Modelling of Disease Dynamics in Complex Network

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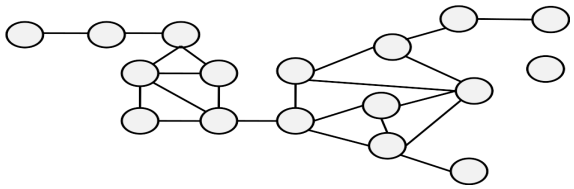
Outline

- Introduction
- Motivation
- Objective
- Proposed Works
- Conclusions
- Future directions
- References

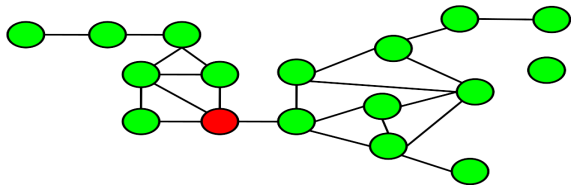
Introduction

- Complex networks are used to describe a large variety of real-world systems i.e. communication, social, biological systems etc.
- Most of the systems are complex and stochastic.
- There is an increasing interest to study the dynamics on networks over dynamical processes.
- Networks parameters play a very important role in analysis of process on network like epidemic spreading , rumor spreading, information propagation.

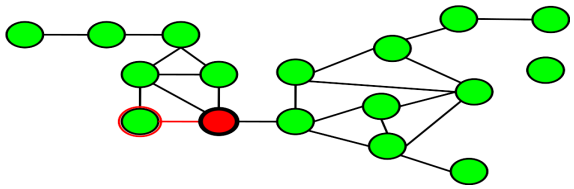
Epidemic Spreading on Network



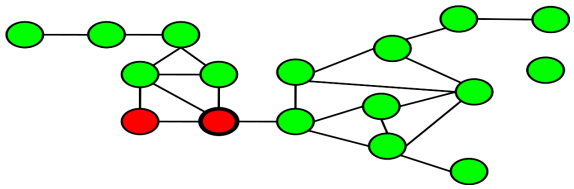
(a) Initial Network without infection



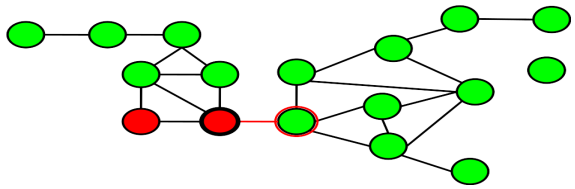
(b) Epidemic Spreading at t



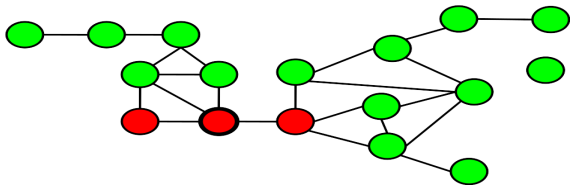
(c) Epidemic Spreading at $t + 1$



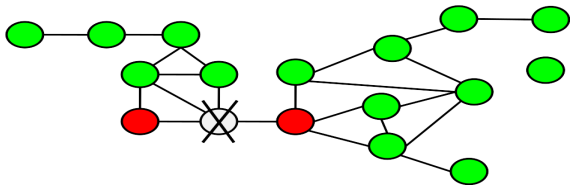
(d) Epidemic Spreading at $t + 2$



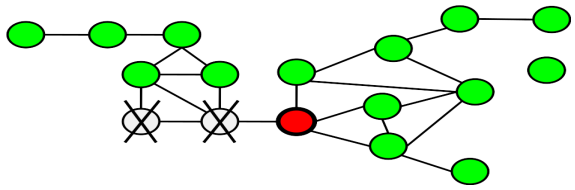
(e) Epidemic Spreading at $t + 3$



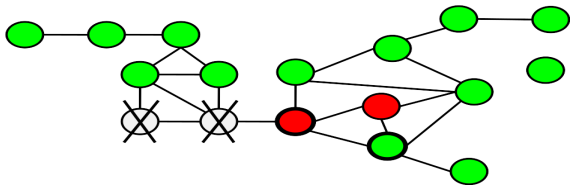
(f) Epidemic Spreading at $t + 4$



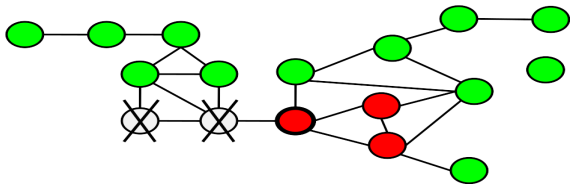
(g) Epidemic Spreading at $t + 5$



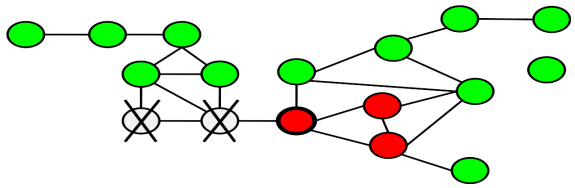
(h) Epidemic Spreading at $t + 6$



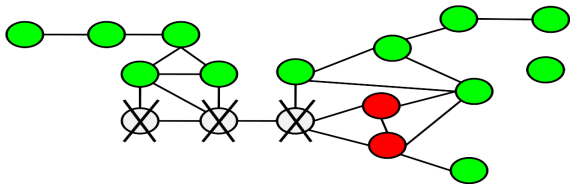
(i) Epidemic Spreading at $t + 7$



(j) Epidemic Spreading at $t + 8$



(k) Epidemic Spreading at $t + 9$



(l) Epidemic Spreading at $t + 10$

Figure: Epidemic Spreading on Network

Motivation

- Challenges:
  - Design of random geometric Network with mobile nodes to show the human movement.
  - Spreading of contagious diseases depend not only contact but environmental condition also.
  - Incorporating seasonal parameter with epidemiological model is not an easy task.
- Diseases spread from one region to another region due to human movement like Zika, Ebola, Corona.
- Seasonal diseases are temperature dependent as diseases spread under certain temperature range.
- Information spreading is almost similar to epidemic spreading on network
- Information is propagated through contacts in network in similar way to epidemic spreading in contact network.

Objectives

- Design frameworks to represent random geometric network with mobile nodes.
- Propose delayed SIR model considering underlying network topology.
- Propose Seasonal SIR model considering homogeneous and heterogeneous underlying network topologies with environmental condition.
- Propose a secured and trusted framework for information propagation on online social networks.

Phase 1
- GNMN
- SIS
- SIR

COVID 19 Spreading

Phase 2
- GNMN
- Delayed SIR
- Critical Threshold

Phase 3
- SSIR
- Homogeneous Network
- Heterogeneous Network
- Basic Reproduction Number

Phase 4
- Information Dynamics on Networks
- Local Trust
- Global Trust
- Credibility

Abbreviation

GNM - Geometric Network with Mobile Nodes
SIS - Susceptible-Infected-Susceptible
SIR - Susceptible-Infected-Recovered
SSIR - Seasonal SIR

Geometric Network with Mobile Nodes

- Modelling of Geometric Network with Mobile Nodes
- Epidemic Spreading considering GNMN as underlying Network
- Results and analysis

Geometric Network with Mobile Nodes (GNMN) model

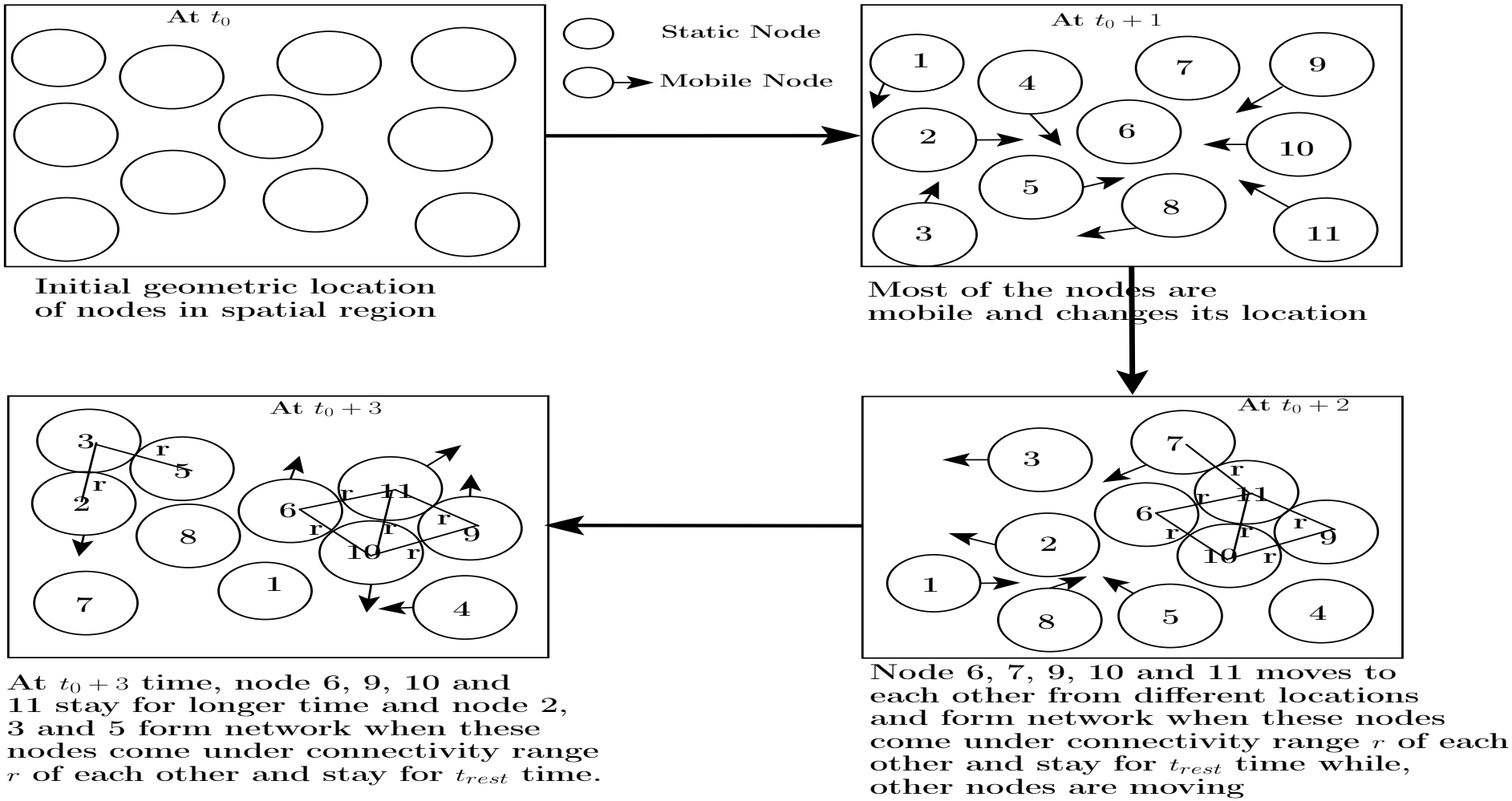


Figure: Mobility and interaction with nodes

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- GNMN consists N nodes uniformly distributed over a two dimentional area $[0, a]^2 \in \mathbb{R}^2$ [1].
- Nodes move with random velocity V.
- Edges connects the pairs of nodes within a given distance from each other, called connectivity radius.
- Epidemics are spread by the infected nodes when they rest for t_{rest} time during movement.
- SIS and SIR model is implemented considering GNMN as underlying network to find the effect of mobility and t_{rest}

[1] Christian Bettstetter, Giovanni Resta, and Paolo Santi. The node distribution of the random waypoint mobility model for wireless ad hoc networks. IEEE Transactions on mobile computing, 2(3):257–269, 2003.

Contd...

Node Distribution of GNMN[1]

$$f_{X,Y}(x,y) = \begin{cases} \underbrace{p_{stat} * f_{(X,Y)}(x,y)}_{f_{stat}} + \underbrace{(1-p_{stat})p_{rest}}_{f_{rest}} & X, Y \in [0,a] \\ + \\ \underbrace{(1-p_{stat})(1-p_{rest})\underbrace{36\frac{xy}{a^4}(1-\frac{x}{a})(1-\frac{y}{a})}_{f_{(X,Y)_{move}}(x,y)}}_{f_{move}} \\ 0 \qquad \text{otherwise} \end{cases} \tag{1}$$

- The pdf defined in Eq 1 reflects spatial structure of node movement.

[1] Christian Bettstetter, Giovanni Resta, and Paolo Santi. The node distribution of the random waypoint mobility model for wireless ad hoc networks. IEEE Transactions on mobile computing, 2(3):257–269, 2003.

Contd...

- The probability of a node to be within the connectivity region, r with respect to another random node during movement, when any node i is at location (x_i, y_i),

$$Pr_M(x_i, y_i) = \int_{y_i - r}^{y_i + r} \int_{x_i - \sqrt{r^2 - (y - y_i)^2}}^{x_i + \sqrt{r^2 - (y - y_i)^2}} f_{X,Y_{move}}(x, y) dx dy \qquad (2)$$

$$Pr_S((x_i, y_i)) = 1 - Pr_M(x_i, y_i)$$

- The probability of having k neighbors of a node at location (x_i, y_i) is calculated as,

$$Pr(x_i, y_i, k) = \binom{N-1}{k} (Pr_s(x_i, y_i))^k (1 - Pr_s(x_i, y_i))^{N-k-1}$$

- The Average probability of a node over the entire area that a node has k neighbors is,

$$Pr(k) = \frac{\int_0^a \int_0^a Pr(x_i, y_i, k)) dx dy}{A}$$

where area $A = a^2$

SIS Model

- In SIS Model[2] , there are two compartments one is susceptible (S) while other is infected (I). Susceptible nodes may be infected with rate $\beta \in [0, 1]$, while infected nodes become susceptible with rate μ where $\beta, \mu \in [0, 1]$
- Infection is transmitted during t_{rest} time
- Applying infection rate and recovery rate on SIS, mean-field equation will be:

$$\begin{aligned} \frac{\partial S}{\partial t} &= -\beta k_i Pr(K = k_i) t_{rest} SI + \mu I t_{rest} \\ \frac{\partial I}{\partial t} &= \beta k_i Pr(K = k_i) t_{rest} SI - \mu I t_{rest} \end{aligned}$$

[2] Hongjing Shi, Zhisheng Duan, and Guanrong Chen. An sis model with infective medium on complex networks. Physica A: Statistical Mechanics and its Applications, 387(8-9):2133–2144, 2008.

SIR Model

- In SIR Model[3] , there are three compartments as susceptible, infected and recovered.
- Applying infection rate and recovery rate on SIR considering GNMN as underlying network, mean-field equation will be:

$$\begin{aligned}
\frac{\partial S}{\partial t} &= -\beta k_i Pr(K = k_i) t_{rest} SI \\
\frac{\partial I}{\partial t} &= \beta k_i Pr(K = k_i) t_{rest} SI - \mu I t_{rest} \\
\frac{\partial R}{\partial t} &= \mu I t_{rest}
\end{aligned}$$

[3] William O Kermack and Anderson G McKendrick. A contribution to the mathematical theory of epidemics. In Proceedings of the Royal Society of London A: mathematical, physical and engineering sciences, volume 115, pages 700-721. The Royal Society, 1927.

Result and analysis

The simulations are done in this work, categorized as follows:

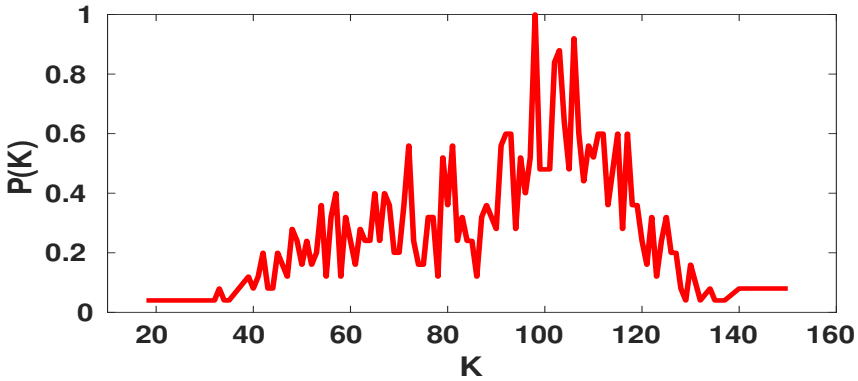
1. RGG model and Geometric Network model with mobility.
2. SIS and SIR model on Geometric Network with mobility
3. SIS and SIR model on Dataset.
4. Analyse the spreading of Covid-19 in Indian states

Results and Analysis

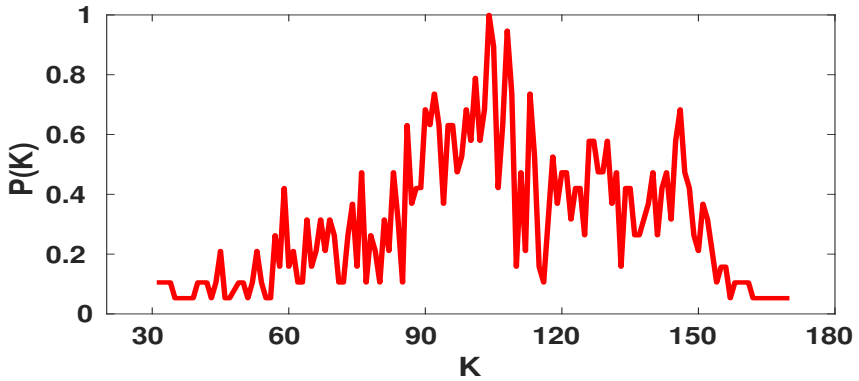
Table: Simulation Parameters for GNMN

Name of Parameter	**Value**
Nodes	2000
Simulation Area($a \times a$)	$2500m \times 2500m$
Square Length(a)	2500m
connectivity region(r)	2m
Spreading Rate(β)	0.8
Recovery Rate(μ)	1
Time of rest(t_{rest})	Random(3,50)s
Threshold time for connectivity($t_{threshold}$)	3s
p_{stat}	0.2
Expected length between two random point	0.521*a
Velocity(V)	Random(1,30)m/s

Result and analysis



(a) DD of GNMN at 3^{rd} time Instances with velocity 21m/s with $t_{rest} = 15s$



(b) DD of GNMN at 7^{th} time Instances with velocity 10m/s with $t_{rest} = 45s$

Figure: Degree Distribution(DD) of GNMN at different time instances

- Degree distribution(DD) for GNMN for two different time instances is plotted to show the effect of random movement of the nodes and t_{rest} on network structure.
- It looks like a Poisson distribution with perturbations.

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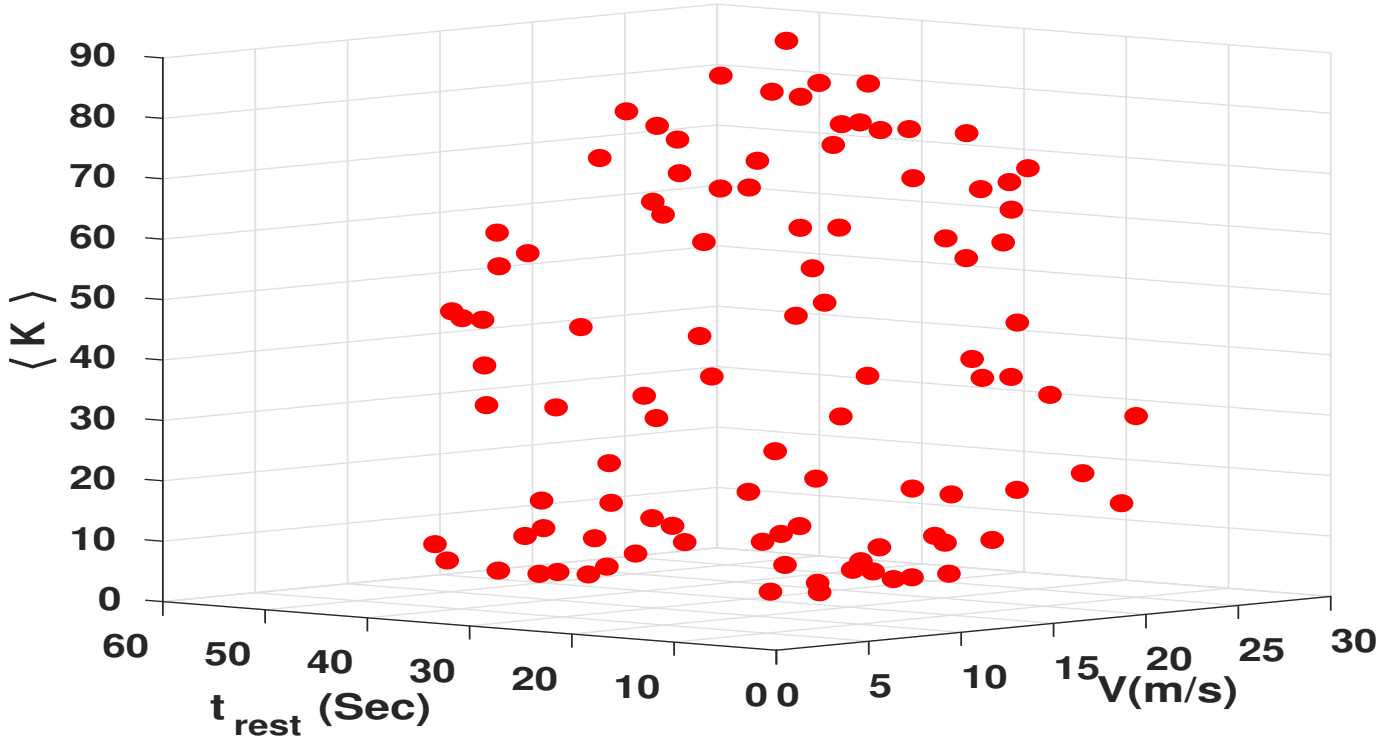
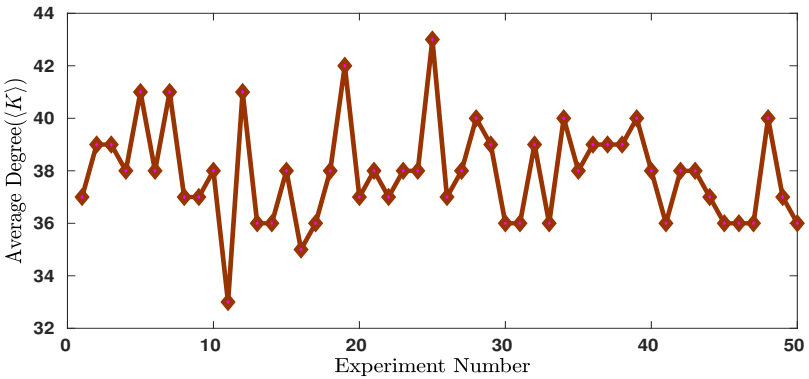


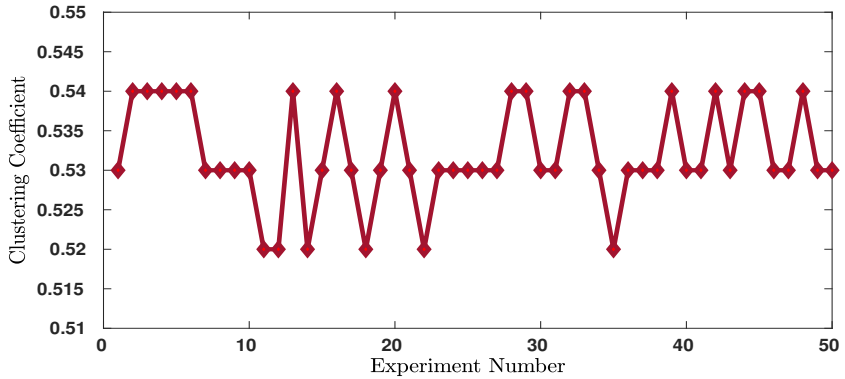
Figure: $\langle K \rangle$ with respect to V and t_{rest} at each time instance

- It is observed that $\langle K \rangle$ increases with the increase of time of rest as more nodes come in contact with the resting nodes within that time.

Contd...



(a) Average Degree of GNMN

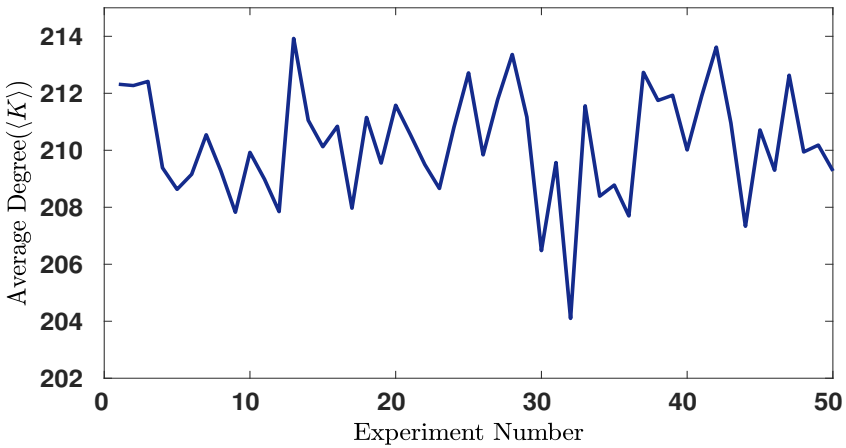


(b) Clustering coefficient of GNMN

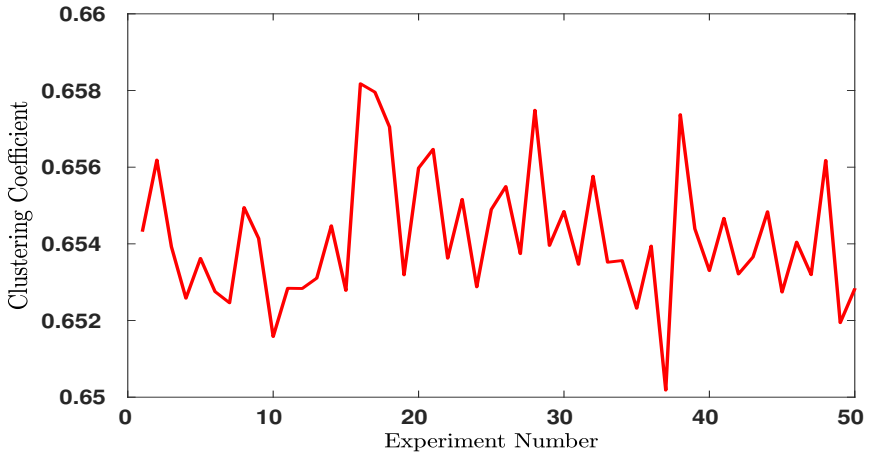
Figure: Network Characteristics of GNMN after 50 experiments

- $\langle K \rangle$ for GNMN vary with high variance with time instances. At some time instances, $\langle K \rangle$ is low and at some instances,$\langle K \rangle$ is high.
- The clustering coefficient of the network is also changing with respect to network structure in GNMN, due to variation in average degree.

Contd...



(a) Average Degree of RGG



(b) Clustering coefficient of RGG

Figure: Network Characteristics of RGG after 50 experiments

Contd...

Table: Average Degree and clustering coefficient of RGG and GNMN

Name of Parameter	**RGG**	**GNMN**
Average Degree	210	38
Clustering Coefficient	0.654	0.533

Analysis of Real World Dataset

Table: **Brightkite Dataset Detail**

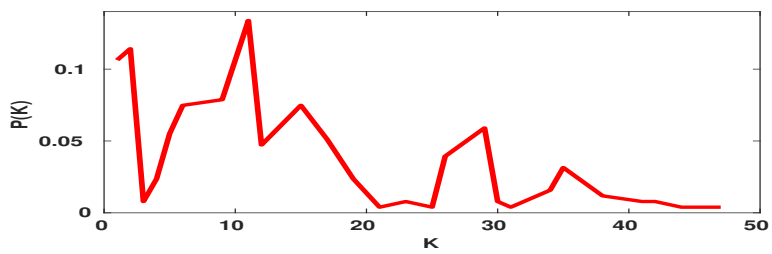
user	check_in time	latitude	longitude	location_id
58186	2008-11-30T22:30:12Z	39.633321	-105.317215	ee8b88dea22411
58186	2008-11-28T17:55:04Z	-13.158333	-72.531389	e6e86be2a22411
58186	2008-11-26T17:08:25Z	39.633321	-105.317215	ee8b88dea22411
58187	2008-08-14T21:23:55Z	41.257924	-95.938081	4c2af967eb5df8
58187	2008-08-14T07:09:38Z	41.257924	-95.938081	4c2af967eb5df8
58188	2010-04-06T06:45:19Z	46.521389	14.854444	ddaa40aaa22411
–	–	–	–	–
–	–	–	–	–
–	–	–	–	–

Dataset statistics after processing

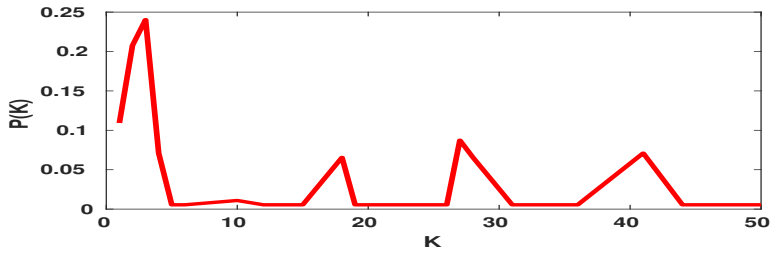
Table: **Brightkite Dataset statistics after processing**

Name of Parameter	**Value**
Total Nodes	58228
Time of rest(t_{rest})	(2-115)days
Velocity (V)	(3-200)Km/h
Connected Nodes in each network	570, 483, 328, 184, 149, 165, 144
Edges in each Network	3282, 2166, 1083, 736, 894, 656, 574
Spatial Region taken($a \times a$)	$25000m \times 25000m$
Average Degree ($\langle K \rangle$) in each region	6, 5, 3, 4, 6, 4, 4

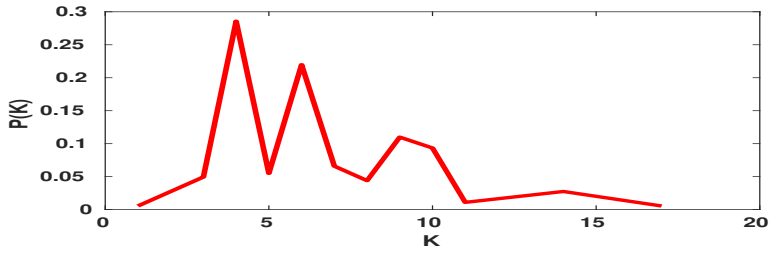
Degree Distribution(DD) of Dataset



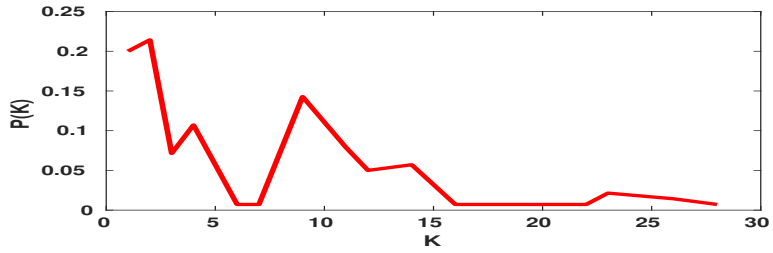
(a) DD of 1^{st} topology of GNMN



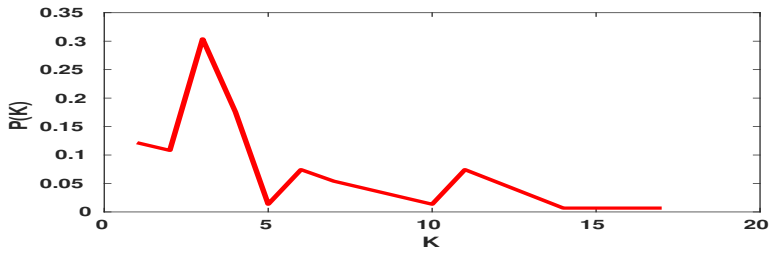
(b) DD of 2^{nd} topology of GNMN



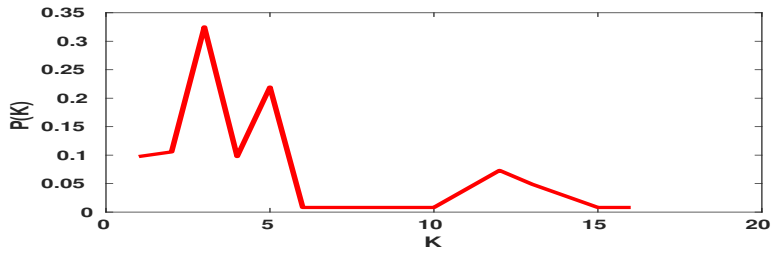
(c) DD of 4^{th} topology of GNMN



(d) DD of 7^{th} topology of GNMN



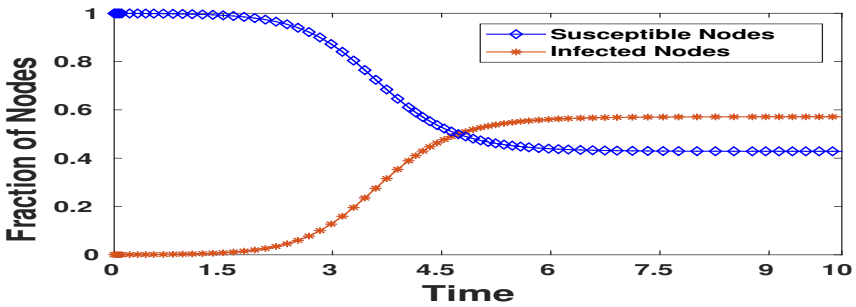
(e) DD of 8^{th} topology of GNMN



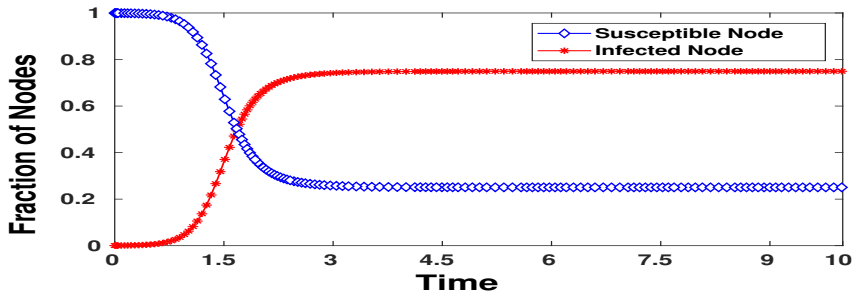
(f) DD of 9^{th} topology of GNMN

Figure: Degree Distribution(DD) of 6-Human Connection Network created using Dataset **Brightkite**

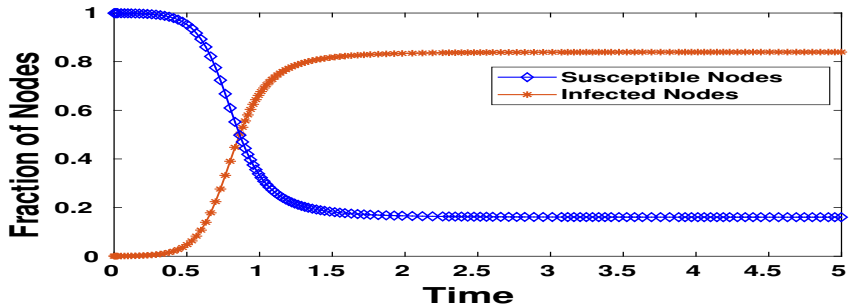
SIS on GNMN



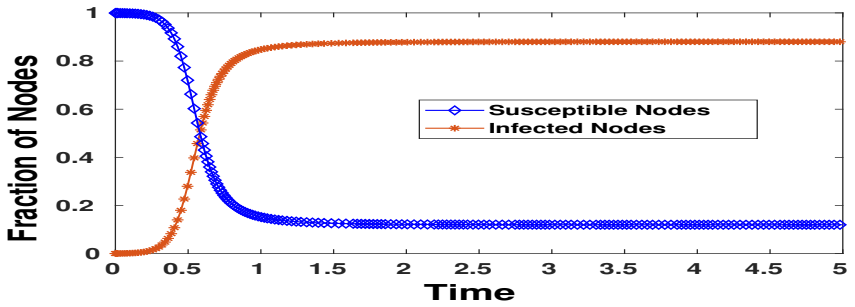
(a)Epidemic Spreading for t_{rest}=5



(b) Epidemic Spreading for t_{rest}=10



(c) Epidemic Spreading for t_{rest}=15

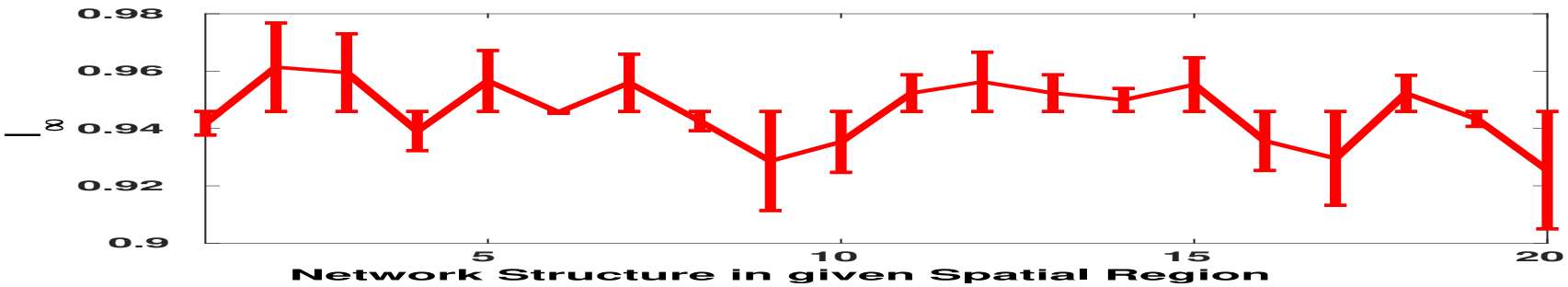


(d) Epidemic Spreading for t_{rest}=20

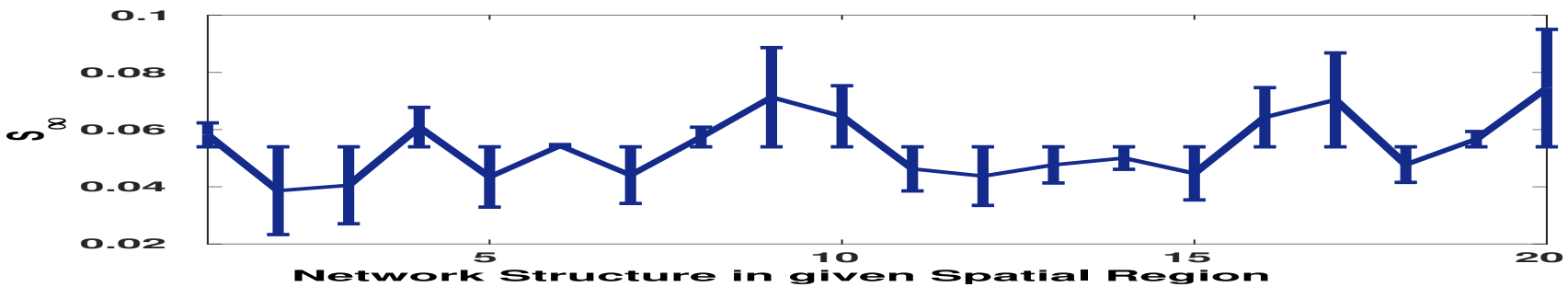
Figure: Effect of t_{rest} time in epidemic Spreading (SIS Model)

- Increasing the t_{rest} leads to faster spreading of the epidemic.

SIS on GNMN



(a) Effect of mobility on I_∞

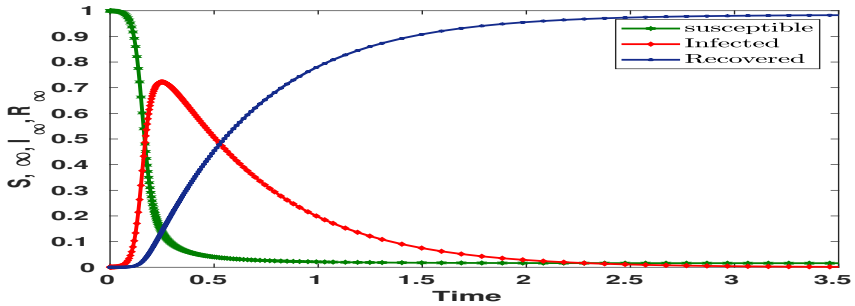


(b) Effect of mobility on S_∞

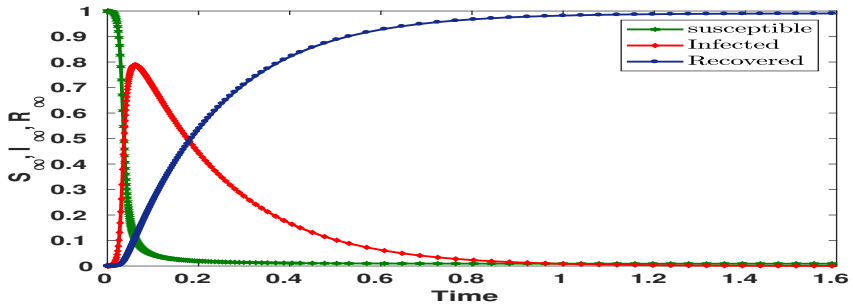
Figure: Effect of Mobility in epidemic Spreading (SIS Model)

- In GNMN, epidemic spread out more quickly at certain time instances when the epidemic is not controlled on time.

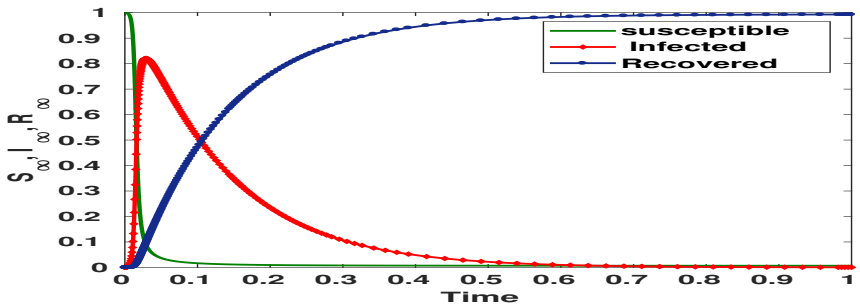
SIR on GNMN



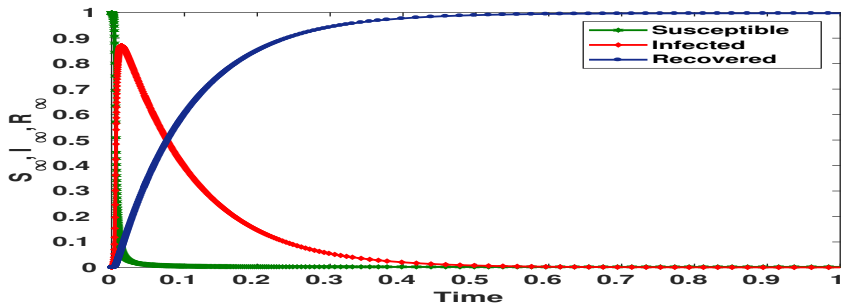
(a)Epidemic Spreading for t_{rest}=3



(b) Epidemic Spreading for t_{rest}=6



(c) Epidemic Spreading for t_{rest}=10



(d) Epidemic Spreading for t_{rest}=15

Figure: Effect of t_{rest} time in epidemic Spreading (SIR Model)

- Increasing the t_{rest} leads to faster spreading of the epidemic.

SIR on GNMN

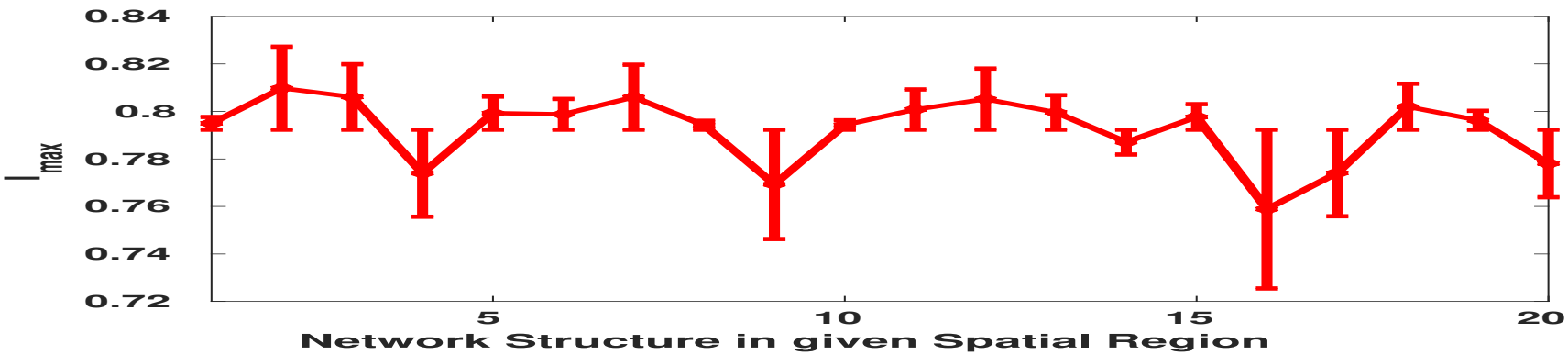
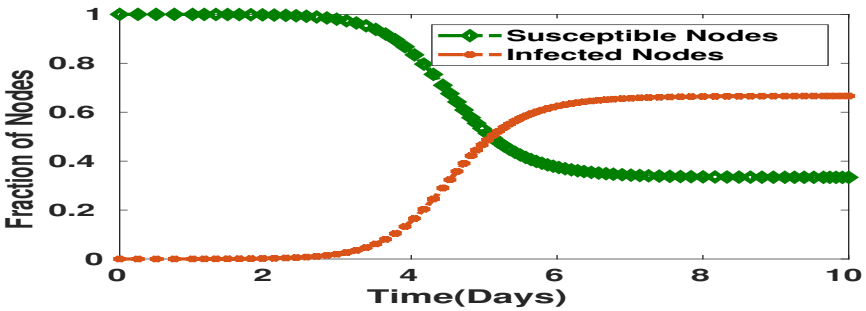


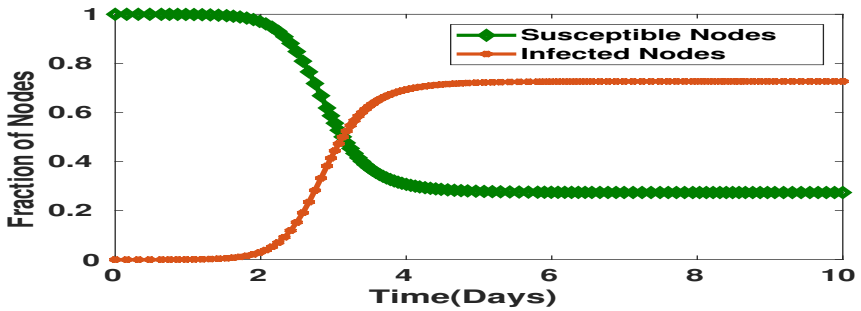
Figure: Effect of Mobility in epidemic Spreading (SIR Model)

- In GNMN, epidemic spread out more quickly at certain time instances when the epidemic is not controlled on time.

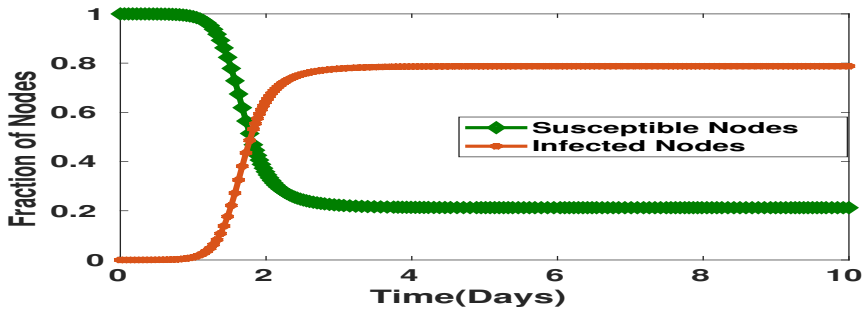
SIS on Dataset **Brightkite**



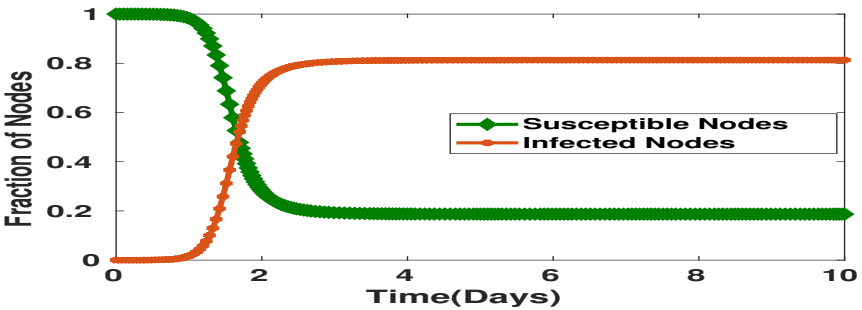
(a)Epidemic Spreading for t_{rest}=5



(b) Epidemic Spreading for t_{rest}=10

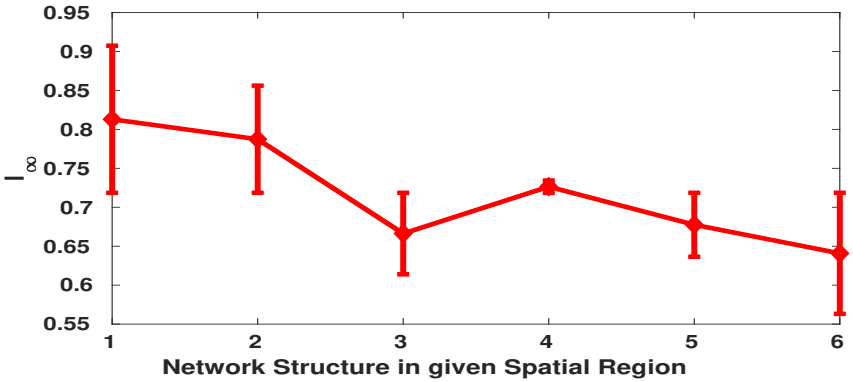


(c) Epidemic Spreading for t_{rest}=15

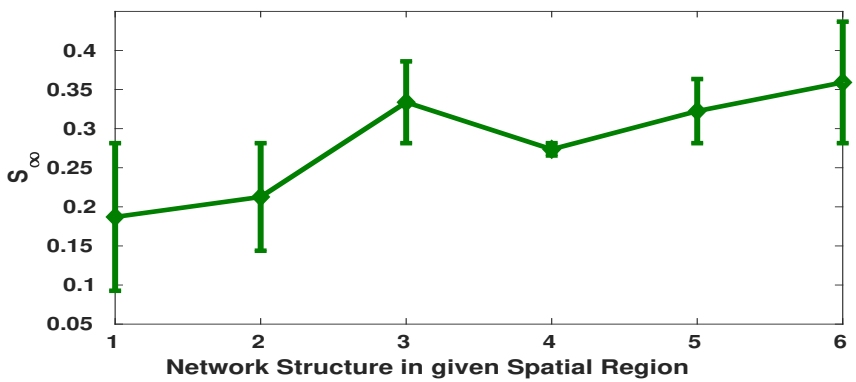


(d) Epidemic Spreading for t_{rest}=20

Figure: Effect of t_{rest} time in SIS epidemic Spreading Model considering Human Connection Network from Dataset **Brightkite**



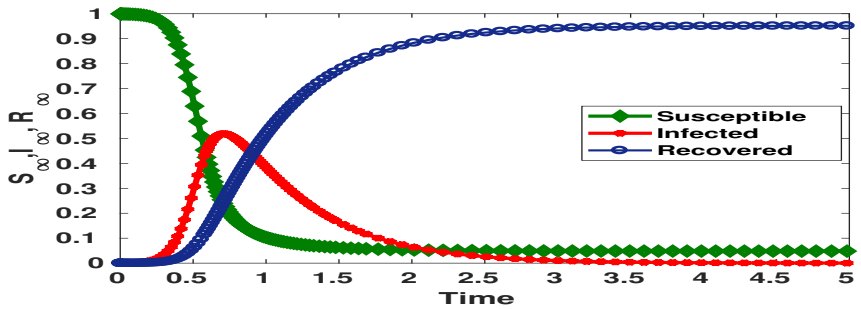
(a) Effect of mobility on I_∞



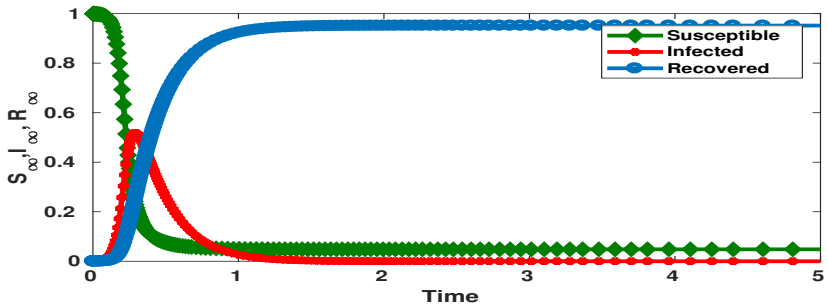
(b) Effect of mobility on S_∞

Figure: Effect of Mobility on SIS epidemic Spreading Model in Human Connection Network from Dataset **Brightkite**

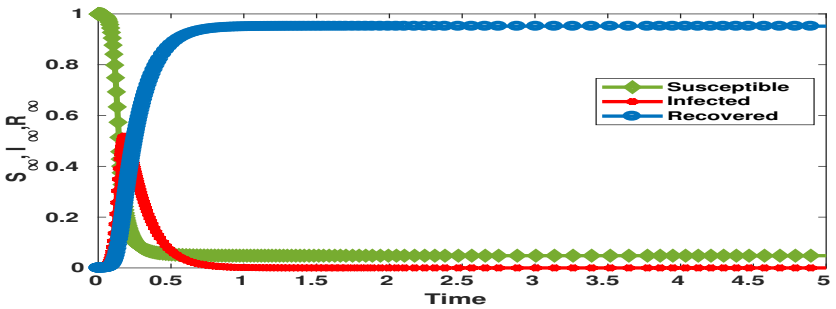
SIR on Dataset **Brightkite**



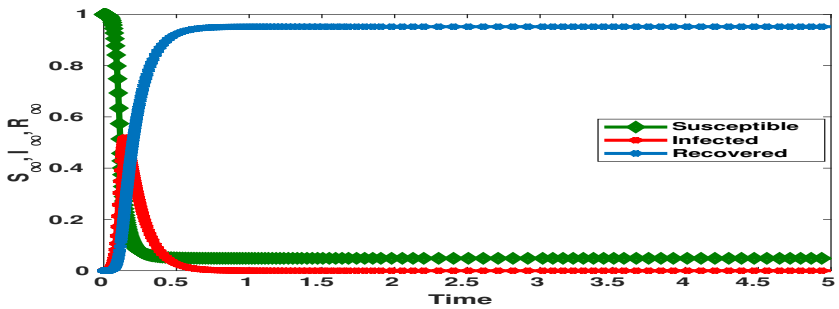
(a)Epidemic Spreading for t_{rest}=3



(b) Epidemic Spreading for t_{rest}=5



(c) Epidemic Spreading for t_{rest}=8



(d) Epidemic Spreading for t_{rest}=10

Figure: Effect of t_{rest} time in SIR epidemic Spreading Model by considering Human Connection Network from Dataset **Brightkite**

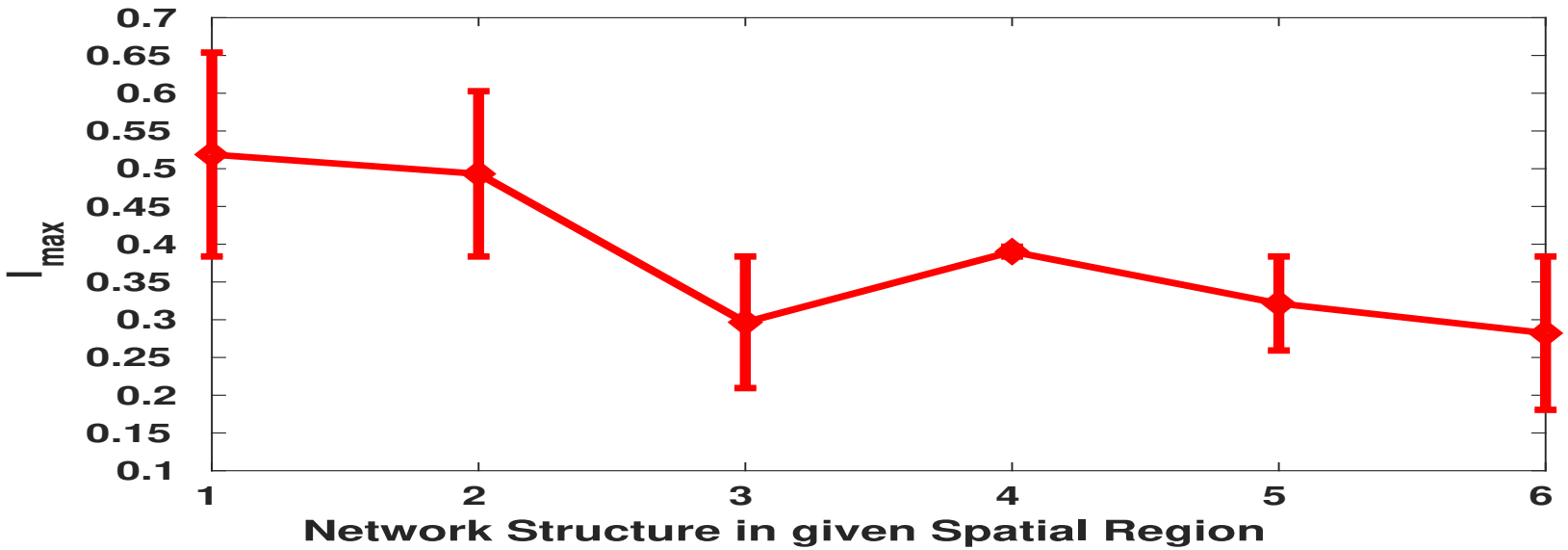


Figure: Effect of Mobility on SIR epidemic Spreading Model in Human Connection Network from Dataset **Brightkite**

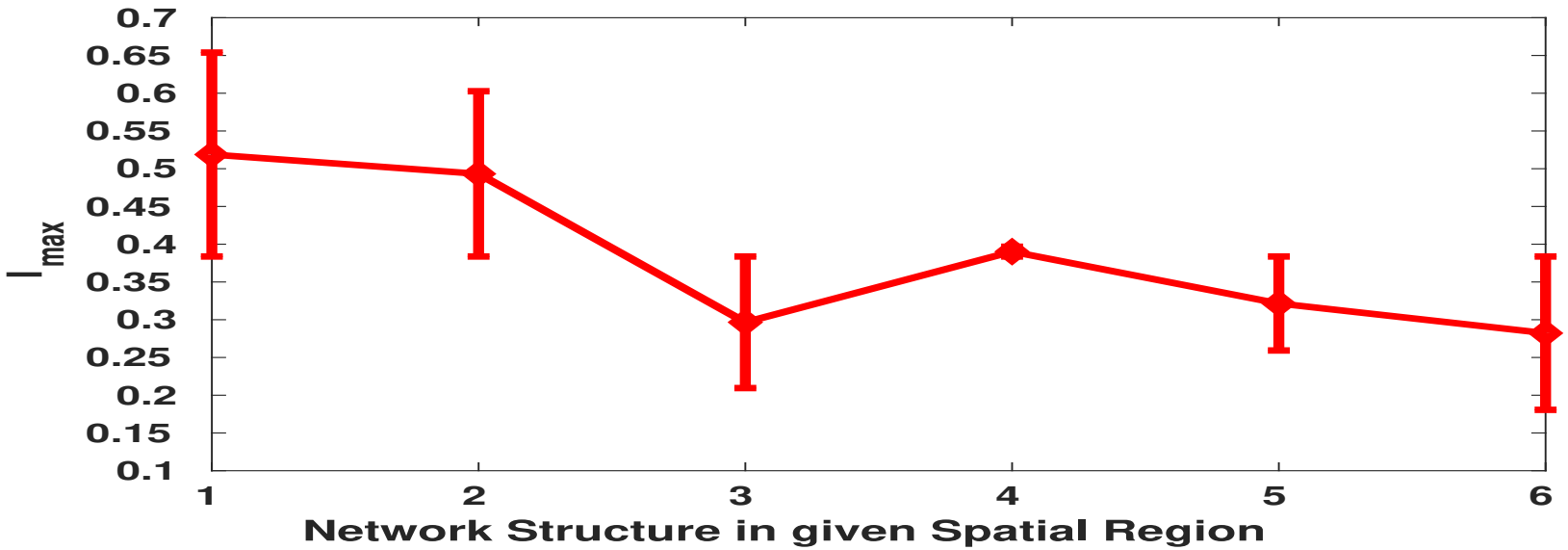


Figure: Effect of Mobility on SIR epidemic Spreading Model in Human Connection Network from Dataset **Brightkite**

Phase 2

- Classical SIR Epidemic Model
- Proposed Delayed SIR Model considering underlying network topology
- Results and analysis

Phase 2

- In the classical epidemiological model, a susceptible person becomes infected instantly after getting in contact with the infected person.
- However, this scenario is not realistic.
- In real, a healthy person become infected with some delay in time not spontaneously after contacting with the infected person.
- Therefore, research is needed for creating more realistic models to study the dynamics of epidemics in the human population with delay.

Classical SIR Epidemic Model

- The classical SIR model is proposed by Kermack and McKendrick[3].

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta S(t)I(t) \\ \frac{dI(t)}{dt} &= \beta S(t)I(t) - \mu I(t) \\ \frac{dR(t)}{dt} &= \mu I(t) \end{aligned}$$

- where, $S(t), I(t), R(t)$ is the fraction of susceptible, infected and recovered population at time t.
- The classical SIR epidemic model does not consider the heterogeneity and topology of complex network.

[3] William O Kermack and Anderson G McKendrick. A contribution to the mathematical theory of epidemics. In Proceedings of the Royal Society of London A: mathematical, physical and engineering sciences, volume 115, pages 700-721. The Royal Society, 1927.

Proposed Work

- In this phase, we have proposed the *SIR epidemic model with delay*.
- Let, G(N, E) defines the network of N nodes that represent the total population and E denotes the connections between nodes representing the interaction between individuals through which epidemic spreads.
- The propagation of disease is explained as:
  - Each healthy node takes a time delay of τ to get infected.
  - A node which gets in contact with the infected person at time $(t - \tau)$ becomes infected after the time delay of τ.
  - The infection rate is represented by β and μ represents the recovery rate where, β and $\mu \in [0, 1]$.
- Let $S(k, t), I(k, t)$ and $R(k, t)$ be the fraction of the susceptible, infected and recovered nodes at time t with degree of k such that, $S(k, t) + I(k, t) + R(k, t) = 1$.

Dynamical behaviors of the model

Now, using the mean-field, rate equations are defined for dynamics of epidemic on network, based on transitions rule with time delay τ,

$$\frac{dS(k,t)}{dt} = -\beta k S(k,t)\Omega_k(t-\tau) \tag{3}$$

$$\frac{dI(k,t)}{dt} = \beta k S(k,t)\Omega_k(t-\tau) - I(k,t) \tag{4}$$

$$\frac{dR(k,t)}{dt} = I(k,t). \tag{5}$$

Where,

$$\Omega_k(t) = \sum_{k=1}^{k_{max}} P(k^{'}|k) I(k,t)$$

$$\Omega_k(t-\tau) = \sum_{k=1}^{k_{max}} P(k^{'}|k) I(k,(t-\tau))$$

$$\Omega_k(t-\tau) = \frac{\sum_{k=1}^{k_{max}} k^{'} P(k^{'}) I(k,(t-\tau))}{\langle k \rangle}. \tag{6}$$

Dynamical behaviors of the model....

- Therefore, from Eq.3, Eq.5 and Eq.6,

$$\frac{dS(k,t)}{dR(k,t)} = \frac{-\beta k S(k,t) \sum_{k=1}^{k_{max}} P(k'|k) I(k,(t-\tau))}{I(k,t)}. \quad (7)$$

- After solving Eq. 7 we get, $\beta = \frac{\langle k \rangle}{\langle k^2 \rangle \tau} > 1$.
- If $\tau \to 0$, then, $\beta_c \to \infty$, it means that epidemic spread quickly to whole population,which is not realistic.
- To make value of β_c countable $\tau + 1$ is used in place of τ, hence, if $\tau > 0$, $\beta > \beta_c = \frac{\langle k \rangle}{\langle k^2 \rangle (\tau+1)}$.

Results and Analysis

- In this section, we discuss the results of our simulations performed using *SIR with delay* model using three different types of underlying networking topologies: Random Graph, RGG with and without mobile agents.
- Various parameters for simulations are listed in Table.

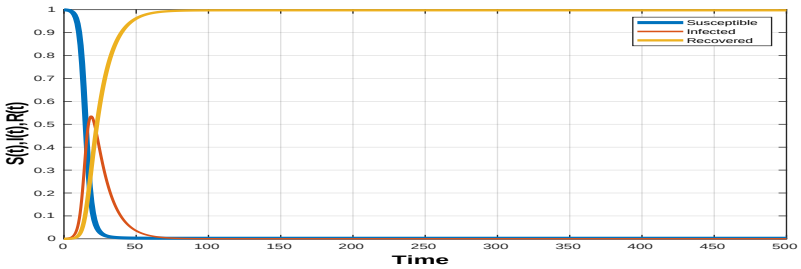
Results and Analysis

Table: Simulation Parameters

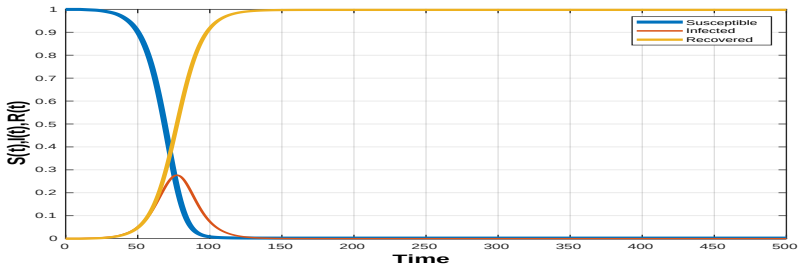
Name of Parameter	**Value**
Nodes	2000
Simulation Area (Square Region)	2500m x 2500m
Length of simulation Area (a)	2500m
Connectivity Radius (r) for (RGG & GNMN)	2m
Spreading Rate (β)	0.6
Recovery Rate (μ)	1
Delay (τ)	[0,10,20,30]
Connectivity probability for (E-R model)	0.2
Expected length between two random point	0.521*a
Velocity (V) for (GNMN)	Random(3, 100)

Results and Analysis

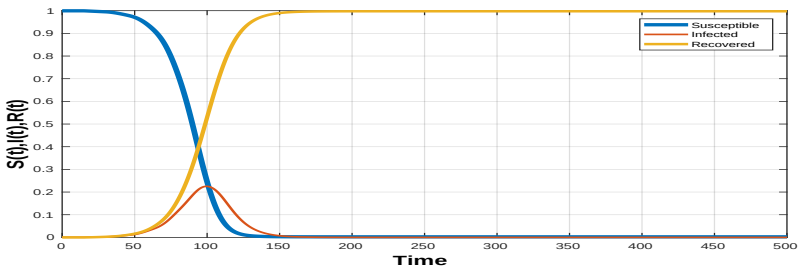
- **Effect of delay in SIR Considering GNMN**



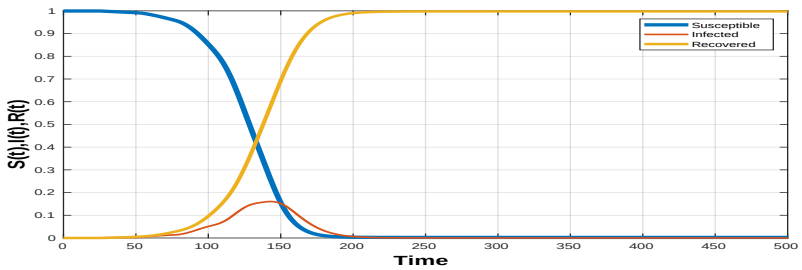
(a) Spreading with Delay 0.



(b) Spreading with Delay 10



(c) Spreading with Delay 20



(d) Spreading with Delay 30

Figure: Effect of delay in SIR considering underlying GNMN

- We observed that with the increase in delay, there is decrease in peak of spreading but the time scale for the existance of disease increases.

Results and Analysis

- **Effect of Delay on Critical Threshold**

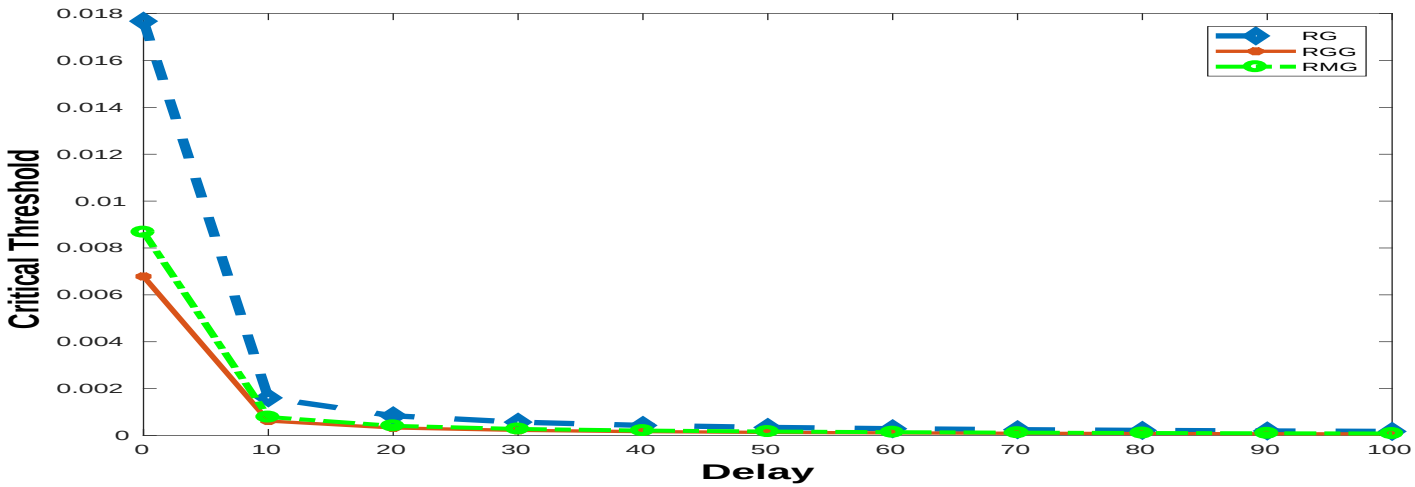


Figure: Effect of delay on critical threshold on RG,RGG, GNMN

- Higher delay may be used to stop the epidemic outbreak against the given spreading rate.

Phase 3

Impact of Seasonal Conditions On Vector-Borne Epidemiological Dynamics

- Proposed Seasonal SIR Model considering underlying network topology
- Results and analysis

Environmental factors of vector-borne epidemic spreading

Many researchers have studied the relationship between the vector population dynamics and the conditions of their habitual environments

- Temperature is one of the main environmental variables influencing vector-borne disease dynamics [4].
- Mordecai et al summerise the temperature dependence of transmission across vectors, pathogens, and environment[5].
- Literature suggests that temperature has an impact on the life cycle of pathogens, especially reproduction and extrinsic incubation period affecting disease dynamics.

[4] Alexander T. Ciota and Alexander C. Keyel.The role of temperature in transmission of zoonotic arboviruses.Viruses, 11, 1013, 2019.

[5] Erin A. Mordecai, Jamie M. Caldwell, Marissa K. Grossman, Catherine A. Lippi, Leah R. Johnson, Marco Neira, Jason R. Rohr,Sadie J. Ryan, Van Savage, Marta S. Shocket, Rachel Sippy, Anna M. Stewart Ibarra, Matthew B. Thomas, and Oswaldo Villena.Thermal biology of mosquito-borne disease.Ecology Letters, 22:1690–1708, 2020.

Proposed Model

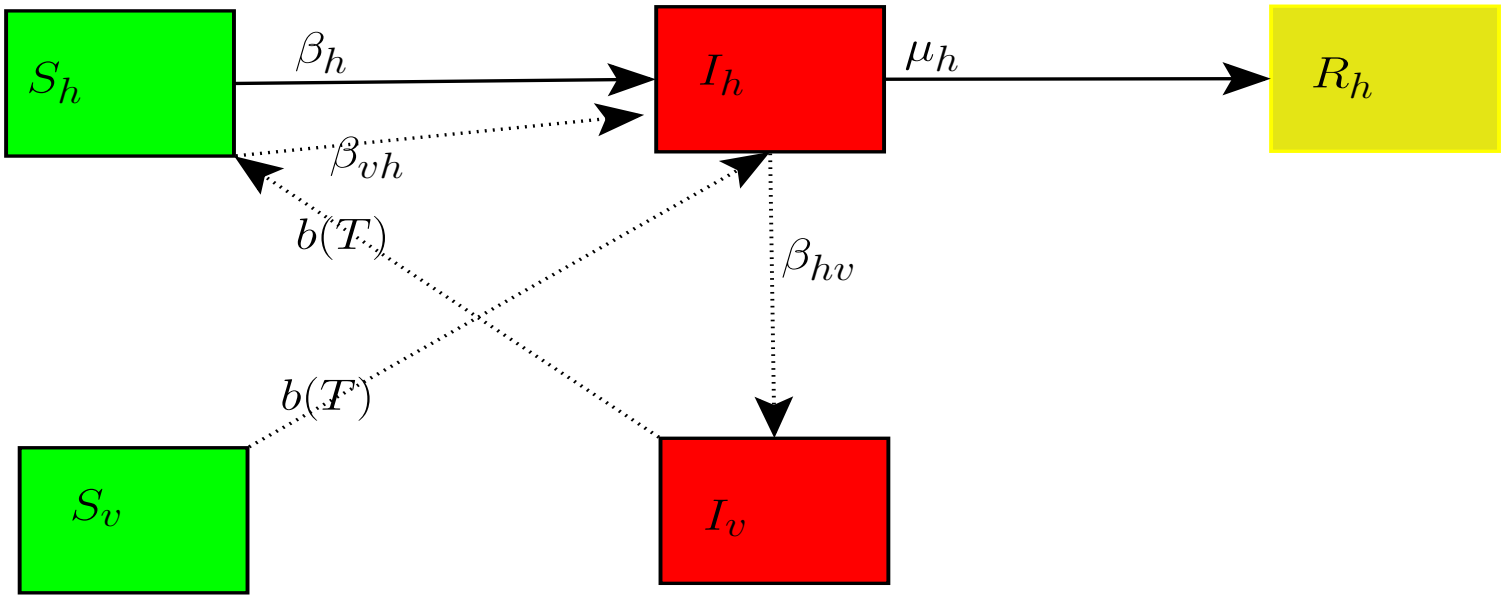


Figure: Block diagram of the Seasonal SIR model. The host population (top) is split into 3 states: Susceptible S_h,Infectious I_h, and recovered R_h. The vector population (bottom) is split into 2 states: Susceptible S_v and Infectious I_v.

Proposed Model

- Vectors are reproduced between temperature range $4.3^{\circ}C$ and $37^{\circ}C$ [5].
- Increase in vector population leads to increment of biting.
- We adopt a Gaussian behavior to model the variation of the biting rate with the temperature. It is expressed as follows:

$$b(T) = b_0 e^{-C(T-T_0)^2} \tag{8}$$

where, C is constant and b_0 is the maximum biting rate at ambient temperature T_0.

- T_0 varies geographically depending upon temperature range and adaptability of vectors.

[5] Erin A. Mordecai, Jamie M. Caldwell, Marissa K. Grossman, Catherine A.Lippi, Leah R. Johnson, Marco Neira, Jason R. Rohr, Sadie J. Ryan, VanSavage, Marta S. Shocket, Rachel Sippy, Anna M. Stewart Ibarra, Matthew B.Thomas, and Oswaldo Villena. Thermal biology of mosquito-borne disease.Ecology Letters, 22:1690–1708, 2020.

Proposed Model

In this section, we integrate the effect of the environmental temperature conditions on the epidemic model.

- There are two type of population: host and vector population.
- Let N_h be the total host population, where $S_h(k,t)$, $I_h(k,t)$ and $R_h(k,t)$ are the fraction of the Susceptible, Infected and Recovered nodes at time t with degree k.
- let N_v be the vector population size and$S_v(t)$ and $I_v(t)$ are respectively the fraction of the susceptible and infected vector at time t.
- Recovered class in the vector population is not considered due to their short lifespan.

Model Formulation

Based on the transitions for heterogeneous networks, the mean-field rate equations are defined as follows:

$$\frac{dS_h(k,t)}{dt} = -\beta_h k S_h(k,t)\Omega_h(k,t) - \beta_{vh} b(T) S_h(k,t) I_v(t) \tag{9}$$

$$\frac{dI_h(k,t)}{dt} = \beta_h k S_h(k,t)\Omega_h(k,t) + \beta_{vh} b(T) S_h(k,t) I_v(t) - I_h(k,t) \tag{10}$$

$$\frac{dR_h(k,t)}{dt} = I_h(k,t). \tag{11}$$

$$\frac{dS_v(t)}{dt} = -\beta_{hv} b(T) S_v(t) I_h(k,t) - \mu_v S_v(t) \tag{12}$$

$$\frac{dI_v(t)}{dt} = \beta_{hv} b(T) S_v(t) I_h(k,t) - \mu_v I_v(t) \tag{13}$$

Model Formulation....

After Solving mean field equation mentioned in Eq. ((9)-(13)), we get

$$\frac{\sum_{k=1}^{k_{max}} kp(k)}{\langle k \rangle}\beta_h k + \beta_{vh} b(T)^2 \beta_{hv} > 1$$

$$\frac{\langle k^2 \rangle}{\langle k \rangle}\beta_h + \beta_{vh} b(T)^2 \beta_{hv} > 1 \tag{14}$$

The left side of the Eq. (14) is the basic reproduction number R_{0_h}.

$$R_{0_h} = \frac{\langle k^2 \rangle}{\langle k \rangle}\beta_h + \beta_{vh} b(T)^2 \beta_{hv}$$

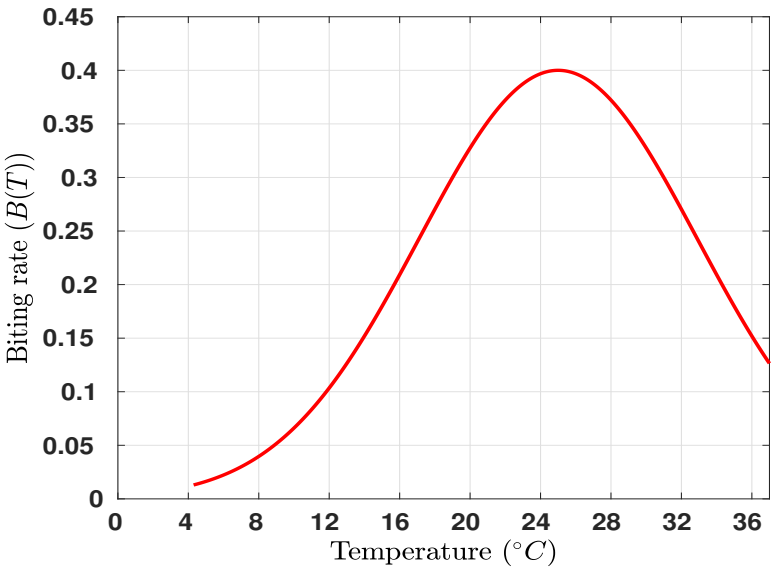
Where β_h, β_{vh} and β_{hv} are constant characterizing the disease, and $\frac{\langle k^2 \rangle}{\langle k \rangle}$ is a constant characterizing the contact network statistics.
Therefore, for a given network, R_{0_h} is proportional to the square of the biting rate i.e. $b(T)^2$.

Simulation Parameters

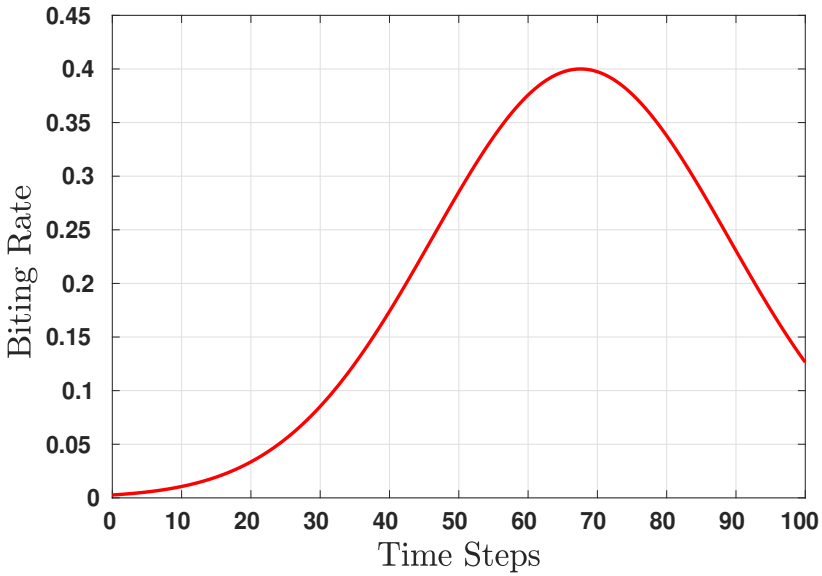
Table: **Values of the parameters used in the simulations**

Name of Parameter	**Value**
Number of nodes for host population	2000
Number of edges to attach for BA model(m)	10
Vector population size	100000
Initial Number of infected host	1
Initial Number of infected vector	100
Host Recovery Rate (μ_h)	1
T_0	$25^\circ C$
Biting rate of vector (b_0) at T_0	0.4
Range of temperature (T)	$[4.3, 37]^\circ C$
C	0.008

Biting of vector population



(a) Biting rate of vector versus temperature



(b) Biting rate of vector population versus Time

Figure: Plot representing the biting rate of the vector population

- Biting increases with the increase of temperature till ambient temperature.

Epidemic Spreading in Heterogeneous Host Population With Vector

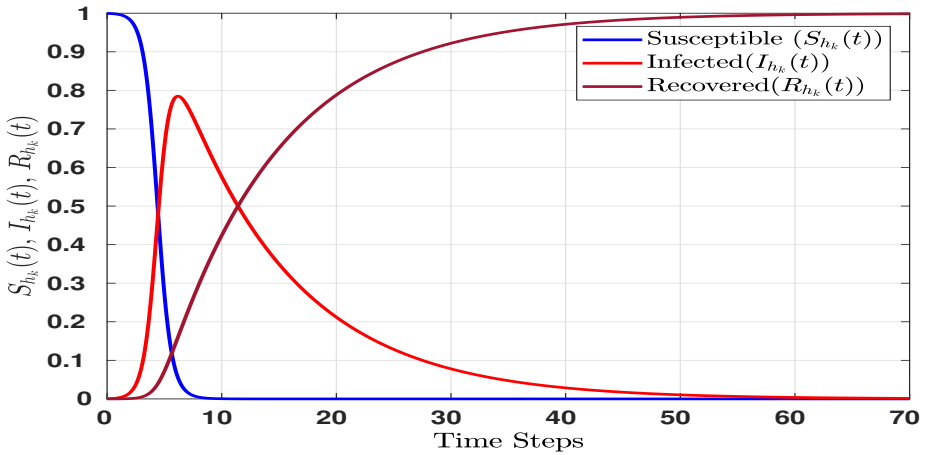


Figure: Evolution of the epidemic spreading considering both routes of transmission (Host-to-Host as well as Host-to-vector interaction).

- The epidemic spreads among host population quickly and last longer when there is two routes of transmissions.

Epidemic Spreading in Homogeneous Host Population

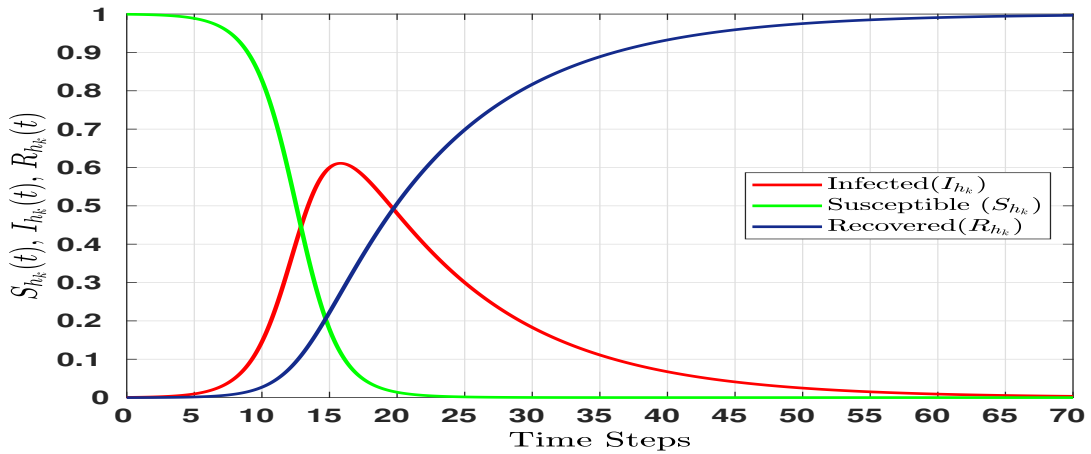


Figure: Evolution of the epidemic spreading in an homogeneous host population.

- In homogeneous contact network, both the peak value of the infected host is low and the time to reach this value is high.

Effect of Temperature on Epidemic Spreading in Host Population

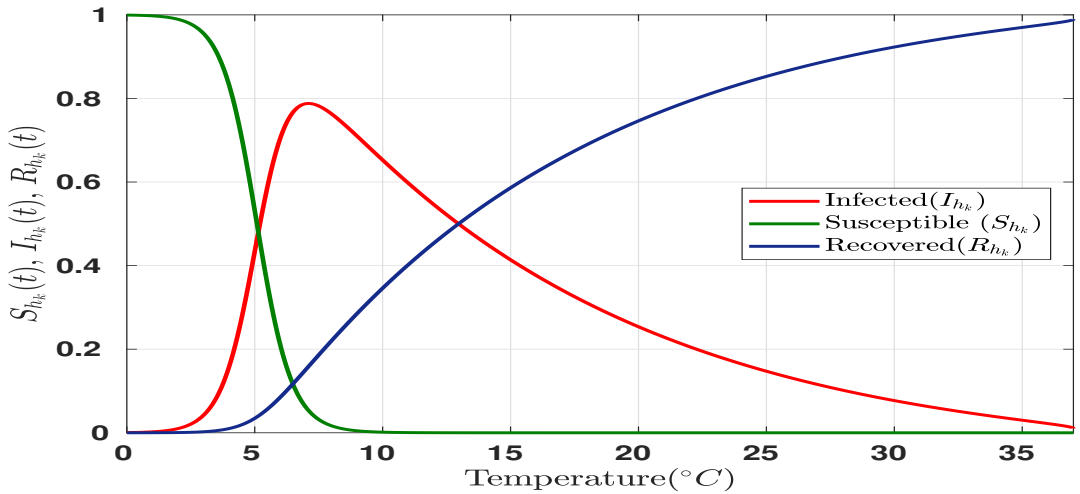


Figure: Evolution of the epidemic spreading in the heterogeneous host population versus the temperature.

- The infection in the host population propagates much faster due to host to host interactions as well as vector to host interactions.

Effect of Temperature on Infection Spreading in Host Using Single Route of Transmission

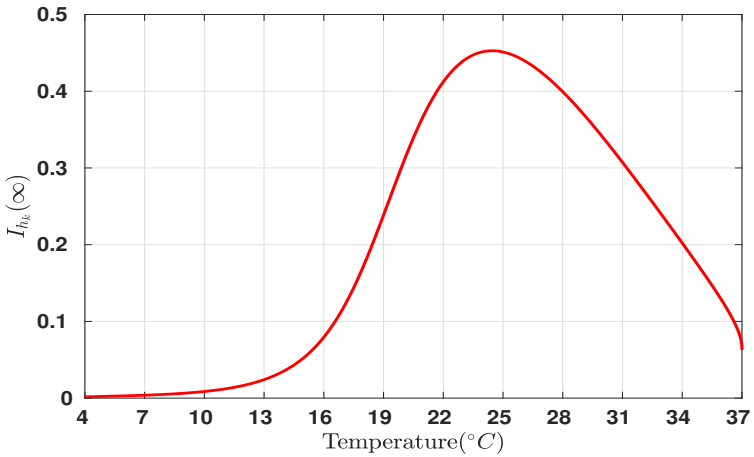


Figure: Epidemic spreading in the heterogeneous host population using single transmission

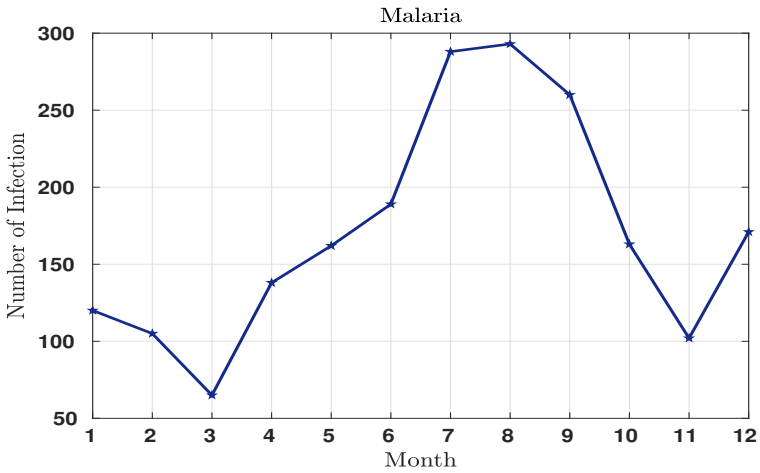
- Epidemic increases till ambient temperature.

Effect of Network Topology on Basic Reproduction Number (R_{0_h})

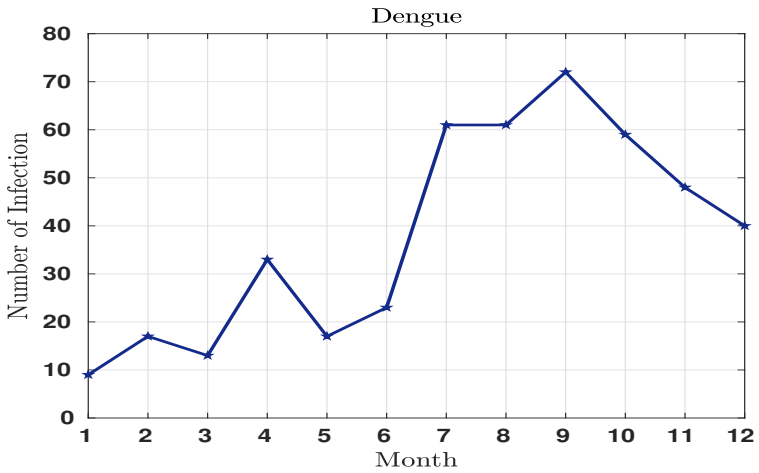
Table: Effect of the network topology on the basic Reproduction Rate(R_{0_h}).

Type of Contact Network	R_{0_h}
Heterogeneous Network (B-A Model)	23.1
Homogeneous Network (WS Model)	18.04

Simulation of Dataset



(a) Infection due to Malaria in each month

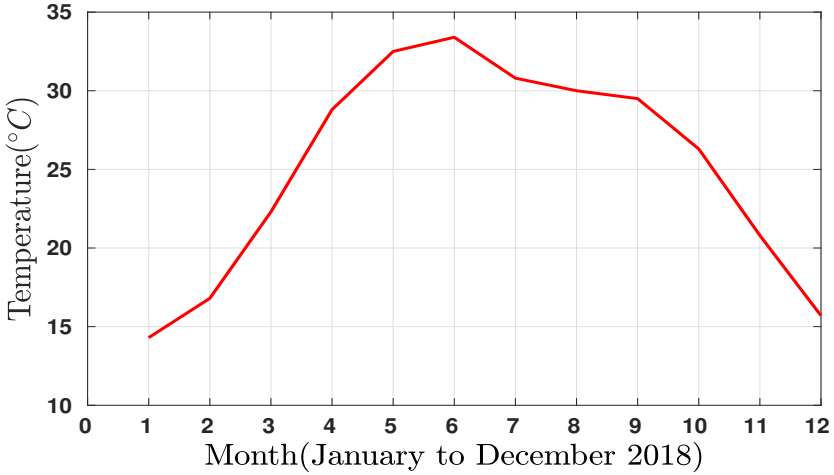


(b) Infection due to Dengue in each month

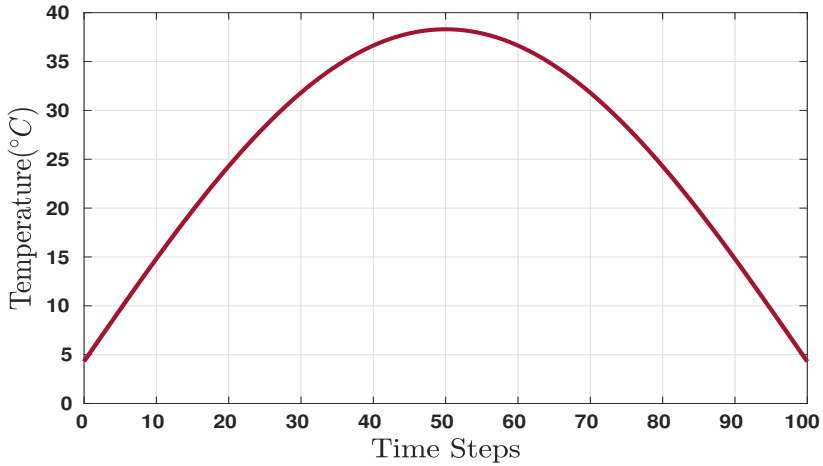
Figure: Evolution of the number of infection during the year for ((a) Malaria , (b) Dengue. Data recorded from the Hospital of New Delhi.

- Impact of disease is maximum between June to October

Simulation of Dataset



(a) Average Temperature of Delhi month wise



(b) Synthetic Model of Temperature

Figure: Average monthly temperatures (a) recorded in Delhi-NCR during the 2018 civil year. Simulated temperature using a gaussian distribution (b)

Example Work

- Information spreading is almost similar to epidemic spreading on network
- Information is propagated through contacts in network in similar way to epidemic spreading in contact network.

Information propagation on Social Network

- In this work we have covered the effect of information dynamics on network specially misinformation or rumor.
- After the development of the internet, people are densely connected with each other to share information rapidly[8].
- Nowadays social network like facebook, twitter is very common for communication among people to do collaborative action.

[8] Matsubara, Yasuko, et al. "Rise and fall patterns of information diffusion: model and implications." Proceedings of the 18th ACM SIGKDD international conference on Knowledge discovery and data mining. 2012.

Network Model

- Consider the network as an undirected graph, $G = (V, E, C, I)$, where V is set of n vertices, such that $V = \{V_1, V_2, ...V_n\}$.
- E is the set of edges, where each edge $e_{ij} \in E$, connects a vertex V_i with the vertex V_j.
- I represents a set of information type, such that $I = \{I_1, I_2, ...I_4\}$.
- C represents a credibility set, such that $C = \{C_1, C_2, ...C_n\}$, where $C_j = \{I_{j_i}, V_j\}$.
- Each vertex V_j has a particular credibility $C_{(I_{j_i}, V_j)} \in C$. It has global impact on network and different from trust.

Trust Relationship

In the proposed model, we consider trust relationships among the users in a network. Each user, V_i keeps track of a trust value T_{V_i,V_j} with each of its neighboring users, $Ne(V_i)$. There are two types of trust are used in this method.

1. Local Trust
2. Global Trust

Analysis of Real World Dataset

- We have simulated the blockchain based information propagation on a real network and synthetic network dataset as underlying networks topology.
- We have taken two real-world network dataset, Facebook data set [9] and LiveJournal social network[10] as mentioned in Table.

Table: Facebook and Live Journal Network Dataset statistics

Name of Parameter	**Facebook**	**Live Journal**
Nodes	46952	3997962
Edges	876,993	34681189
Average clustering coefficient	0.0851	0.2843
Mean Shortest Path	5.7	6.5
Number of triangles	122,852	177820130

[9] Leskovec, Jure, and Julian McAuley. "Learning to discover social circles in ego networks." Advances in neural information processing systems 25 (2012): 539-547.

[10] Yang, Jaewon, and Jure Leskovec. "Defining and evaluating network communities based on ground-truth." Knowledge and Information Systems 42.1 (2015): 181-213.

Analysis of Real World Dataset.....

- Various other parameters used for seed nodes to propagate information are listed in Table. These parameters are used to initialize the node identity with different credibility score according to info type.
- Taking inspiration from **PEW Research Center** report, the distribution of topics among nodes followed by using the same pattern[11].

Table: Simulation Parameters

Cred_Score	random (0-1)
Info_type	[Pol,Tech,Movie,Research]
Information generating nodes (Seed Nodes)	100

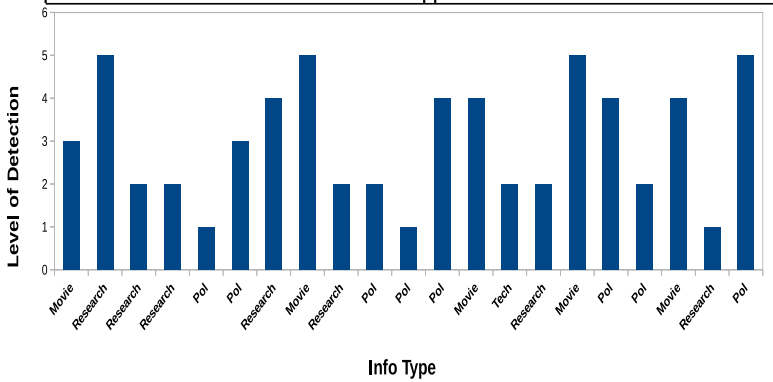
[11] PEW Research Centre, 2018. http://www.pewinternet.org/.

Analysis of Real World Dataset.....

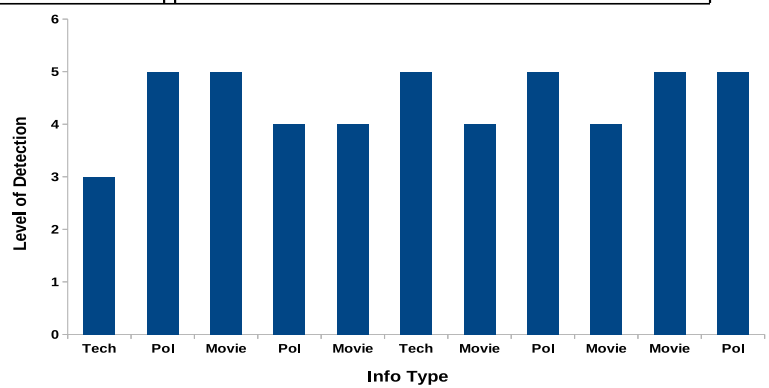
- We evaluate our model using real datasets from Facebook and Live journal. Our model achieves an accuracy of 83% on the Facebook dataset and 89% on Live journal dataset.

Table: Average Level of Detection

Info Type	Average Level of Detection(Facebook)	Average Level of Detection(Live Journal)
Pol	3	5
Tech	2	4
Research	3	
Movie	4	5



(a)Level of Detection in Facebook network



(b) Level of Detection in Live journal network data

Analysis on Synthetic Network

- We also perform an experiment on two synthetic networks considering E-R network model and BA model of a scale free network.
- To generate a random network and scale free network we have to consider various parameter listed in Table.

Table: Simulation Parameters for Synthetic Network

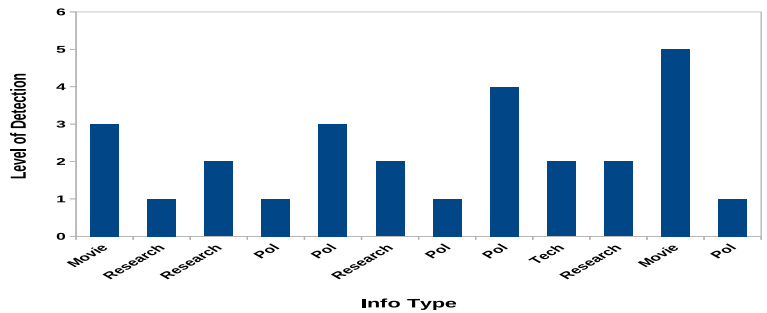
Name of Parameter	**Value**
Nodes	2000
Cred_Score	random (0-1)
Info_type	[Pol,Tech,Movie,Research]
Connecting probability (p) (for $E-Rmodel$)	0.2
Number of edges to attach from a new node to existing nodes (m) (for BA Model)	10
Message generating node (Seed Nodes)	100

Analysis on Synthetic Network ..

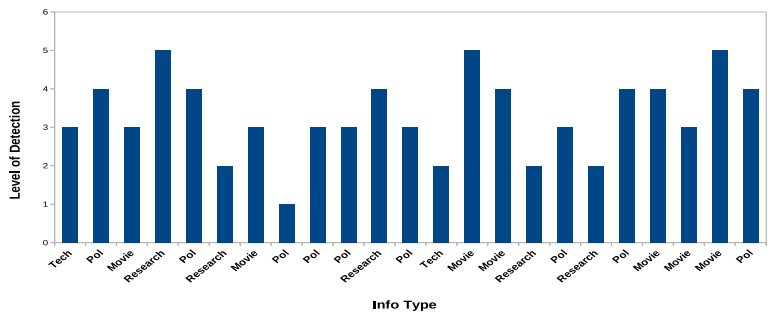
- We also evaluate our model using E-R Network Model and BA Network Model. Our model achieves accuracy of 77% in case of E-R Network Model as underlying topology and 89% in the case of BA Network Model

Table: Average Level of Detection in Synthetic Network

Info Type	**Average Level of Detection in Scale-Free Network**	**Average Level of Detection in E-R Network**
Pol	2	4
Tech	2	3
Research	2	3
Movie	4	4



(a)Level of Detection in Scale-Free Network



(b) Level of Detection in Random Network

Conclusions

- A geometric Network with Mobile Nodes is proposed.
- Increasing movement and t_{rest} time increases the spreading.
- SIS and SIR Model is performed considering GNMN as underlying contact network.
- A delayed SIR model is proposed considering delay in infection and incorporating the underlying network parameters
- Delay in infection decreases the critical threshold of spreading
- A seasonal SIR model is proposed considering dual route of transmission and environmental temperature condition.
- Basic reproduction number R_0 is derived in term of biting rate which is function of temperature.
- A model is proposed to study the spreading of COVID-19

Future Direction

- This work may be extended for future work based on the random mobility, such as the effect of the mixing rate and the connectivity fluctuation parameter.
- This work may be extended to include infection delay and recovery delay simultaneously.
- The work may be extended for dynamic network.
- The work may be extended to consider other environmental features such as humidity.

List of Publications

Journal Publications

J1. **Arquam, Md**, and Anurag Singh. "Epidemic Spreading in Geometric Network with Mobile Agents." *Acta Physica Polonica B 51.9 (2020)*: 1853.

J2. **Arquam, Md**, Anurag Singh, and Hocine Cherifi. " Impact of Seasonal Conditions on Vector-Borne Epidemiological Dynamics." *IEEE Access 8 (2020)*: 94510-94525.

Conference Publications

C1. Singh, Anurag, Bhasin Samriddhi, , Gakhar, Bhanu, **Arquam, Md**. "Modeling the effect of Quarantine and Isolation forCOVID-19 Spreading." *International Conference on Sustainable and Innovative Solutions for Current Challenges in Engineering & Technology* Springer Cham, 2020.

C2. Agrawal, Rimjhim, **Arquam, Md**, and Anurag Singh. "Community detection in Networks using Graph Embedding." *Procedia Computer Science* 173 (2020): 372-381.

C3. **Arquam, Md**, Anurag Singh, and Hocine Cherifi. "Integrating Environmental Temperature Conditions into the SIR Model for Vector-Borne Diseases." *International Conference on Complex Networks and Their Applications*. Springer, Cham, 2019.

C4. **Arquam, Md** and Anurag Singh "Challanges in Network Modeling of communicable and Noncommunicable Diseases in Complex Network." *Proc. ICEIT Conference on Advances in Mobile Communications, Networking and Computing*, New Delhi, April 11-12, 2019.

C5. **Arquam, Md**, Anurag Singh, and Rajesh Sharma. "Modelling and analysis of delayed sir model on complex network." *International Conference on Complex Networks and their Applications*. Springer, Cham, 2018.

Communicated

1. **Arquam, Md**, Anurag Singh, and Rajesh Sharma. "A Blockchain-based Secured and Trusted framework for Information Propagation on Online Social Networks." Under review in SNAM(Social Network Analysis and Mining)

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Thank
you