Epidemic Control with Temporal Immunization and Limited Vaccine Budget

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ABSTRACT

In the ongoing effort to curb the spread of COVID-19, there is a global drive towards creating an effective vaccine against the virus. Once a vaccine is created, however, its distribution becomes an important problem to address. An effective distribution can save time and energy, letting us reach herd immunity with the least amount of resources spent, even if vaccines provide temporary immunity. Here, we develop an algorithm that takes into account a limited budget and temporary immunity in order to most effectively curb the spread of a virus, such as COVID-19. This algorithm works by using an immunization pattern function, a cost function, and a risk function, and minimizing the work needed to reach a certain level of immunity in the network. Experiments based on the data from known networks, such as UCI's Karate Club Network [9] or large networks from Stanford's SNAP datasets [4] show how our algorithm works in both small and large settings. We can also tune the algorithm so that it is robust enough to work in a variety of situations.

1 INTRODUCTION

1.1 Background

Vaccines are considered one of the most effective methods to prevent the spread of an epidemic. However, distributing the vaccines under a limited budget remains an open problem, as an effective distribution would prevent the spread of an epidemic as much as possible. This can be a hard problem since it can involve another silent problem to solve: How do we find the people that are exposed to the epidemic and how do we decide who are the most vulnerable people that should have the highest priority of vaccine injections? Besides, considering that some vaccines can only give people a temporary resistance against the epidemic, or temporary immunization, the vaccine distribution problem can be even harder under a limited vaccine budget. For example, there have been several COVID-19 cases identified as a reinfection case [3], which indicates that even if a vaccine is created, the resistance against the COVID-19 may only be temporary.

1.2 Related Works

There have been some works focusing on the vaccine distribution problem.

In [2], the author focused on the networks and populations with broad and scale-free degree distributions. Then the author proposed an effective immunization strategy that immunizes random acquaintances of random nodes to study the critical threshold for immunization analytically. This work is useful to us because the algorithms require no knowledge of the node degree distribution as well as other global knowledge to give the immunization strategies, which can be a useful start for designing an algorithm that can be tested in a variety of networks. However, this work assumes an SIR model in the experiment, which limits the generality of the strategy over different kinds of epidemic spread patterns.

The author of [5] concentrated on the optimal vaccine allocation with five outcome measures: deaths, infections, year of life lost, contingent valuation, and economic costs. Then the author used a model parametrized with survey-based contact data and mortality data from influenza pandemics to find the optimal vaccinations. One of the advantages of this work is that it divides people into different age groups to minimize transmission. However, the disadvantage of this model is that it assumes a model of transmission dynamics for different age groups.

The topic of [6] is a focus on the prevention of an epidemic in a network. Considering that giving some target nodes immunization can be more effective than immunizing a random subset of nodes, the author oppugns the assumption that the selected nodes can be completely immunized. Instead, if the method to prevent the spread of the epidemic is just some infection-prevention resources, such as masks, instead of permanent vaccines, it will be a challenge to distribute the fixed amount of resources across the nodes in the network to minimize the spread (new infections) of the epidemic. One of the advantages of this work is that it introduces the concept of fractional immunity under a limited budget, which can be a real situation that few works focus on now.

In [10], the author focused on real-time decisions to immunize healthy nodes with some nodes that have been already been infected. The advantage of this work is that it allows real-time decisions with the progressing infection process while most of the other previous works for controlling the propagation of epidemic are pre-emptive, which immunizes people before the start of the epidemic.

In [11], the author noticed that most existing studies of vaccine distribution policies are based on the assumption that pre-emptive strategies are developed with prior epidemiological models, which may fail to adapt to the new epidemiological patterns and cannot take advantage of the health care surveillance data. Therefore, the author (1) formulated the data-driven immunization problem, (2) proposed an efficient approach to align the contact network with the surveillance data, (3) developed the algorithm that approximates the guarantee for immunization. The advantage of this that it relies on the health care surveillance data instead of prior epidemiological models, which makes the method data-driven.

In addition to this, there are other works focusing on detecting the most vulnerable people that are exposed to the epidemic, which

is exactly the silent problem when solving the vaccine distribution problem.

In [7], the author attempted to reconstruct the propagation of an activity (epidemic) in a temporal network. One of the advantages of this work is that it assumes the temporal network, which can be more reasonable for long-time real-world social networks since it only contains information about when two nodes interacted with each other, while most existing works are assuming that the network does not change during the whole process. Another advantage is that it only requires a sample of nodes that have been reported as infected instead of the perfect, complete, noise-free data. In addition, it requires no exact propagation model as the prior knowledge.

In [1], the author focused on the efficient and effective strategy of detection of healthcare-acquired infections outbreaks by monitoring selected people and locations. Although the problem that this paper focuses on seems to be a little different, the big picture of identifying most vulnerable people is still consistent with our work, and one of the biggest advantages of this paper over the others is that this paper first introduces the monitoring rates (or immunization frequency) into the detection problem.

1.3 Our Contributions

However, all the works above, except for [6, 8], focus on long-term immunization methods, like vaccines, while failing to consider the fact that even long-term immunizations can be invalid after a certain period of time. Besides, for a new, large-spread epidemic like COVID-19, the production speed of the vaccines may be low at the initial time, which raises the problem of how to control the spread of epidemic with temporal immunization vaccine and limited budget. To the best of our knowledge, we are the first to consider the temporal immunization pattern function and limited vaccine budget into consideration together, which instead exactly meets the situation we are facing against the large-spreading COVID-19.

2 PROBLEM FORMULATION

Given the temporal network $G(V, E)$, V is the set of nodes in the temporal network and $\|V\| = m$ is the number of nodes in the temporal network. As for the edges, an edge $e = (u, v, t)$ describes that node $u \in V$ and $v \in V$ have an interaction from u to v at time t. Then $E = \{(u, v, t) | u, v \in V, t \in T\}$ is the set of edges (interactions) in the temporal network, while $\|E\| = n$ is the number of edges (interactions) in the temporal network. Furthermore, we will use the set $E(t_i) = \{(u, v, t) | t = t_i\}$ as the set of interactions at time t_i. For all temporal edges (interactions), the initial time will be t_0 and the final time will be t_N, which involves t_0, t_1, t_2, ... ,t_N timestamps in the whole simulation process.

However, temporal graphs can be hard for us to perform the analysis and distribute the vaccines with limited budget. Therefore, we need to convert the temporal graphs to stable graph. Specifically, we will use the following method shown in Figure 1 as the method to convert the temporal graph to traditional stable graph, which then allows us to apply existing graph algorithms.

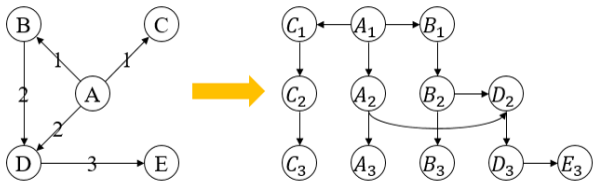

Figure 1: Convert from temporal graph to stable graph

Basically, the idea is that for each node $v \in V$ we will create the copy for each node for $t_0, t_1, t_2, \ldots, t_N$: $v_{t_0}, v_{t_1}, v_{t_2}, \ldots, v_{t_N}$. By creating the copy for the nodes, we will get a stable graph $H(V_H, E_H)$ where $\|V_H\| = N \times \|V\|$. As for the edges, for each edge $e = (u, v, t) \in E$, we will create the edge from u_t to v_t, which represents that u and v have an interaction (edge) at time t. Furthermore, for every node $v \in G$, we also need to create a series of the edges (v_{t_0}, v_{t_1}), (v_{t_1}, v_{t_2}), ... , $(v_{t_{N-1}}, v_{t_N})$ in $H(V_H, E_H)$ which represents that each node $v \in V$ is the same node at different time.

One example of the method to convert the temporal graph to traditional stable graph are shown in Figure 1, we have five interactions in the temporal graph $E = \{(A, B, 1), (A, C, 1), (A, D, 2), (B, D, 2), (D, E, 3)\}$. We can convert the nodes $V = \{A, B, C, D, E\}$ to different nodes and then convert the temporal graph to stable graph.

In addition, there also exist a line-list I that contains the already infected cases, where $u \in I$ means that u has been confirmed to be infected with the epidemic before time t_0. Supposing $V(I) = \{u | u \in I\}$ is the node set that has been confirmed with the epidemic, we will have $V(I) \subset V$.

Here, one thing to notice is that the line-list I is given to us at time t_0, which means that we will not influence the propagation process using vaccines before t_0. However, as the epidemic continues to spread among the population after t_0, we can start to give immunizations to people to prevent infection as well as influence the propagation process of the epidemic.

As for the propagation process, we will use the **independent cascade (IC) model** to model the process of infections after t_0, which means that for any healthy node v at any time t, if there exist n neighbors that are infected, then the probability that v will also get infected at time $t+1$ is $p(v, t) = 1 - (1-p)^{\|V_H(E_H(,v))\|}$, where $\|V_H(E_H(,v))\|$ is the number of v's neighbors that get infected, p is the probability that v's neighbor infect v independently if v is not immunized, and $p(v, t)$ is the probability that v gets infected at time t.

Next, we will define the temporal immunization pattern of the epidemic. Here, we will define the decay of the immunization as a function of t: $R(t)$, where $R(t) \in [0, 1]$ at any time t, and for each specific node $v \in V_H$, we will have $R(v, t)$ as the temporal immunization pattern for node v at time t. Then with the temporal immunization pattern, we will have the probability that v will get infected at time $t+1$ is $p(v, t) = 1 - (1 - (1 - R(v, t))p)^{\|V_H(E_H(,v))\|}$. Intuitively, the higher $R(t)$ indicates a higher immunization level. And for node v, the $R(t)$ will be $R(v, t)$. Here, a $R(v, t) = 1$ means that v will not be infected at time t, while $R(v, t) = 1$ will lead to

$p(v,t) = 1 - (1 - (1 - R(v,t))p)^{\|V_H(E_H(,v))\|} = 0$ means that v will not get infected at time T.

Next, we will measure the risk that one specific person faces as a risk function $D(v)$. Here, we can consider $D(v)$ as the priority that we need to give immunizations to since they are in higher risk if infected with the epidemic. One thing to notice is that is $D(v)$ only measures the risk (for example, death rate) after this person is infected with the epidemic instead of the high probability of being infected. For example, older people may be in higher risk of death when infected with the epidemic, while the probability of being infected is not taken into consideration in risk function $D(v)$.

Next, we will define the budget of the vaccine. Here, the budget of the vaccine at each timestamp t is $B(t)$, where we have $B(t) << m$ and $\sum_t B(t) << m$. Intuitively, we can explain it as we can have at most $B(t)$ people injected with vaccines every day. Here, we only allow the same people (node) to be vaccinated no more than once every day (this can be reasonable in real-life situations) but we allow the vaccine to be administered to the same people (node) every day once (although seems not efficient, this can also be reasonable since we can give those people in high risk of infection, such as doctors and nurses, multiple vaccinations to keep them healthy).

In this problem, what we want to find are the nodes to vaccinate at time t, expressed as $Vaccine(t)$, and $Vaccine(t)$ satisfies $Vaccine(t) < B(t)$. Specifically, we will have $t_0 < t < t_N$ for $Vaccine(t)$.

However, it's worthy to notice that since our vaccination is given over time. During this time, more infected cases can also emerge. Therefore, we may also need to extend the infected line-list to $t > t_0$. Here, considering that we are assuming an IC model in propagation, we will use the expectation of the probability that each node is infected $E[I(t)]$ to calculate the $E[I(t+1)]$. Specifically, we will have the $E[I(t+1)]$ simulated based on $E[I_t]$, which means that given expectation of the line-list at time t as $E[I_t]$, we will have the expectation of the line-list at time $t+1$ as $E[I_{t+1}]$, where f follows the propagation model of IC model.

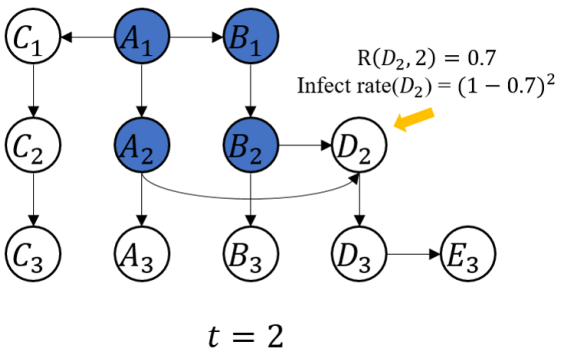

Figure 2: The example of infect rate

Here, we can speculate the $E[V(I(t+1))]$ given $E[V(I(t))]$ with the basic IC model: Given the line-list $I(t_0)$ and temporal network $G(V,E)$, we will convert the temporal network $G(V,E)$ to stable network $H(V_H, E_H)$. Then the vulnerable nodes $InRisk(t)$ are the nodes that have interactions with the $I(t)$ at time t, or $InRisk(t) = \{v|(u,v,t), t = \text{t}, u \in I(t)\}$.

Here for each node v at time t, we consider the set of edges $E(,v) = \{(u,v,t)|v = v, t = t\}$ and $V(E(,v))$ as $V(E(,v)) = \{u|(u,v,t), v = v, t = t\}$. Then the probability that v will get infected at $t+1$ can be intuitively considered as

$$p(v,t) = 1 - ((1 - R(v,t))p)^{\|V(E(,v))\|} \tag{1}$$

And therefore the $E[V(I(t+1))]$ will satisfies

$$E[V(I(t+1))] = E[V(I(t))] + 1 - \sum_v 1 - ((1 - R(v,t))p)^{\|V(E(,v))\|} \tag{2}$$

Here, we will also add the risk function $D(v)$ to the equation, which we can intuitively written as

$$E_{Risk}[V(I(t+1))] = E_{Risk}[V(I(t))] + \sum_v D(v)(1 - ((1 - R(v,t))p)^{\|V(E(,v))\|}) \tag{3}$$

Therefore, with the assumptions above, we can formulate our problem as follows:

Problem 2.1. *Given the temporal network $G(V,E)$ and therefore the stable network $H(V_H, E_H)$, line-list I, immunization pattern function $R(t)$, Risk function $D(v)$, and the vaccine budget $C(t)$, find the best nodes to give vaccine injections $Vaccine(t)$, which satisfies*

$$\arg \min_{Vaccine(t)} E_{Risk}[V(I(t_N))] - E_{Risk}[V(I(t_0))] \tag{4}$$

where

$$E_{Risk}[V(I(t+1))] = E_{Risk}[V(I(t))] + \sum_v D(v)(1 - ((1 - R(v,t))p)^{\|V(E(,v))\|}) \tag{5}$$

and $Vaccine(t)$ satisfies $Vaccine(t) < C(t)$ for any $t_0 < t < t_N$.

3 ALGORITHM

3.1 Convert from Temporal Graph to Stable Graph

First, we will show the pseudo code for converting the temporal graph to stable graph.

Algorithm 1 TemporalToStable

Input: $G(V,E)$
1: **for** $t \in \{t_0, t_1, ..., t_N\}$ **do**
2: **for** $v \in V$ **do**
3: $V_H \leftarrow V_H + v_t$
4: **end for**
5: **for** $e = (u_e, v_e, t_e) \in E$ **do**
6: **if** $t_e == t$ **then**
7: $E_H \leftarrow E_H + (u_t, v_t)$
8: **end if**
9: **end for**
10: **for** $v \in V$ **do**
11: $E_H \leftarrow E_H + (v_{t-1}, v_t)$
12: **end for**
13: **end for**
Output: $H(V_H, E_H)$

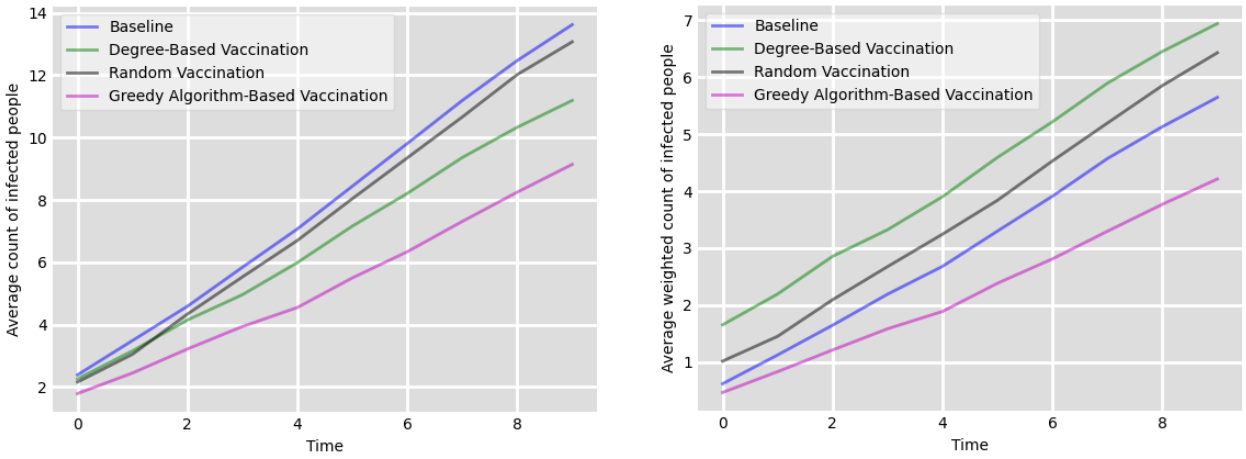

Figure 3: The results of the GreedyVaccine on Karate graph, left is the number of people infected at each time stamp, right is the sum risk of people infection at each stamp. We can see that GreedyVaccine outperforms the other baselines

3.2 Greedy Algorithm

Here, we want to design our algorithm using the greedy algorithm to find the $Vaccine(t)$ at each time t, which means that for each time $t_0 < t < t_N$, we will find the nodes that can minimize $E_{Risk}[V(I(t+1))] - E_{Risk}[V(I(t))]$ greedily. Specifically, we will update the $GreedyValue = D(v)(1 - ((1 - R(v,t))p)^{\|V(E(,v))\|})$ of each node at every timestamp, then pick the priority nodes as the ones with the highest GreedyValue, and "vaccinate" them. We will use $C(t)$ vaccines every day instead of adjusting the number of people vaccinated every day to prepare for another potential breakout.

Here, we want to show that at each timestamp t, by picking the priority nodes as the ones with the highest GreedyValue, and "vaccinate" them, we will achieve a $1-\frac{1}{e}$ guarantee over the optimal performance.

Theorem 3.1. *At each timestamp t, the effect of $Vaccine(t)$ that reduces the expectation of the risk, $\sum_v D(v)(1-((1-R(v,t))p)^{\|V(E(,v))\|})$ is a sub-modular function.*

Proof. For $S \subset T$ in the $Vaccine(t)$, since T distributes more vaccines than S, then $\forall v \in S$, we also have $v \in T$. And for $v \notin S$ but $v \in T$, we will have $D(v)(1 - ((1 - R(v,t))p)^{\|V(E(,v))\|}) \geq 0$, which means that $\sum_v D(v)(1 - ((1 - R(v,t))p)^{\|V(E(,v))\|})$ is a monotone function. Besides, since both $D(v)$ and $(1 - ((1 - R(v,t))p)^{\|V(E(,v))\|})$ are non-negative, we will also have $\sum_v D(v)(1-((1 - R(v,t))p)^{\|V(E(,v))\|})$ will also be a non-negative function.

Next, for $S \subset T$, we also have the relationship that $\sum_{v \in S+e} D(v)(1-((1-R(v,t))p)^{\|V(E(,v))\|}) \leq \sum_{v \in T+e} D(v)(1-((1-R(v,t))p)^{\|V(E(,v))\|})$, which means that the effect of $Vaccine(t)$ has diminishing returns. Therefore, we will that $\sum_v D(v)(1 - ((1 - R(v,t))p)^{\|V(E(,v))\|})$ is a monotone function, which indicates that by using the greedy algorithm, we can guarantee a $(1 - \frac{1}{e})$ performance. □

Then, we will give our VaccineGreedy algorithm as follows:

Algorithm 2 VaccineGreedy

Input: $H(V_H, E_H), I, R(t), D(v), C(t)$
for $t \in \{t_0, t_1, ..., t_N\}$ **do**
  GreedyList = $\emptyset$
  for $v_t \in V_{H,t}$ **do**
    if v_t has not been infected yet **then**
      $GreedyList[v_t] = D(v_t)(1 - ((1 - R(v_t,t))p)^{\|V(E(,v))\|})$
    else v_t has already been infected
      $GreedyList[v_t] = 0$
    end if
  end for
  while $\|Vaccine(t)\| < C(t)$ **do**
    $v_t^* = \arg\max_{v_t}\{GreedyList[v_t]\}$
    $Vaccine(t) = Vaccine(t) \cup v_t^*$
    $GreedyList[v_t^*] = 0$
  end while
end for
Output: $Vaccine(t)$

4 EXPERIMENTS

4.1 Setup

For the experiments, we expect to compare with three baselines: Without vaccines, giving vaccine injections randomly, and giving the vaccine to the nodes with the highest degree. Then, we will run our algorithm with the three baselines to see if our method and algorithm can give better results. The expected results will be:

(1) We can reduce the expected new infection numbers, which means that the newly infected cases $E[V(I(t_N))] - V(I(t_0))$ will be smaller than the numbers in the three baselines.
(2) Our algorithm can run efficiently with a relatively low complexity, which means that our algorithm can successfully

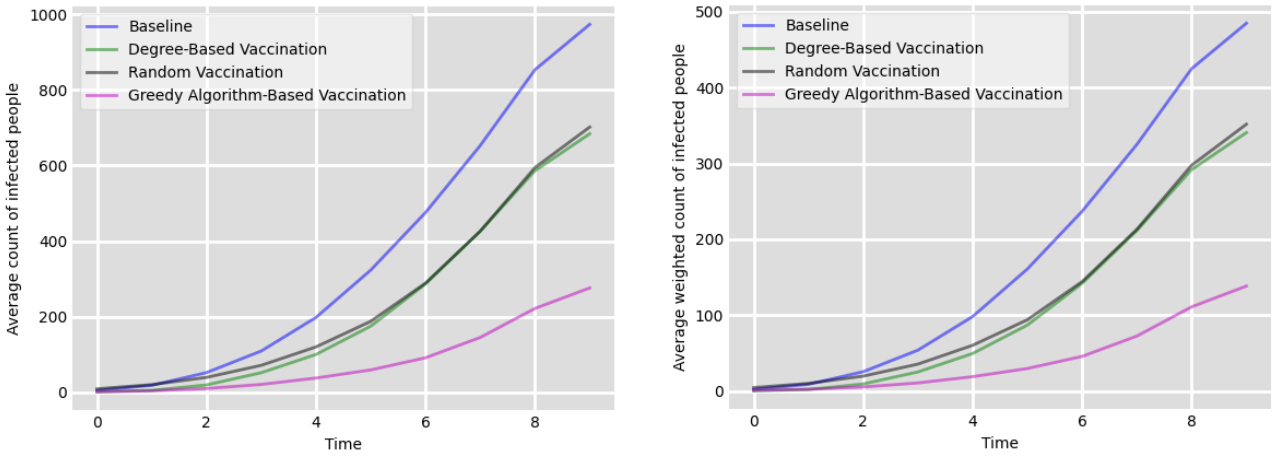

Figure 4: The results of the GreedyVaccine on Oregon graph, left is the number of people infected at each time stamp, right is the sum risk of people infection at each stamp. We can see that GreedyVaccine outperforms the other baselines

run on the large dataset with tens of thousands of nodes and millions of edges.

The outputs of our experiments will be shown with two plots. One will be the raw counts of the Infections and the other will be the weighted counts that weigh the counts by the total amount of danger that is present in the infected nodes.

4.2 Datasets

We performed the experiment on two datasets: KARATE dataset with 34 nodes and 156 edges [9], and OREGON dataset with 10670 nodes and 22002 links [4]. All datasets are based on IC model. The details of the dataset are shown in Table 1.

Table 1: Datasets

Dataset	Nodes(m)	Edges(n)
KARATE	34	156
OREGON	10670	22002

Specifically, both two datasets are initially the stable graphs. Therefore, we will first convert the graph from stable graph to temporal graph by selecting the edges in the original graph with $p = 0.2$ at each timestamp. Then we will get a temporal graph as the input, which allows us perform our experiments on temporal graph.

Besides, without loss of generality, we will set the risk function $R(v)$ as uniform distributed random numbers between 0 to 1, and set the R(t) as a linear decrease function like

$$R(v, t) = 1 - 0.2 \times (t - t_0) \tag{6}$$

where t_0 is the date that node v was immunized. Therefore, at the date that node v is immunized, the $R(v, t_0) = 1$. Then $R(v, t_0 + 1) = 0.8$ after one day, $R(v, t_0 + 2) = 0.6$ after two days, ... until $R(v, t_0 + 5) = 0$ after 5 days and later.

4.3 Results

Here, we will show our experiment on both the Karate graph and the Oregon graph. Although both of the graphs are stable graphs initially, we use the method described in Section 4.2 to convert the graph from stable graph to temporal graph by selecting the edges in the original graph with $p = 0.2$ at each timestamp, and then start our algorithms on the temporal graph. Specifically, we will then convert the temporal graph to stable graph using the algorithm described in Algorithm 3.1.

4.3.1 Karate Graph. First, we performed our experiment on the Karate graph shown in Figure 3. The sub-figure shown on the left is the number of the people get infected at each timestamp, and the sub-figure shown on the right is the sum of the risk of the people that get infected at each timestamp. Here, we are setting our Budget of the vaccines as 5 total, which will be distributed on day 1,3,5,7,9. Form the figures, we can see that our Greedy Algorithm Based Vaccination is always performing better than the Baseline (no vaccine), random vaccination baseline, and the Degree-based Vaccination, which indicates that our VaccineGreedy outperforms the other vaccine distribution methods.

4.3.2 Oregon Graph. Running the same experiment on the Oregon graphs showed a larger difference between the vaccination techniques. With the same Budget of the vaccines as the Karate graph, we see in Figure 4 that degree-based and random vaccinations both outperformed the baseline (with no vaccine), but the greedy algorithm outperformed all other baselines by a large margin. Even when accounting for the overall risk, we observed a much lower level of infections in the greedy algorithm. With the larger graphs, runtime became far more noticeable. Here, the greedy algorithm did not add an extensive amount of computation in comparison to the others, taking just under thirty seconds longer than vaccinating randomly with a graph of over 10,000 nodes.

5 CONCLUSION

After observing the different graphs, we can generally conclude that the greedy algorithm improves on all three baselines. This is especially seen on the larger graphs, as the greedy algorithm continually updates at each time step to control the flow of the epidemic and slow it down as fast as possible. This leads to a best case of the greedy algorithm lowering the infection rate by a margin of up to 50% compared to the baseline code.

5.1 Further Work

As we continue experimenting on different types of graphs, we can improve on the greedy algorithm in several ways:

(1) We could also account for the fact that persons that are at high risk may not necessarily infect as many people as someone that is at a low risk. This may be due to earlier hospitalization or even death of the high-risk individuals. It would be a matter of accounting for a 'death' and a 'recovered' status in future experiments.
(2) Finally, we can test a changing graph, as with the inclusion of laws regarding how high-risk locations, such as bars as restaurants, the greedy algorithm can take into account different avenues that the epidemic can have to spread

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