Spatial Explicit Model to Visualize the Spread of Epidemic Disease in a Network

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Abstract. The development of the visualization tool of any infectious spreading disease requires an elegant graphical user interface which can show the result of simulation at every time steps. The goal of this work is to provide an effective way to visualize epidemic diseases, e.g., flu, cholera, influenza, etc. in a network for the decision makers to determine the level of epidemic threats in any vulnerable zones. The Gravity and Susceptible, Infected and Recovered (SIR) epidemic models are used to draw a network on the map and simulate the disease status. Thus the results obtained are visualized to give a clear picture of spreading behavior of a disease. This visualization tool provides an understanding for the epidemical analysis of diseases through graphs and network statistics.

Key words: Susceptible Infected Recovered, gravity model, visualization tools, network

1 Introduction

The epidemic of any infectious disease can be better understood by decision makers if they are provided with a proper tool to visualize this. If we consider an example for a

new outbreak of infectious disease in a particular geographical region it is always crucial for a decision maker to come out with epidemic scenarios. In fact, visualization of the vulnerable zone plays an important role for understanding populations from serious epidemic hazards. As a result of simulation of diseases in a network, early visualization of such threats can be obtained. Hence, a well-developed decision support system with simulations to identify the vulnerable zone has become a common area of interest in this field. The growing interest in simulation modeling techniquea has been used in the context of visualizing epidemic diseases. A review of some existing epidemic disease visualization tools using different technologies follows. GLEAMviz [1] visualization software has been made to visualize epidemic levels on a worldwide scale. This project uses the multi scale mobility model from the airport listed in International Air Transport Associations (IATA) database for the disease transmission route. Geographical Information Systems (GIS) and electronic disease surveillance databases [2] are extensively used to visualize the impact of epidemics of geographical regions. Furthermore, social network analysis [3] is also used for epidemic simulations for disease transmission in human beings. Although the above mentioned technologies provide epidemic visualization they need huge data sets about diseases and are not flexible to be applied in different emerging contagious diseases because they rely on epidemic network data sets [4]. Hence a decision support system that can provide policy makers with the ability to create epidemic scenarios in absence of disease routes for an emerging contagious disease seems to be essential. To address this problem an epidemic visualization system with simulation is proposed. The purpose of this tool is to visualize epidemic disease networks through simulation results. The specific goals are listed as follows:

- To use gravity model for epidemic disease network formation;
- To use SIR for epidemic modeling; and
- To visualize epidemic scenarios on a map.

The epidemic disease network is formed by using the gravity model. This model provides the rate of disease transmission across distance. The strength of disease transmission is decreased with the increase in distance Zipf in the 1940s [5] has provided a theoretical motivation for movement between cities 1 and 2 being governed by a $\frac{P_1 P_2}{d}$ relationship, where P is the respective city population and d is separation distance. The strength of the movement is affected by the size of the population and their separations. Hence, in our tool we used distance as an important factor to construct the network. The closer the nodes the denser is the network. The visualization of epidemic diseases for deci-

sion support system using Susceptible(S), Infected(I) and Recovered(R) (SIR) epidemic model is one of the main components of this tool. It is a good modeling tool for many infectious disease like small pox[6], influenza and measles, etc.; where every population can be categorized into three different stages[7].It has three stages and in a population which are prone to disease are in Susceptible stage. Those who carry the disease and transmit the disease to others are in Infected stage and those who are immune or recovered from the disease and those removed from the population are in Recovered stage. In the tool the three stages of the model are depicted in the nodes which in this case are cities on the map. This tool is intended for general purpose epidemic disease visualization to decision makers at different disease transmission rates, epidemic distances,simulation timesteps and infection probabilities. The results thus obtained are visualized on a map. The system uses two dimensional coordinates of cities in the map to draw a network underlying the principle of gravity model[8].The system is very flexible to change the network as per the necessity of decision makers, whereas previously developed technologies requires data as a fixed source for the network formation. Section 2 introduces network topology. Section 3 is about the SIR epidemic model, Section 4 provides the system description, Section 5 describes the implementation of the system, Section 6 describes simulation and analysis, Section 7 is about user study and evaluation, Section 8 discusses about the limitations of the system and Section 9 draws conclusions.

2 Network Topology

The strength of interconnection of two nodes is determined by how closely they are located. The affiliation between the cities is the function of the distance and thus the network is built upon physical proximity between them. The force of epidemics decays with the increase in distance [9].The spread of any infectious disease can be depicted by human travel pattern between two cities. An analogy with the physics law, it is expected that disease transmission increases with decrease in geographical distance [10]. The generic model for the gravity is described as:

$$F_{i,j} = G\frac{M_i M_j}{d_{i,j}^2}$$

where G is the gravitational constant: M is the mass of the bodies: i,j and d is the distance between them. In the context of this work the force of an epidemic is taken as the link formation between the two nodes, i.e., two nodes will construct the link if

they fall into the range of the epidemic distance. This means connectivity completely depends upon closeness of the cities. Fig. 1 visualizes the network of cities with two different epidemic radius and its degree distribution.

(a)   (b)
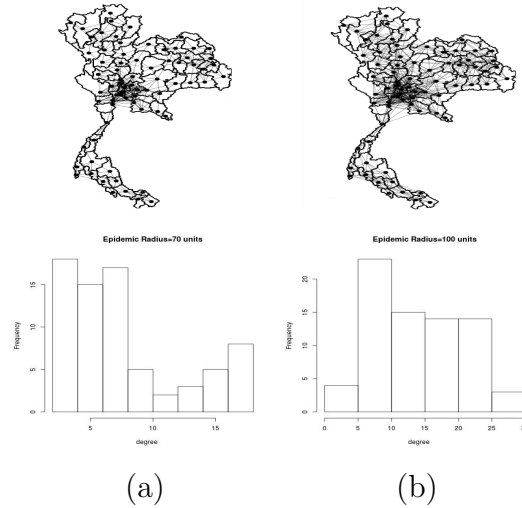
Fig. 1. Example of epidemic network . (a) Networks with 70 units epidemic radius. (b) Networks with 100 units epidemic radius.

3 Epidemic Model

The core of the system is based upon epidemiological states of the cities. Hence the connection among different cities is a vital part of network formation. The transportation network is also an important role for the disease carrier[11].Every connected city is susceptible to the disease. Those cities which are already infected will either stay infected or will change the status to be recovered. The spreading process of disease can be understood as: at each time step the susceptible nodes becomes infected at a rate of β; the infected nodes will be recovered at a rate of γ. The transmission of the disease in the nodes is $S \xrightarrow{\beta} I \xrightarrow{\gamma} R$. SIR model is represented by the differential equation as [12][13]

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

Each state is fraction of population at a particular timestamp. The population is one of the stages at a particular time. This model is particularly meant for fast spreading disease and for a constant population. Fig. 2 visualizes the mode of spread of disease stages.

Fig. 2. SIR epidemic model.

The overall composition of the cities in a map will be of three different kinds of categories: susceptible cities, infected cities and recovered or removed cities.

4 System Description

4.1 Methodology

The system is developed by integrating the Geographical Information System (GIS) shape files for reading the map, graph theory for analyzing the network and SIR epidemic model for the simulation. The input of the system is epidemic radius, disease transmission rate , simulation timestep and infection period. The computation of the network data is done by the open source boost library[4] and for the visualization open source 2D Cairo graphics[5] is used. The system first reads the GPS position of the cities and locates on a map. Then after getting the input for the epidemic radius it draws the network on top of it. The user can then select any city on a map as an epidemic outbreak and provide the transmission probability[14] and simulation timestep and can see the epidemic visualization on a map.

4.2 Simulation Model

In the SIR epidemic model the cities on the map are classified according to their states: susceptible(S), infected(I) and recovered(R).The epidemic spreads through the links between the cities. The spreading process of disease can be understood as: At time (t=0) the node infects its neighboring susceptible nodes with the random probability(p) less than the transmission probability(tp). At time (t=1) the neighbor node gets infection and at time (t=2) the initial node which has transmitted the disease passes the infectious period and becomes immune or recovered in the system. The overall scenario can be viewed in the figure below:

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[4] http://www.boost.org/
[5] http://www.cairographics.org/

At time = 0   At time = 1   At time = 2

(a)   (b)   (c)

Fig. 3. S,I and R are the Susceptible, Infected and Recovered nodes of the disease network. (a) Infected nodes transmits the disease. (b) Susceptible nodes receive infection. (c) Recovered nodes recover from infection.

Pseudocode for the infection and recovered status

```
program Infective and Recovered nodes (Output)
  {Get the transmission probablity,infectious period from a user
   For every nodes which is infected state:=1};
   var
    nodes: 0..maxNodes;
    statusVector;
    timeVector;
    transmissionProbablity,randomProbablity: Real;
   begin
    nodes := 0;
    statusVector:= 0;
    timeVector  := 0;
   repeat
    randomProbablity:= rand() / (RAND_MAX+1))*-1;
    if(randomProbablity<transmissionProbablity)
     {
       statusVector:=1; //infects the randomly selected outdegree nodes
       timeVector :=timeVector+1;
     }
```
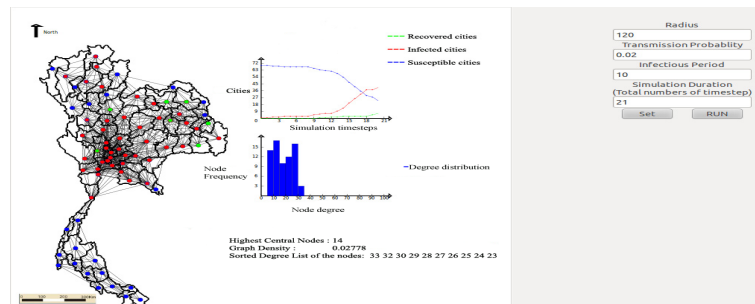
```
   if(timeVector>infectiousPeriod &&  statusVector==1)
    {
       statusVector:=2; //Nodes will be recovered or removed
    }
   nodes:= nodes+1;
   until nodes = maxNodes;
end.
```

  The model works undertaking two major widely used components in epidemiology
called as infectious period to produce the symptoms of disease in the nodes and trans-
mission probability to transfer the disease from infected to the susceptible nodes. Thus
the epidemic visualization system, that enhanced by this model, will have sufficient
information to simulate the disease and create epidemic scenario in a disease network.

5 Implementation

The proposed system is made which allows the user to enter the epidemic radius,
transmission probability, infectious period of the disease and simulation time steps.
The network is then drawn by calculating the Euclidean distance between the pairs
of the cities. From,the whole cities user can select any of them as an outbreak of the
epidemic and run the simulations and the result is dynamically visualized on the map
for every timestep. At the same time the user can also see the graph density, degree
distribution and epidemic curves in the interface. Figure below is the User interface of
the prototype.

Fig. 4. Screenshot of the epidemic disease visualization of the proposed system.

6 Simulations and Analysis

Fig. 5. SIR Simulation result for 60 unit epidemic radius

In figure(a), Susceptible curve decreases rapidly with the increase in transmission probability, with the increase in simulation timesteps the curve starts to decrease and after some period the curve flattens out. In figure(b), Infected curve increases rapidly with the increase in transmission probability and reaches the peak of the infection, as the number of simulation timeteps increases the infection curve also falls down rapidly. It starts to decrease and finally the curve reaches to minimum 0 and flattens out where no infection is seen. Similarly in figure(c) the recovery node is only seen after the infectious period of the outbreak in this case the infectious period of the disease is four days. It is observed from the figure(c) that the recovery curve also increases rapidly with the increase in transmission probability and after some period the curve reaches to the peak and becomes constant.

7 User Study and Evaluation

Users of this prototype system are only few members including the developer and we have not verified results yet. However we think this prototype will be able to create the epidemic scenarios for decision makers without explicitly requiring the network construction data. Apart from the user study the evaluation of this prototype has been

done with the existing visualization tool Epigrass[6] and Gleamviz[7]. The results of the evaluation follows:

1. **Ability to visualize SIR epidemic disease:** The developed prototype fully supports this feature by asking the user to set up their parameters in the tools. GleamViz and Epigrass can also support this feature moreover they can be modeled for all types of epidemic disease.

2. **Ability to visualize the disease in a local scale:** The developed prototype and Epigrass fully supports this feature by prompting the user to load their specific GIS shape files and to run the simulations whereas GleamViz provides the global level epidemic visualization.

3. **Ability to create epidemic scenarios:** All of these tools support this feature.

4. **Ability to create the disease network with the Euclidean distance between the nodes:** This is an interesting feature of the prototype where the network is drawn underlying straight line distance between the two nodes. Due to this reason the prototype does not require the network construction data else it only needs the epidemic radius from the user. Whereas Gleamviz requires multi scale mobility model of the International Air Transport Association (IATA) database for the network formation and Epigrass uses the transportation and passenger flow data for the network formation. To the best of our knowledge in the absence of the network data in GleamViz and Epigrass both cannot simulate and visualize the epidemic disease.

7.1 Comparision of the prototype with the existing visualization tools

Table 1 provides a comparision of the prototype with the GLEAMViz and EpiGrass visualization tools.

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[6] http://sourceforge.net/projects/epigrass/
[7] http://www.gleamviz.org/

Table 1.

Criteria	Prototype	GLEAMviz	EpiGrass
Visualization of spatial data	Yes	Yes	Yes
Visualization of models	Yes	Yes	Yes
Visualization of simulated results	Yes	Yes	Yes
Types of epidemic disease	Contagious acute infectious disease	Every kind of epidemic disease	Every kind of epidemic disease
Data for disease network formation	No network data requirement	IATA databases	Transportation and passenger flow data
Software modularity and extensibility	Yes	Client server based online tool	Yes

The strength of the prototype is to draw a network for the disease simulation in the absence of the network data which is not present in either of the two systems. The prototype calculates the Euclidean distance between the nodes within the epidemic radius and draws the network on the map. Currently the prototype is only applicable for the visualization of acute infectious disease which has a very short exposed period. Table 1 compares the important feature of the popular epidemic visualization tools with the prototype.

8 Limitations

The prototype is developed using SIR epidemic model. This model also has shortcomings because it does not consider the immigrants and emmigrants of the population and assumes the total population as constant [15]. In the prototype we have cities and assume the population is well mixed and the same in all parts of the country which is completely impossible in a real situation. In the developed prototype the latent period for acquisition of infection and the start of infectiousness has not been addressed due to which the chronic infectious disease cannot be modeled. The diseases with latent periods that can be modeled using the extensible SIR model with latent period called SEIR epidemic model cannot be used by this prototype. However the prototype can be useful for the decision makers to observe and create the scenarios for the acute infectious disease having a very short exposed period like influenza, chicken pox, distemper.

etc. In the current version of the system we can only address the SIR model but in our upcoming version of the system we will also be able to provide the flexiblility to change the infectious disease model like SEIR, MSIR, SIS and SIQR to visualize the epidemic spread of the disease.

9 Conclusion and Future Work

This research proposes the visualization of the epidemic disease using a simple epidemic and gravitational model. To accomplish this a prototype is developed without explicitly requiring predefined network construction data. The epidemic spread as a result of simulation is visualized in the map. The usage of graph theory has become very useful to visualize the epidemic network, degree distribution and finding the central nodes in the network. The developed prototype can visualize the states of every node at the given time stamp. This tool is very flexible for visualizing SIR modeled infectious disease for a given transmission rate and epidemic radius. Currently, this prototype cannot address all the epidemic diseases. In the current context we also lack the real epidemic data to test with our system generated results. Due to this reason we cannot ensure that the prototype can be very accurate with its simulated results. However in the upcoming version the prototype will come out with tested real data and also be capable of visualization for other existing epidemic models. Therefore the proposed visualization approach is enhanced in the further development of the tool.

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