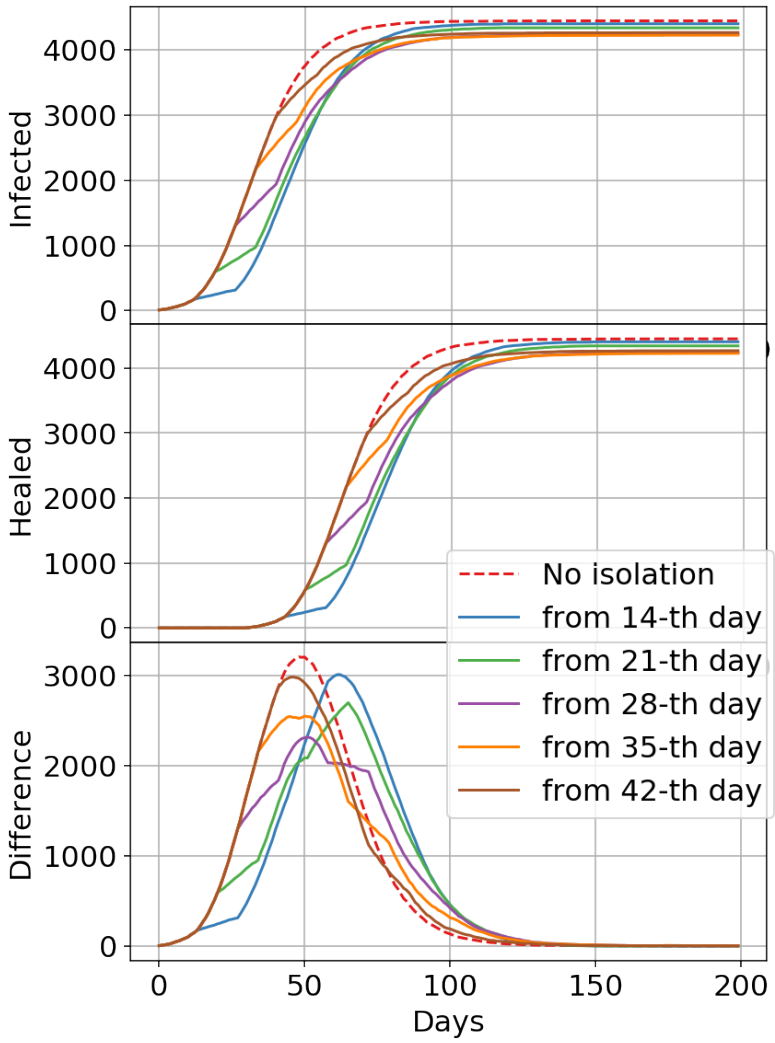

Figure 11: 2-week isolation.

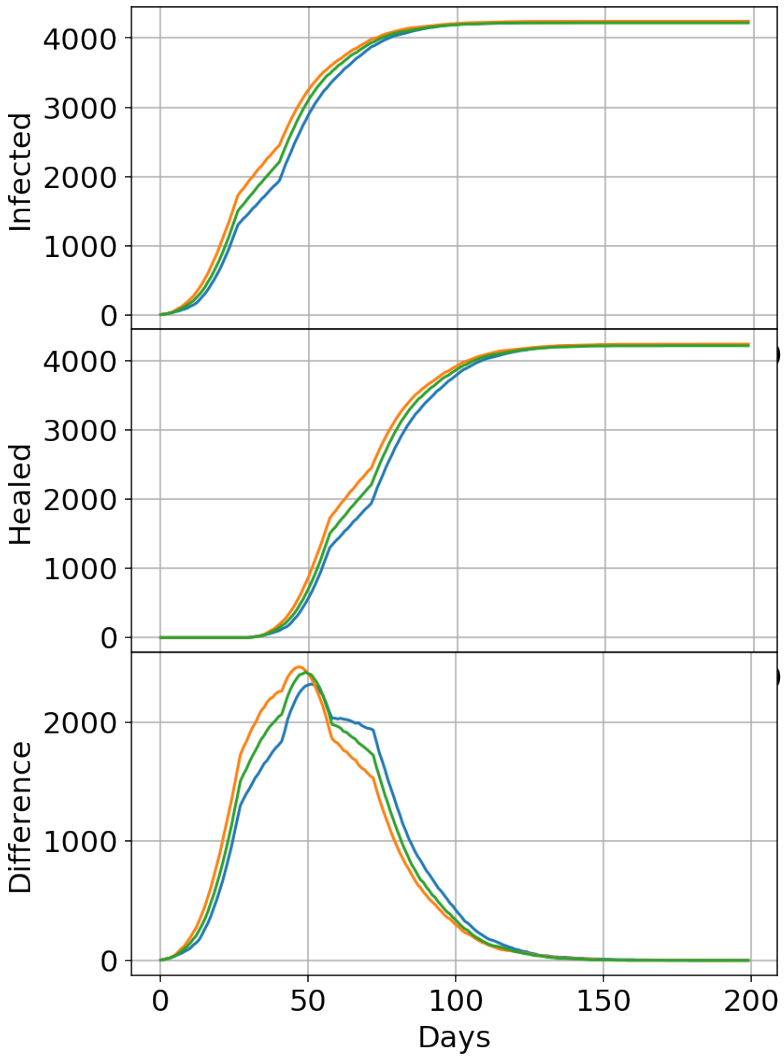

Figure 12: The variability of the infection process on 2-week isolation with 28-day delay showed by running the simulation with three different random seeds.

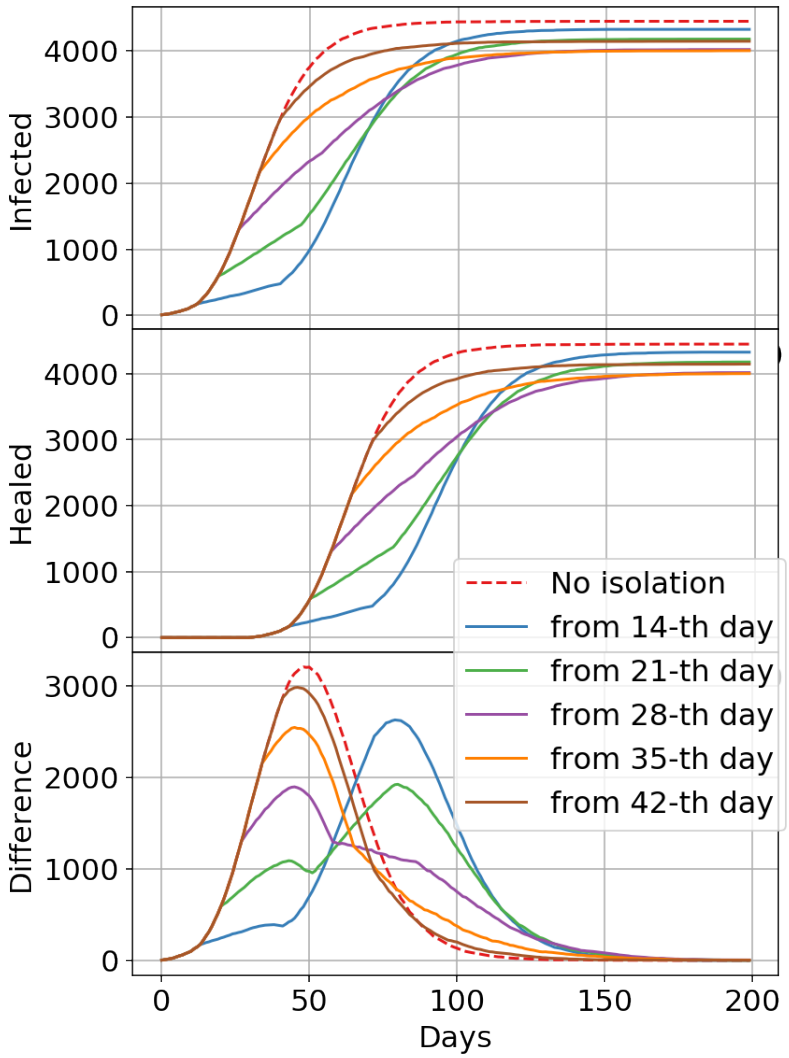

Figure 13: 4-week isolation.

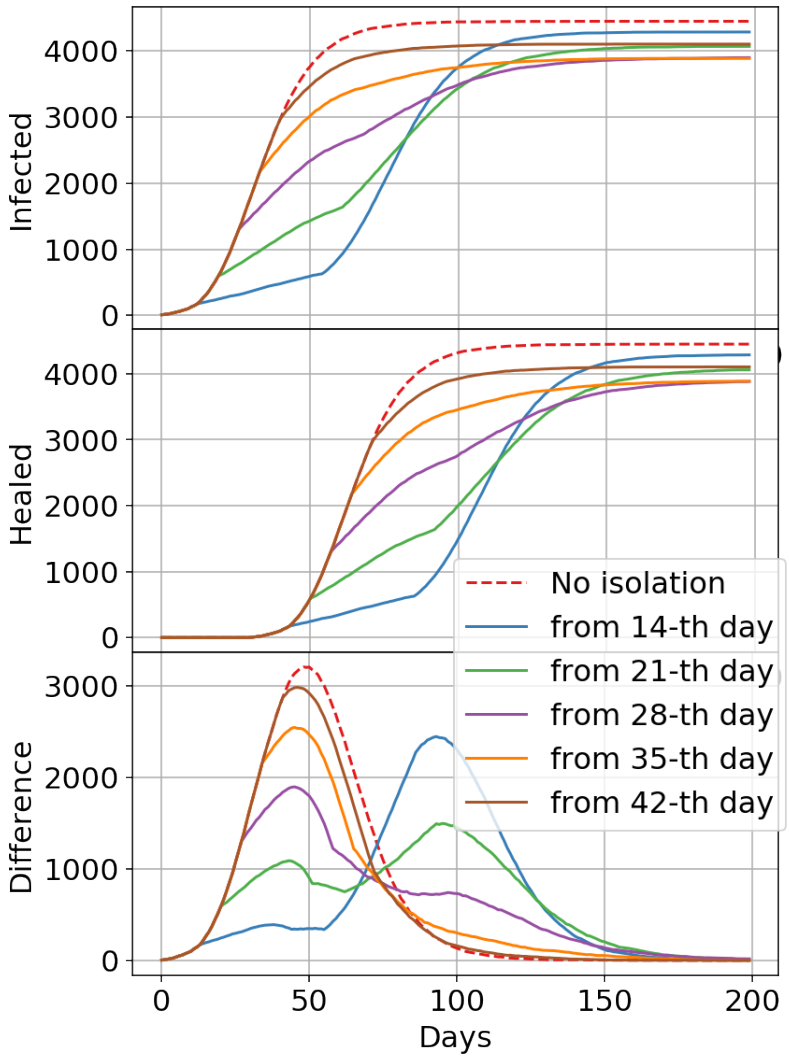

Figure 14: 6-week isolation.

On the figure 15 one may see that results are similar on 10,000 nodes. For 6-week isolation, the total numbers of infected are 8881, 8446, 8004, 7812, 7997, 8342 and the maximum numbers are 6462, 4332, 2866, 4407, 5545, 6252 for, respectively, no isolation, 14-, 21-, 28-, 35-, 42-day delays.

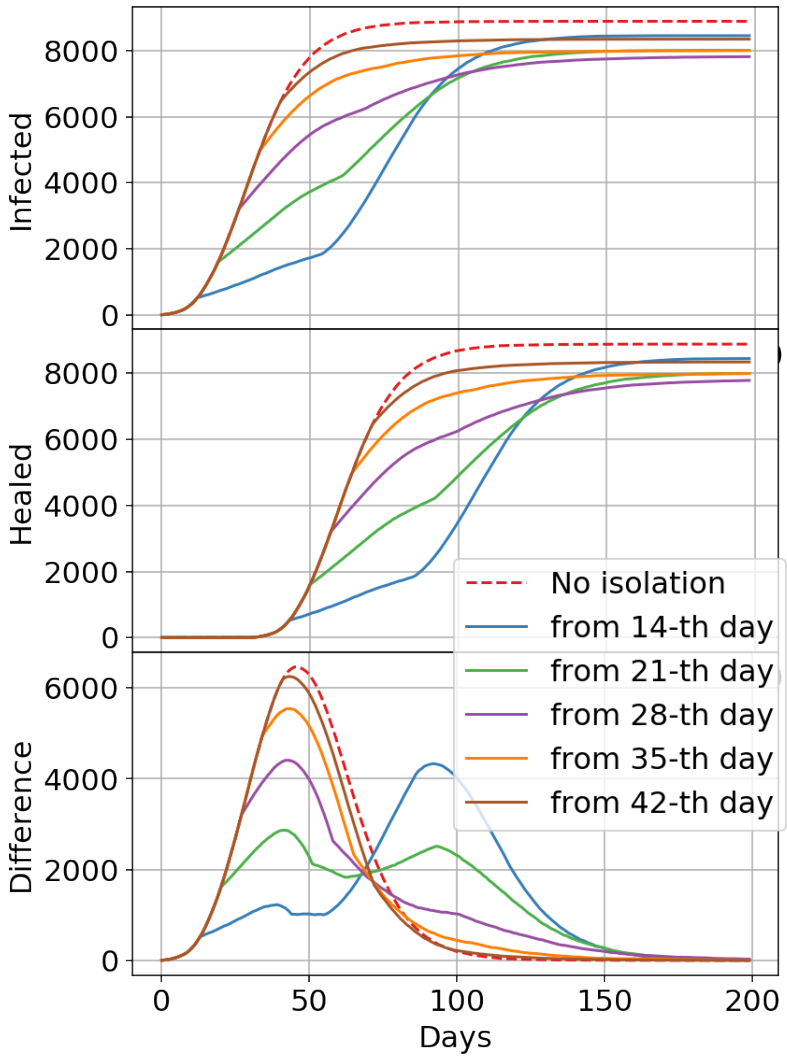

Figure 15: 10,000 nodes. 6-week isolation.

5 Conclusion and Recommendations

The experiments we conducted, show that the goals to decrease total number of infected and to decrease share of lethal cases among infected (problem 1 and 2 stated in 3) are not antagonists to each other. Firstly, the values of both criteria get better when the delay increases starting from zero. Secondly, they get worse when the delay becomes essentially large. Thirdly, a good compromise can be found because the optimal values are achieved at close to each other delays.

That compromise for isolation with length from 2 to 6 weeks is with the delay between 21- and 35-day delay.

Alas, to use the recommendation to start an isolation at some day of epidemic, we need to know the day of the beginning of epidemic, which is usually unknown. Fortunately, I, the amount of infected at the current day t_{today} can be estimated. Also, we know n, the size of population. Thus, we can run "no isolation" simulation on n-node graph to the day t_{sim}, when the number of infected in the simulation is equal to I. Then $t_{today} - t_{sim}$ is the estimation of the day of the epidemic beginning.

For example, a town with population 5,000 people registers first infected. The town knows that they can afford 4 week isolation. They could randomly select a group of citizens and run the virus test on them. After running suggested in this paper "no isolation" simulation, the town computes the day of the epidemic beginning. Table 2 tells them that to minimize the maximum number of infected they have to start the isolation around 28-th day of the epidemic, which is approximately when 27% of population is infected.

References

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