InfecTracer: Approximate Nearest Neighbors Retrieval of GPS Location Traces to Retrieve Susceptible Cases

Chandan Biswas
Indian Statistical Institute, Kolkata
chandanbiswas08_r@isical.ac.in

Debasis Ganguly
IBM Research, Dublin, Ireland
debasis.ganguly1@ie.ibm.com

1 INTRODUCTION

Epidemics, such as the present Covid-19 pandemic, usually spread at a rapid rate. Standard models, e.g., the SIR model [1], have stressed on the importance of finding the susceptible cases to flatten the growth rate of the spread of infection as early as possible. In the present scientific world, location traces in the form of GPS coordinates are logged by mobile device manufacturing and their operating systems developing companies, such as Apple, Samsung, Google etc. However, due to the sensitive nature of this data, it is usually not shared with other organizations, mainly to protect individual privacy. However, in disaster situations, such as epidemics, data in the form of location traces of a community of people can potentially be helpful to proactively locate susceptible people from the community and enforce quarantine on them as early as possible.

Since procuring such data for the purpose of restricted use (possibly by government organizations) is difficult (time-consuming) due to the sensitive nature of the data, a strong case needs to be made that how could such data be useful in disaster situations. The aim of this article is to demonstrate a proof-of-the-concept that with the availability of massive amounts of real check-in data, it is feasible to develop a scalable system that is both effective (in terms of identifying the susceptible people) and efficient (in terms of the time taken to do so). We believe that this proof-of-the-concept will encourage sharing (with restricted use) of such sensitive data in order to help mitigate disaster situations.

In this article, we describe a software resource to efficiently (consuming a small run-time) locate a set of susceptible persons given a global database of user check-ins and a set of infected people. Specifically, we describe a system, named InfecTracer, that seeks to find out cases of close proximity of a person with another infected person. Since a naive approach of pairwise checking on billions of check-in records is clearly not scalable, we employ an indexing-based solution (similar in principle to what is used in standard web search systems). First, we index billions of check-in records (analogous to indexing web pages). Second, a number of records in this index is marked to be infected (due to available information of reported infection). Third, given the location trace of each infected person (analogous to a keyword-based query executed on a web search system), we find out a list of susceptible people (analogous to the 10 blue links found by Google in response to a query). Merging the results for each infected person in a community thus gives a list of all susceptible people for whom appropriate measures can then be undertaken.

As a different use-case, it is also possible for an individual end-user to formulate a query (comprised of a set of his personal check-in records) and then find out if he had come in close contact (in terms of the space and time of his own check-ins) with another infected person. This individual can then impose appropriate measures on himself, such as self-isolation or visiting a GP.

2 APPROXIMATE RETRIEVAL APPROACH

The objective of the retrieval approach is then to find the set of ghost-users given a real user, because as per the ground-truth of the simulated data these (pseudo) users came in close contact with a known infected user.

In a real life situation, one has a massive database of user check-ins of a population out of which it is known that a number of persons are infected. The goal is to rapidly find the candidate set of people who came in close contact with the infected. However, a brute force search to locate the candidates would take a huge time (since it is a quadratic time complexity operation).

In our approach, we undertake an approximate nearest neighbor search approach to solve the problem. The two main research questions in this setup are:

1. How does efficiency (run-time) vary with the fraction of people infected, e.g., if 10% of a population gets infected, is this still a feasible solution?

2. What is the effectiveness of the approximate nearest neighbor search? Since it is an approximate method, it can make mistakes. Is there a satisfactory bound on the error rate?

2.1 Extraction of the data

The geo-locations of users (which in real life can be obtained from GPS locations of smart phones) are then represented as 3-dimensional points (2 space dimensions corresponding to the location on the Earth’s surface and 1-time dimension measured in epoch seconds). The path traced in this 3 dimensional space-time corresponds to the activity phase of a single user. The idea is shown in

[Figure 1: A simple visualization of a 2d space-time world]
Figure 1 shows a simple visualization of a 2d space-time world (the space-time in our case is 3d). Each person is shown as a path (curve) in this space-time, i.e. each person changing his position (x coordinate) with respect to time (which is ever increasing meaning that the curves monotonically increase with respect to the x coordinate, or in other words the curves never loop down). The figure shows two intersections in this graph one of which is an intersection of a healthy person with an infected one (leaving him at a high risk of infection). The job of the program is to automatically find all such possible intersections given a massive list of such person location traces (curves in the space-time) and a given list of infected people (query curves like the one shown with red in the figure).

If you want to generate your own data (using a different simulation approach then read the Appendix section). Else to conduct experiments on the provided dataset, simply execute
gunzip data/*
wc -l data/data.txt
wc -l data/data.txt.ext
You should see the following output
266909 data/data.txt
1601454 data/data.txt.ext

2.2 Indexing the Data
The indexing step enables a very fast retrieval of susceptible cases. To perform the indexing step you then need to execute
python index_checkins.py -d data/data.txt.ext
   -i simusers.idx
where you specify the data file (comprising the user-id, locations, time-offsets) and the index file to save the data.

2.3 Retrieval of Candidate Infected Persons
The next step is to retrieve the susceptible cases. The program simulates the case that a fraction of the population (whose data exists in the index already) has been infected. The ‘retrieval’ program formulates and executes a query for each of these infected people and reports a list of 3 most susceptible persons that came in close contact (in terms of space and time) with an infected person. You simply need to execute
python retrieve_susceptibles.py -d data/data.txt.ext
   -i simusers.idx -s 0.01 -n 266909
where you specify the data file (to simulate infected people), the index file (to retrieve susceptible people) and the fraction infected (in the example set to 0.01 or 1%). The last argument is the number of real users in the data (this is useful for the program to compute the ground-truth information and compute recall).

The program prints out output in the following format (the search time is reported in seconds):
Reading data file...
Loading user ids...
Loading user data...
Number of users infected: 2669
Search time = 0.055400
Avg. Recall = 0.9332

The main usefulness of the program is the lightning fast search through millions of check-in locations identifying the susceptible people in real quick time. Exact brute force distance computation involves scanning through billions of check-in locations for each infected person (a new query), which is not scalable. Pandemics can be better fought if susceptible people to catch an infection are quickly identified and quarantined. We believe that this tool can contribute to such a cause. We also observe that the recall achieved is satisfactory.

3 SIMULATION EXPERIMENTS WITH CHECK-IN DATA
To reproduce the simulation results with the code provided in the repository, download the Foursquare2 global check-in data in the project folder. After the files are downloaded execute the script ‘prepdata.sh’ to create the data file (named ‘data.txt’) by following command
sh prepdata.sh

3.1 Generating Simulated User Overlap Data
The real FourSquare check-in data is not directly applicable for our study because it is much less likely that two Foursquare users would check-in to the same location (a point-of-interest, e.g. a museum/restaurant) at near about the same time. However, to model an infectious disease spread, we need to have users that came in close contact with each other (in terms of both space and time). We undertake a simple simulation model to generate pseudo-user interactions (likely contacts). First, we filter the ‘data.txt’ file to retain only one check-in per user. This makes the simulation algorithm easier to manage. Next, for each user ‘U’ (having a unique id), we generate a set of mutually exclusive ‘pseudo-users’ or ‘ghost-users’, which comprises the ground-truth information for each user. Note that since all the original/real user check-ins were sufficiently apart

2https://drive.google.com/file/d/0BwrgZ-IdrTetZ0I30ZER2ejl3VX/view
InfecTracer: Approximate Nearest Neighbors Retrieval of GPS Location Traces to Retrieve Susceptible Cases

in space-time coordinates, it is likely that the neighbourhood of a user comprised of the ghost-user check-ins are also far apart (in which case one can rely with sufficient confidence on the simulated ground-truth data). For each user ‘U’ we generate $p+n$ number of ghost-user in $\delta$ neighbourhood, out of them ‘$p$’ number of ghost-users are belong to $\epsilon$ neighbourhood, if user U is positively infected person then these ‘$p$’ ghost-users will be considered as vulnerable person, whom we need to identify, and remaining ‘$n$’ people will be considered as non-suspicious persons as they are in safe distance from the infected person ‘U’. In Figure 2 we presented a visualization of simulated ‘ghost-users’ corresponding to a real infected user (red person in the figure).

To generate the simulated data, simply execute

```
sh addusers.sh data.txt
```

### 3.2 Preliminary Results

To address the correctness of our algorithm we employ ‘Recall’ as evaluation metric because the task of finding susceptible users is a recall-oriented task (false positives are acceptable but not the false negatives). While the parameter $\epsilon$ controls the number of people to whom the disease spreads from a single person, the parameter $\delta$ controls the number of false positives (intentionally introduced to see if the algorithm can filter out the true positives from the false ones). In Table 1, we present some results for our initial sets of experiments.

**Table 1: Some preliminary results with variations in the number of infected persons (total number of persons in the dataset being 266909). The number of pseudo-susceptible users (the ground-truth) was set to 5 in the simulations.**

| #Infected (%) | $\epsilon$ | $\delta$ | #Retrieved | Time(s) | Recall |
|---------------|------------|----------|------------|---------|--------|
| 2669 (1%)     | 1          | 2        | 5          | 0.0774  | 0.9036 |
| 5338 (2%)     | 1          | 2        | 5          | 0.1569  | 0.9016 |
| 8007 (3%)     | 1          | 2        | 5          | 0.2559  | 0.9010 |
| 10676 (4%)    | 1          | 2        | 5          | 0.3087  | 0.9052 |

**REFERENCES**

[1] Katherine Turner. Introduction to infectious disease modelling. Sexually transmitted infections, 87, 11 2010.