Statistical model checker for Epidemics Progression on Complex Network

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A Thesis Submitted to
Indian Institute of Technology Hyderabad
In Partial Fulfillment of the Requirements for
The Degree of Master of Technology

Under the guidance of
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June 2016

Declaration

I, Ravi Prakash, declare that this thesis titled, 'Statistical model checking for Epidemics Progression on Complex Network' and the work presented in it are my own. I confirm that this work was done wholly or mainly while in candidature for a thesis research.Any part of this thesis has previously been submitted for a degree or any other qualification at this University or any other institution, this has been clearly stated.I have consulted the published work of others, this is always clearly attributed.I have quoted from the work of others, the source is always given. With the exception of such quotations, this thesis is entirely my own work.I have acknowledged all main sources of help.Where the thesis is based on work done by myself jointly with others, I have made clear exactly what was done by others and what I have contributed myself.

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This Thesis entitled 'Statistical model checking for Epidemics Progression on Complex Network' by Ravi Prakash is approved for the degree of Master of Technology from IIT Hyderabad.

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Acknowledgements

I would like to express my deepest appreciation to all those who provided me the possibility to complete my thesis. A special gratitude gratitude to my thesis adviser Dr. M V Panduranga Rao for his constant encouragement, patience and immense knowledge. Without his guidance and persistent help, this dissertation would not have been possible.I thank the Almighty, my family and friends for their support and constant encouragement.

Dedication

This work is dedicated to my parents and all of my friends without whom none of my success would be possible.

Abstract

In this thesis uses the susceptible-infected-recovered (SIR) model to show how the epidemic spread over the complex network , which can be used for the early prediction for epidemic spread,so we can determine the proper cause of the action ..The propagation of epidemics on a small-world network with and without immunization has been shown.Immunization helps to control the outbreaks of the epidemics.Our approach is to using the modeling the SIR model with Discrete event simulation which is one way to simulate the complex systems, which allows us to ask the interesting queries regarding how the epidemics spread over the time,at what time will be the peak time for spread and many more. In this work we uses the one of java lib. i.e. Graph Stream for our purpose to generate the small world network and we have also uses MultiVesta tool which is a Statical model checker tool.This work can be use in application of modeling the human disease as well as modeling the computer malware because it has similarity with spreading the human disease as the computer viruses.

Contents

Chapter 1

Introduction and Motivation

Infectious disease has been a major threat to human societies for a long time. According to world health report 2007 each year human influenza rapidly spread all over the world within the week or months and causes 5 million cases of illness and about 250,000 to 500,000 deaths. Disease can cause infections in all age groups its depends on the type of disease. Even though the exact number of infections, illness and death is unpredictable.Each epidemic has a different way of spreading depending on the type of disease and its factors like latent period of disease and its infectiousness. Spreading of disease is also depending on the structure of the network i.e. how the individuals are connected and key spreader of disease in the network. If early detection of disease spreading is possible then we can determine the proper cause of the disease spreading and can take necessary actions to reduce the impact of disease threats, which is possible by the Epidemics models.

We modeled the epidemic model with Discrete event simulation and integrated with Multivesta which is able to answer the query like:

- What is the number of infected people at a particular time?
- What is probability that a person B will infect after person A being infected?
- What is the probability that at least one among nodes $v_1, v_2, \ldots, v_k$ will be infected between times t_1 and t_2?
- What is the probability that node v_1 will be infected within t time units of the node v_2 getting infected?

- What is the probability that the total number of nodes to get infected under vaccination scheme A is at least k times the number under vaccination scheme B?
- What is the probability that all nodes will recover before time t? [IMP: Expectation version: What is the expected time before which all nodes will recover?]
- What is the probability that a given node is infected if $r\%$ of its neighbours are vaccinated?
- Compare the expected number of nodes that will eventually get infected if a given vaccination scheme is introduced at times t_1, t_2, t_3 etc.

Social structure is most important to understand the spread of infectious diseases in the network i.e. connections of individuals also called as contact network. Connections are often modelled by a random graph or random network. In this type of networks nodes represents the individuals and edges represents the connections between the nodes(individuals).Dynamics of the disease spreading over the network is depends on the factor called degree distribution of nodes, degree distribution means individuals is connected with how many other individuals. We have use Watts and Strogatz random model for our analysis. This model have a special properties like it have low clustering coefficient but one node can reach to another node in less steps which makes more real to structure than others network model.

It has been shown that most empirical networks display heavy-tailed degree distributions, so it conclude that in a large population there is a small proportion of individuals who have many links, thus imposing a threat of infecting more individuals.

In epidemiology an important concept is basic reproduction number sometimes also called basic reproductive ratio, which is donated by R_0, it represents the severity of disease spread. R_0 is having range in between the 0 and 1 to represent the severity of infection. If $R_0 \leq 1$ then infection will die out in the long run but when R_0¿1 epidemic will occur in population.

Any form of vaccination is able to reduce the reproduction number in order to prevent the disease from spreading, so it possible when early detection is possible.We have uses the various strategies to vaccinate the people base on the centrality of network such as degree centrality,betweeness centrality and closeness centrality. we have also comparing the results with these strategies including no vaccination .

In this thesis uses compartmental SIR epidemic model in which people are divided into the three group i.e susceptible, infected and recovered . we modeled this epidemic model with the Discrete Event simulation in which system states are changes at a fixed time

steps, and after the we have integrated with the MultiVesta which is a Statical model checker tool for Discrete event simulation.

We will discuss the Preliminaries and previous work in the chapter-2 which include discussion about the epidemic model, discrete event simulation, random network models and overview of Multivesta.In chapter-3 will discuss about the implementation details of our work and chapter-4 will discuss about the Results and conclusion of our work.

Chapter 2

Preliminaries and previous work

In this section we will go through the discussion about the epidemic models , Network analysis, Random network models,Discrete Event Simulation and overview of SMC and Mutivesta.

2.1 Network Analysis

When we are dealing with large networks that exhibit apparently random structure, Analysis of structure of network gives idea about what we are dealing with. We will discuss about the several metrics of Network analysis.

2.1.1 Clustering Coefficient

Clustering coefficient is used to measure the degree to which vertices in the network tends to cluster to each others. Clustering coefficient means at what extend neighbors of a vertex is connected to each other, it can be use to spread the information over the social network.

There are two version of measuring clustering coefficient one is local and other is local view. Local view gives an indication of the embeddedness of single nodes whereas global view is designed to give an overall indication of the clustering in the network.

2.1.2 Centrality

Centrality is used to measure which vertices is the more important than others node. Importance of vertex is depends on what kind of network we are dealing, like dealing

with network of persons ,so in this scenario centrality will give us influencing person in the network. Finding out which one is the most central node is important because :

1. It can help in spreading the information in faster way on the network.
2. It can help in stopping the epidemics.
3. It can help in protecting the network from breaking.

There are some concepts of centrality,

1. Degree Centrality
2. Betweenness Centrality
3. Closeness Centrality

2.1.3 Degree Centrality

In Degree Centrality,this strategies consider the node which having the higher degree will be considered as most central node on the Network .

2.1.4 Betweenness Centrality

Betweenness is a centrality measure of a vertex within a network. Betweenness centrality states that the number of times a node acts as a bridge along the shortest path between two other nodes. Betweenness of a node N in a network G=(N,E) G=(N,E) with N nodes can be computed as,

First for each pair of nodes(s,t), computes the shortest paths between them.Second determine the what fraction of shortest path pass through the node for which we want to calculate the centrality, now sum of the all this pair of nodes(s,t).

We can represents the betweeness centrality in more compact way as:

$$B_c(n)=\sum_{s\neq n\neq t} \sigma_{s,t}(n)/\sigma_{s,t}$$

where $\sigma_{s,t}$ is the total number of shortest paths from node s to node t and $\sigma_{s,t}$(n) is the number of those paths that pass through n .

2.1.5 Closeness Centrality

2.2 Random Network

In this section we will discuss briefly about the random graph or random network for more details can refer book [1].

Random network is a simple connected graph in which pairs of vertices are connected by the some probability. Random Network are now considered as important concept because random network or graph allow us to model the many real word scenario such as construction of contact network of human relations which provides the platform to analysis the different parameter like which individual is more influencing in the network.

2.2.1 Erdos-Renyi Random Graph Model

E-R model is used for generating the network in which edges are set between nodes with equal probabilities. In this model start with n isolated nodes and connect the node pairs with probability p , all node have aprox same number of links.

2.2.2 Small-World Network

A small-world network is defined as a network where the typical distance between two randomly chosen nodes is separated with 6 degree (in terms of average path). This concept is also called as the 6 degree separation which is given by the Stanley Milgram in 1967.Watts-Strogatz gives a small world model to construct the random network.Watts-Strogatz model has been for work as graph.

Algorithm for construction of Watts and Strogatz network model is [1]:
Consider a set of n vertices $v_1, v_2, ..., v_n$ and an (even) number k. In order to ensure that the graph will have relatively few edges (i.e., it is sparse),choose n and k such that $n \gg$ k $\gg \ln(n) \gg 1$.

1. Order the n vertices into a ring and connect each vertex to its first $k/2$ left-hand (clockwise) neighbors, and to its $k/2$ right-hand (counterclockwise) neighbors,leading to graph G .

2. With probability p, replace each edgeu, v with an edge u, w where w is a randomly chosen vertex from $V(G)$ other than u, and such that u, w is not already contained in edge set of (the modified) G.

The resulting graph is called a Watts-Strogatz random graph or simply called as the WS graph). We also refer to a $WS(n, k, p)$ graph.

2.2.3 Discrete Event Simulation

A discrete-event simulation (DES) models the operation of a system as a discrete sequence of event in time, where each event will occur at a particular instance in time and marks a change of state in the systems or more precisely we can say system state can change only a countable number of point in time.These points in time are when event occur, an event is an instantaneous occurrence which may change the system state. There are two approach to advance the time while modeling the Discrete Event Simulation one is the fixed-increment time advance and another is the Next-event time advance.

1. Fixed-increment time advance
2. Next-event time advance

2.2.3.1 Fixed-increment time advance

In this type of DES simulation time is divided into the discrete time,means time increment with the fixed time steps.If events occurring between time increments is going to considered to an increment boundary. This approach has been used in our work to model the epidemic.

2.2.3.2 Next-event time advance

In this type of Discrete event simulation, we determine times of occurrence of future events,simulation time advances to next events which is executed.Occurrence of event changes the event list.We continue this until the stopping criteria is satisfied. So in this simulation time is jumped from one event time to another.

2.2.3.3 Component of the Discrete Event Simulation

There are some basic components of the DES as,

- Simulation Clock :It holds the current simulation time.
- System state: Variables used to describe state.

- Event list times of future events for each event type
- Statistical counters to accumulate performance measures
- Events: causes of system changes

2.3 Epidemiological Models

There are number of epidemiology models like SIR,SIRS,SIS,SEIR. Everyone having different modeling approach, but we will discuss SIR model in detail.

2.3.1 SIR Model

SIR model is a compartment based model which divides the whole population into three different groups S,I and R as component of the population .

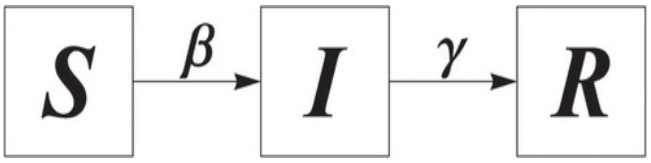

FIGURE 2.1: SIR Models

Susceptible(S) means the people of this group are portion of population who are able to catch the disease. I (infected) is the group of people who are already infected and going to responsible for transmission of infection to the group of susceptible, and R(recovered) is the group of people who recovered from the disease and having the permanent immunity or who died due to illness.

Equations of SIR model,

where β=transmission rate and γ =mean recovery rate

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI \tag{2.1}$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - \gamma I \tag{2.2}$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I \tag{2.3}$$

There is some assumption of SIR model

1. Population is constant i.e. S (t)+I(t)+R(t)=N where is N is the total population and t is the time .
2. Every individual is connected with others i.e. all individuals having the same probability of contracting the disease with same rate β .
3. Once individual get recovered means individual gets permanent immunity.

By the model equation, rate of transmission of the disease is proportional to the rate of encounter of susceptible and infected individual. Recovery rate is only proportional to the infected individual is the mean recovery rate γ and $1/\gamma$ is the mean infective period. In SIR model incubation time is assumed negligible and the rates of infection and recovery are much faster than the characteristic time associated to births and deaths. initial condition in SIR model is

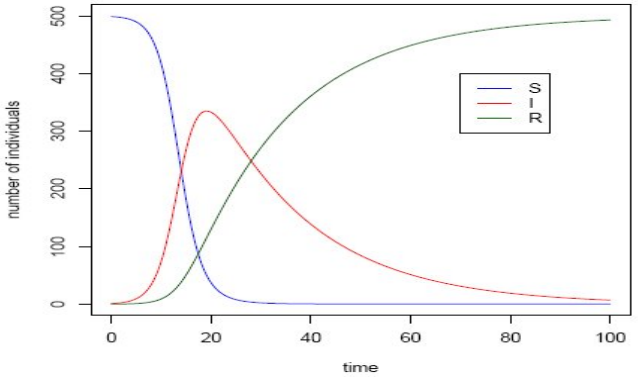

FIGURE 2.2: SIR model characteristics

Figure 3.2 represents the temporal behavior of the proportion of the individuals in each compartments of SIR model. Graph shows that as the time will pass susceptible individual population will decrease and the group of infected will increase up to sometime and then it will decrease after vaccination or medical cure, and individuals of recovered will increase as the time pass.

Problem with SIR model is that this model assumed that everyone is connected with each other which is not realistic, and the social network of SIS model unstructured due this result may vary from the actual at large scale.

2.3.2 SIS model

This model assumed that disease does not confer permanent immunity to infected individuals after getting recovered. Recovered individuals again included in the susceptible

group. So this model divided the population into two compartments, S and I. SIS model is suitable for describe the behavior of epidemics produce bye the bacterial agent such as plague , meningitis , and venereal disease and it also suitable for the disease like malaria. In SIS model it also assumed that population is constant as SIR model, so we can write the equations for SIS model

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI + \gamma I \tag{2.4}$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - \gamma I \tag{2.5}$$

As we know the population is constant i.e. S+I=1, so we can merge the above two equation into single equation

$$\frac{\mathrm{d}I}{\mathrm{d}t} = (\beta - \gamma)I - \beta I^2 \tag{2.6}$$

SIS model concluded that if I_0 is small and β¿γ, the solution is a logistic growth which is going to saturate before the whole population is infected. Saturation value (I_s)= β¿ γ/ β . So by this can show that basic reproduction R_0=β /γ, this is going to set the condition for epidemic to persist.

2.3.3 SIRS Model

SIRS model is an extension of SIR model that is does not confer a permanent immunity to the recovered individual, according to this model recovered individuals will again join to the group of susceptible.

We can write equations as,

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI + \lambda R \tag{2.7}$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI + \gamma I \tag{2.8}$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I - \lambda R \tag{2.9}$$

This model consider the fact that after getting recovered from the infection not give a card to permanent immunity because its very much chance that recovered get non immune so individual go to the susceptible group, but this model have some same assumption like SIR model i.e. . Population is constant and probability of contracting individuals is same means everyone is connected with others and connections are unstructured.

2.3.4 SIER Model

This model is also a kind of SIR model with more compartments S,I,E and R. This model take care of extend period or latent period of disease, so this define an extra compartment E.

2.4 Model Checking and Multivesta

Model checking is the one of the technique for automatically verifying correctness properties of finite-state systems.basically there are two types of the model checking,

- Numerical Model Checking
- Statistical model checking.

2.4.0.1 Numerical Model Checking

Numerical model checking is based on State space exploration based,in numerical model checking we visit each and every state of system to analysis the system.This model provides the accurate system analysis but its very costly and too much time consuming .Numerical model is not suitable for the larger network, for larger network statistical model checking is more suitable.

2.4.0.2 Statistical Model Checking

Statistical techniques, involving simulation and sampling, have been in use for decades to analyse stochastic systems.Statistical Model Checking (SMC) refers to a series of techniques that monitor several runs of the system with respect to some property, and then use results from the statistics to get an overall estimate of the correctness of the design[5].

Statistical model checking is fast, and it scales much better than in compare of numerical model checking for the larger network and its easy to implement but this model checking techniques is not accurate for the small network. model checking to larger networking.

2.4.1 Multivesta

MultiVeStA is an efficient statistical analysis tool which can be easily integrated with existing discrete event simulators, and improve them with distributed Statistical Analysis and Statistical Model Checking capabilities.

MultiVesta is a java based statistical analysis tool which can be easily integrated with existing discrete event simulators, it also provides the capabilities of distributed Statistical Analysis and Statistical Model Checking .Multivesta tool is the an extension of the existing VeStA and PVeStA tools. MultiVesta supports models like PCTL, CSL and MultiQuaTEx queries which are very powerful. We can ask several logical queries using MultiQuaTEx query language. MultiVesta not supports only normal boolean queries but also supports Until and Parametric queries.Most of the part of MultiVesta is a black box for us.

2.5 Previous work

In this section we will discuss about some previous work which are related in some sense of our work.

Preventing and controlling outbreaks of infectious disease an author Christopher L. Barrett come up with an efficient algorithm for simulating the spread of contagion in large realistic social network using individual based models. The data set is using by the author is provide by the united census which is a synthetic data .The structure of network use by the author is inform of person and locations i.e. in network there is an edge between the person and location when person visited that particular location. Basic idea of algorithm is,

1. Individuals can affect others only if there is interaction between the individual at the same location and at same time.
2. Individuals health state changes are deterministic, and can be precomputed.
3. There is a minimum latent period (hidden time) means it is the time that must pass between a person get infected and person is able to infect others.

M.N.Kuperman provides the mathematical analysis of Disease spreading model and also shows the impact of these disease models by using random networks such as by using E-R random network model and small world network [4].

Elisa canazani provide the detailed the analysis of infectious disease and analysis about the causing factors for epidemics, comparing the pros and cons of different-2 epidemic models.[5].

Author Christopher L. Barrett, Stephen Eubank and Madhav V. Marathe given the idea about Simdemics which is an interaction-based multi-agent approach to support taking decision on epidemics for large urban region.Simdemics is based on idea that a better understanding of key parameter in the social contact network which will give the better insights into dynamics of disease and in taking decision for intervention strategies.Simdemics details the demographic and geographic distribution of disease and provides the decision making information by formulating the things (1)consequence of a biological attack or natural attack (2)what is the demand for health services (3) feasibility and effectiveness of response options.[3]

An another paper titled 'Probabilistic Model Checking of Disease Spread and Prevention which is more related to our work.In this paper author investigates the benefits of model checking upon contact networks,they model of disease spreading through the population. They demonstrate how to characterize a disease as it is spread in terms of the portions of the population that it affects, as well as how to evaluate and explore preventative and controlled measures to limit the diseases effects.They have also uses the several vaccination strategy for this work.[6]

Chapter 3

Implementation of Discrete Event Simulator and its integration with multivesta

3.1 Modeling Discrete Event Simulator for SIR model

To simulate the SIR model, basically there is two events i.e. changing from susceptible categories to infected and infected to recovered state when these events occur it changes the state of system at a time. We are using fixed incremental time steps discrete event simulation in which time is increment by the fixed steps.Event occurring in between the time t_1 and t_2 is going to consider on the next increment boundary time.In our implementation initially we set the all nodes as the susceptible and also set the initial time for their status is 0.
At a particular time if node is susceptible then there is chance that this node will get infect if there neighbors are infected, so probability of one infectious node infecting its susceptible neighbor, given that it is infected for t time units, is

$$\text{prob(infection)}=1-(1-\text{ infection\_rate})^t$$

In our model it is assumed that every infected node is equally likely, means have the same infection rate, if node get infected on that time we will are updating the infection time of the node with the current simulation time .

If the status of the node is infected then this node will go into the recovered state with some recovery rate γ at time step t. and after that we increment the current simulation with fixed time steps.

To implement the SIR model on DES we have use the Random Network model as contact network which simulate the network as the social structure. Random network model has been used in our work is Watts and strogatz model which having the special properties like it have low clustering coefficient but the average length is shorter. We have use a Graph Stream java lib. to generate this network.

3.1.0.1 Simulation Parameters

This simulation has the following parameters based on the SIR.

- Number of node (N)
- Average degree(k)
- Rewiring probability(p)
- Infection Rate
- Recovery Rate

We have also implement the vaccination strategies like degree centrality,betweeness centrality and closeness centrality to control and prevent the epidemic.

3.2 Integration with MultiVesta

To Implementing Statistical model checking for SIR model we need DES simulator for SIR model and MultiVesta.

The linking between Discrete event Simulator and Multivesta is show in above figure .We have implemented a class NewConnector which extends the NewState class of MultiVesta.NewConnector class is use to link between the our DES simulator and MultiVesta and it works as intermediate class for us.New connector having the object of of main simulation class SIR-model.This class keep track of all the simulation variable which are relevant for MultiQuaTEx queries.

MultiVesta provides two variations for model checking: Stepwise Simulation and Whole simulation. In stepwise simulation it checks for the properties of system after each

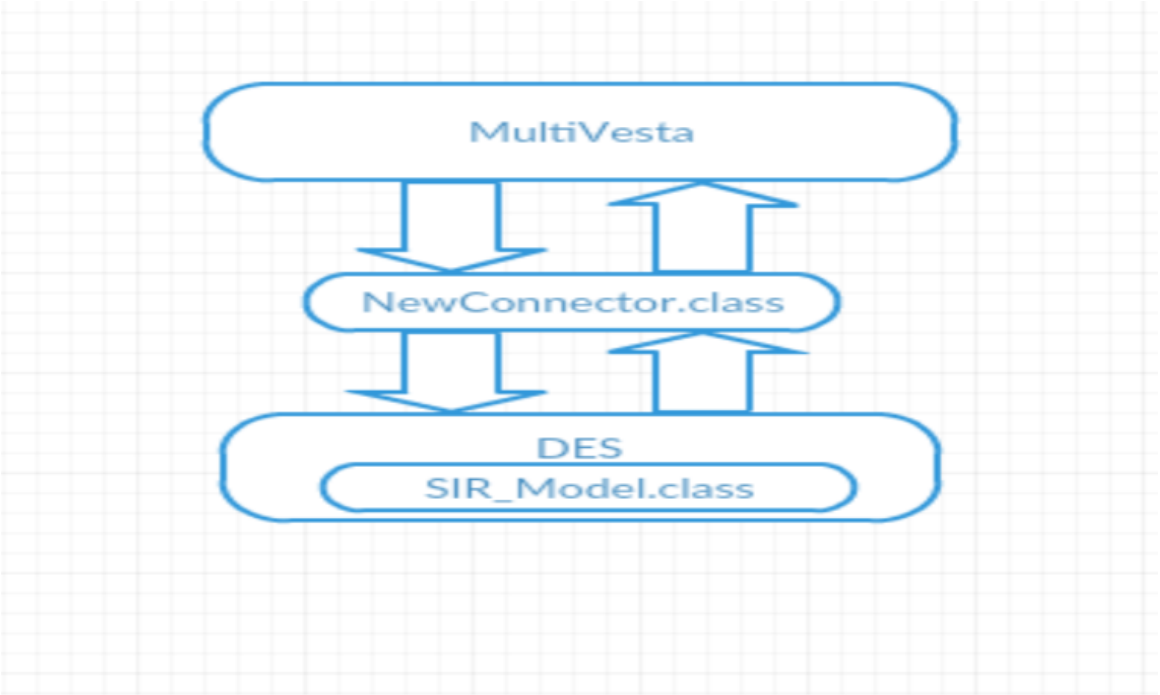

FIGURE 3.1: Integration between DES simulator and Multivesta

discrete step of simulation but in case of Whole simulation, the properties is going to checked if and only after the simulation is completed.

Chapter 4

Results and Analysis

4.0.1 Experimental setup

We have taken a fixed graph of 1,00,000 nodes which generated by using the watts and strogatz model,and initially we have fixes 10 initially infected node for our all type of queries. and have taken the 30,000 as total number of vaccination.

For running MultiQuaTEx queries and getting results we Need MultiVesta client and server model to run the MultiQuaTEx queries .We have Provided a server list and port number.We have to start server in one terminal and on another we have to run the client.

- Server Command
  java -cp .:lib/* vesta.mc.NewVestaServer 49141(PortNumber) In this command we provide classpath of MultiVesta.jar where we start Ves-ta server.

- Client Command

  java -cp .:lib/* vesta.NewVesta -sd core.NewConnector -m ModelName

  -f quatex/queryname.quatex -l ServerList/Server -bs 10 -ms 100 -a 0.005

  -d1 0.0004 -se core.NewEvaluator -osws ONESTEP

  In this Command we provide classpath of NewVesta class which is inside Multi-Vesta.jar that contain main function. -sd is for state-descriptor.

  -m is for ModelName(usually initial setting file).

  -f is for File Name of QuaTEx query.

  -l is for Server List here we provide server file name so that we connect to that server which is running on other terminal.

-bs is for Batch-Size we use batch size 10 in over experiment.

-ms is for Maximum-Simulation we use 100 simulation i.e 10 batch of 10 simulation.

Using MultiQuaTEx queries we studied several things regarding epidemic progression on Network.

- **Example 1** What is the probability that node n_1 will infected before node n_2 at the end of the simulation for different vaccination schemes.

- **MultiQuaTEx Syntax**
  rval(1): returns true if the simulation is completed and false otherwise.
  rval(8) and rval(9) : return simulation time when node n_1 and node n_2 get infected respectively.

```
AbeforeB() = if { s.rval(1)==1.0 } then if { s.rval(8) >s.rval(9) }then {1} else
{0} fi else # AbeforeB() fi ;
eval E[ AbeforeB()];
```

- **Result**

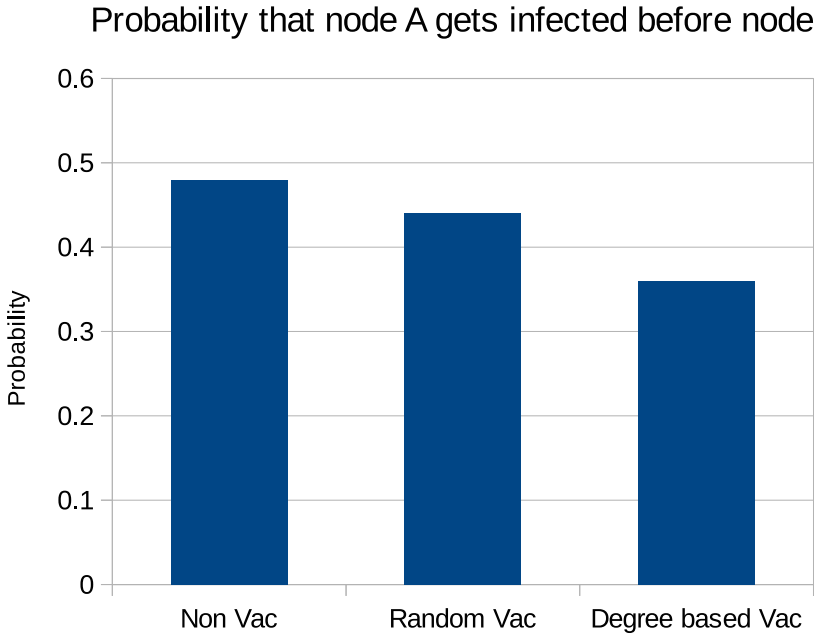

FIGURE 4.1

- **Analysis:**
  Probability of getting node A get infected before node B is high in the case of no vaccination to nodes , and as we can also see that that degree base vaccination is better than random vaccination of nodes.

- **Example 2** What is the probability that node A and node B will infect between time t_1 and t_2.

- **MultiQuaTEx Syntax**
  rval(1): returns true if the simulation is completed and false otherwise.
  rval(9) : return simulation infection time when node A and node B get infected respectively.

```
AStatBtw() = if { s.rval(1) == 1.0 } then if { s.rval(9) >=20 && s.rval(9) <=30}
then {1} else {0} fi else #AStatBtw() fi;
eval E[ AStatBtw() ];
```

- **Result**

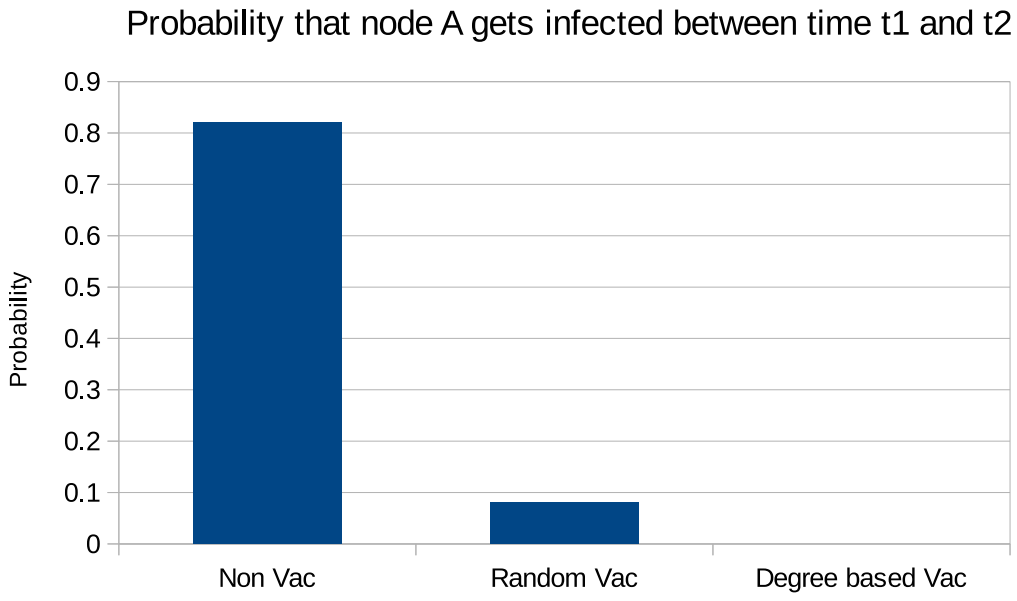

FIGURE 4.2

- **Analysis:**
  Probability of getting node A and node B getting infected in between time t_1 and

t_2 is much higher in case of non vaccination than random vaccination, here in case of degree base vaccination the probability is 0 .So we can conclude that degree vaccination is better in that case.

- **Example 3** What is the probability that atleast 75 % of node will remains uninfected between time t_1 and t_2.

- **MultiQuaTEx Syntax**
  rval(5): returns the current simulation time.
  rval(11) : returns the percentage of the nodes which are not infected at the current time.

```
noninfect(x)= if {s.rval(5)>= x } then if {s.rval(11)>= 0.75} then {1} else {0}
fi else #noninfect({x}) fi;
eval parametric(E[noninfect(x)],x,15,3,100);
```

- **Result**

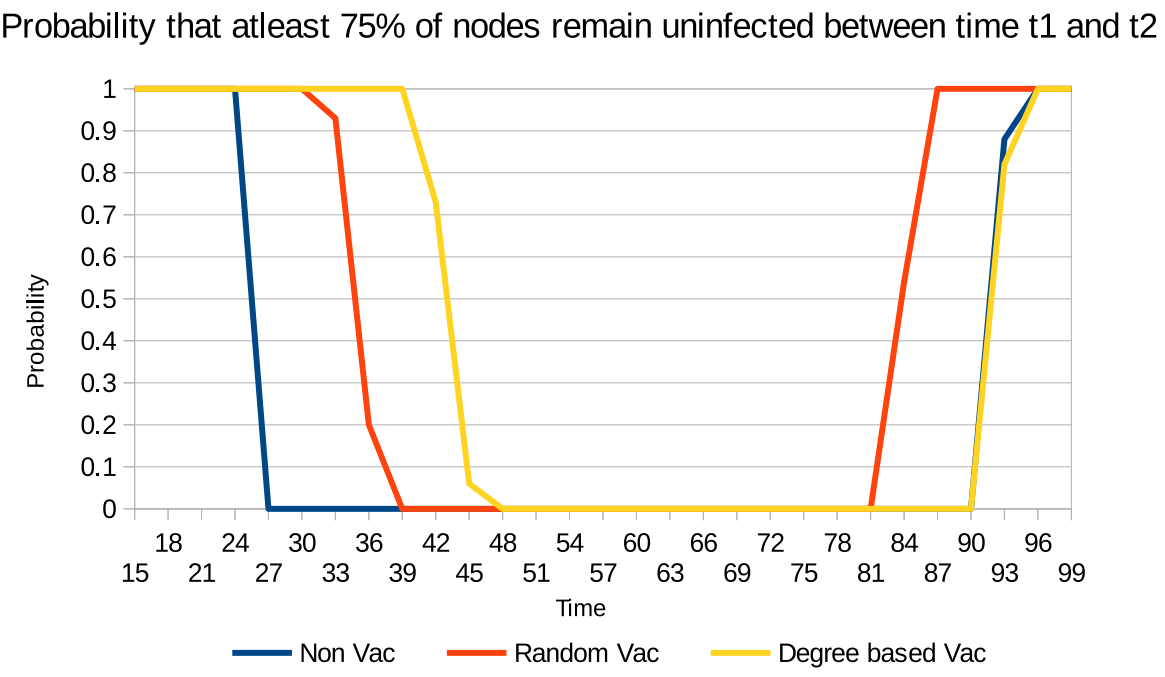

FIGURE 4.3

- **Analysis:**
  As we can see by the result that between time t_1 and t_2 , in case of non vaccination nodes gets infected to early in compare of degree base and random vaccination.

- **Example 4** What is the probability that at least one node among $v_1.v_2, ...v_k$ will infect ?

- **MultiQuaTEx Syntax**
  rval(5): returns the current simulation time.
  rval(12) : returns the infection time of each node $v_1, v_2, v_3, ...v_k$.

```
multinode(x)= if {s.rval(5)>= x } then if {s.rval(12)>=1} then {1} else {0} fi
else #multinode({x}) fi;
eval parametric(E[multinode(x)],x,5,3,32);
```

- **Result**

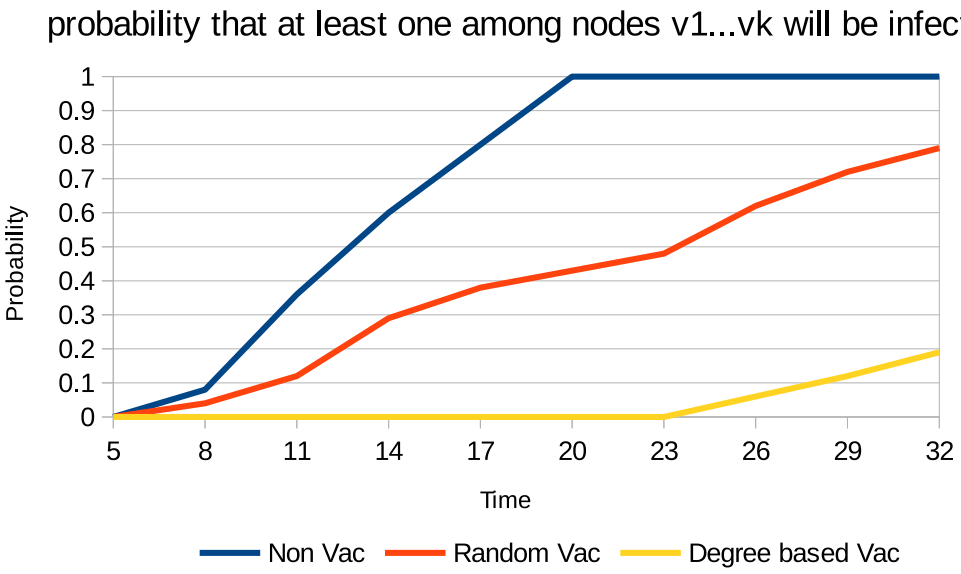

FIGURE 4.4

- **Analysis:** As we can see by the result that nodes get infected early in non-vaccination case and random base vaccination , but random vaccination is much better than non_vaccination case, and degree base vaccination is better than these two.

- **Example 5** Number of node get infected when vaccinations is introduced at time t=14?

- **MultiQuaTEx Syntax**

  rval(5): returns the current simulation time.

  rval(2) : returns number of infected node.

```
nrInfect() = if { s.rval(5) == 14 } then { s.rval(2) } else # nrInfect() fi ;
eval E[ nrInfect() ] ;
```

- **Result**

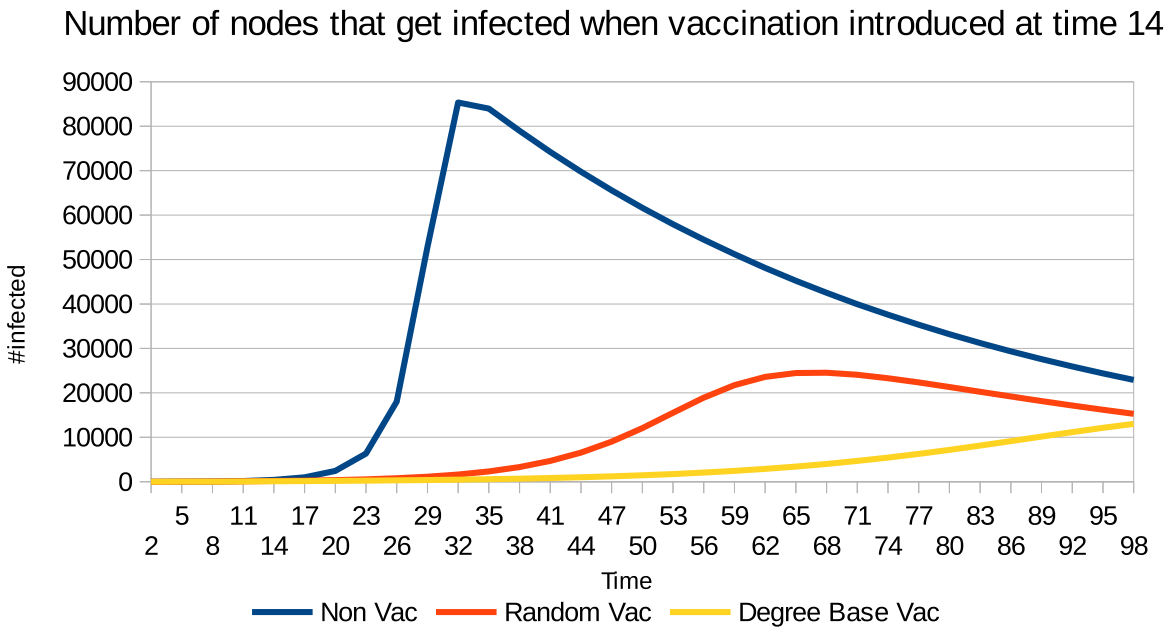

FIGURE 4.5

- **Analysis:** As we can see by the result lesser number of nodes gets infected if we apply the vaccinations at time t=14 .

- **Example 6** What is the probability that given node is infected if 25% neighbours of nodes are infected?

- **MultiQuaTEx Syntax**

  rval(13): returns ratio of vaccinated node and non vaccinated node for given node.

  rval(14) : returns node infected is infected or not

```
vacNeighbor() = if { s.rval(1) == 1.0 } then if { s.rval(14) < 1050 &&
s.rval(13)>=0.25} then {1} else { 0 } fi else #vacNeighbor() fi;
eval E[vacNeighbor()];
```

- **Result**

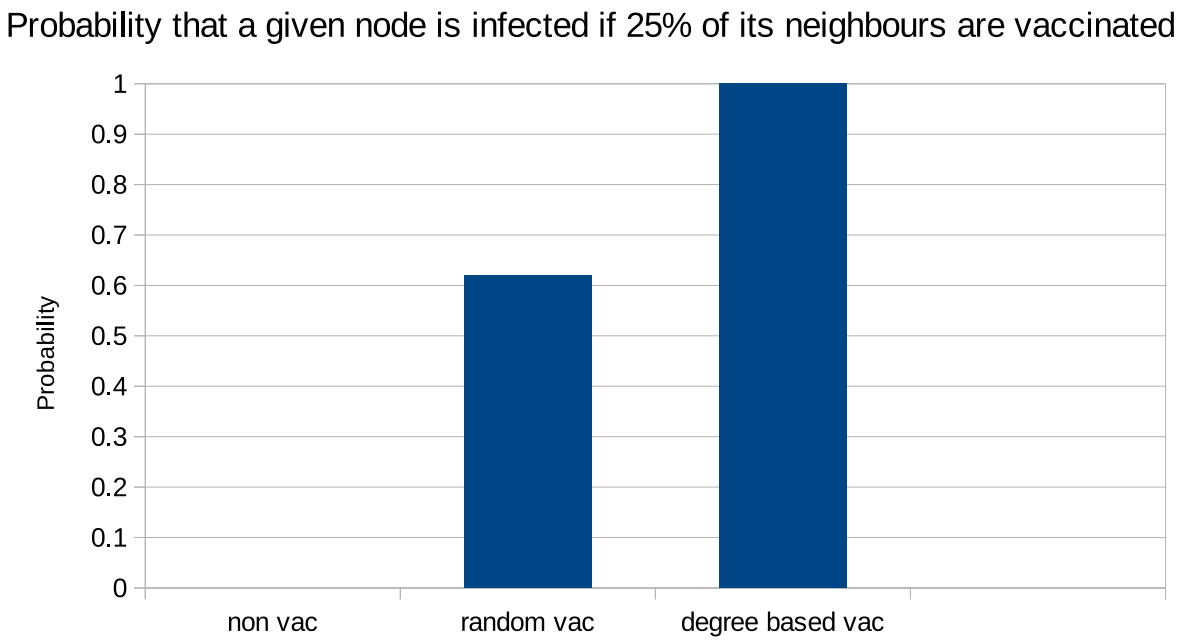

FIGURE 4.6

- **Analysis:** As we can see by the result, first for non vaccination is zero because its not satisfying the criteria of vaccination, second thing is that in this case random vaccination is working better than degree distribution.

4.1 Conclusion :

We demonstrated a linking of the MultiVesta statistical model checker with the Discrete event simulator for SIR model on complex network, which show how epidemic progress on the social network,like at what rate epidemic spread, at what time epidemic will and high any more things we can analysis by using this. These combinations show how power full statistical model checking is and how we can apply SMC in real scenario to model the complex systems.

Chapter 5

References

[1] van Steen, Maarten. "An Introduction to Graph Theory and Complex Networks." Copyrighted material (2010).

[2] Kuperman, Marcelo N. "Invited review: Epidemics on social networks." Papers in Physics 5 (2013): 050003.

[3] Barrett, Christopher L., Stephen Eubank, and Madhav V. Marathe. "An Interaction-Based Approach to Computational Epidemiology." AAAI. 2008.

[4]Barrett, Christopher L., et al. "EpiSimdemics: an efficient algorithm for simulating the spread of infectious disease over large realistic social networks." Proceedings of the 2008 ACM/IEEE conference on Supercomputing. IEEE Press, 2008.

[5] BARRETT, CHRIS, et al. "EXACT STOCHASTIC SIMULATION OF EPIDEMICS ON COMPLEX SOCIAL CONTACT NETWORKS."

[6] Lee, Taesik, Hyun-Rok Lee, and Kyosang Hwang. "Identifying superspreaders for epidemics using R0-adjusted network centrality." Proceedings of the 2013 Winter Simulation Conference: Simulation: Making Decisions in a Complex World. IEEE Press, 2013.

[7] Coburn, Brian J., Bradley G. Wagner, and Sally Blower. "Modeling influenza epidemics and pandemics: insights into the future of swine flu (H1N1)." BMC medicine 7.1 (2009).

[8] Huang, Samuel. "Probabilistic model checking of disease spread and prevention." Scholarly Paper for the Degree of Masters in University of Maryland (2009).