Vol.11.Issue.2.2023 (April-June)

http://www.bomsr.com

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RESEARCH ARTICLE

BULLETIN OF MATHEMATICS AND STATISTICS RESEARCH

A Peer Reviewed International Research Journal

INTERNATIONAL STANDARD SERIAL NUMBER 2348-0580

Analysis on SAE(AI)ITRD -Epidemic model over the complex network

Varshinipriya M[1], Padmavathi Ramamoorthi[2]

[1,2] PG & Research Department of Mathematics

Sri Ramakrishna College of Arts & Science(Autonomous) Coimbatore-641006, India

DOI:10.33329/bomsr.11.2.49

ABSTRACT

A SAE (AI) ITRD model over a complex network is being framed to study the spreading dynamics of a disease with awareness using a Markov chain approach. Most of the spreading disease like COVID, Hepatitics etc., follows SE(AI)ITRD Spreading process. The model is well suitable to study disease with awareness. The basic reproduct number R_0 is found using the next-generation matrix. The model is verified through numerical simulation. keywords: Epidemiology, Aware- ness, Complex networks, Markov chain.

1 INTRODUCTION

Epidemiology is the method used to find the causes of health outcomes and diseases in populations.In epidemiology,the patient is the community and individuals are viewed collectively.John Snow was conducting a series of investigations in London that warrant his begin considered the ”father of field epidemiology.”Twenty years before the development of the microscope,Snow conducted studies of cholera outbreaks both to discover the cause of disease and to prevent its recurrence.

Epidemiologic studies may be

- Descriptive, organizing data by time, place, and person;
- Analytic, incorporating a case-control or cohort study;
- Experimental.

The WHO’s pandemic alert system ranges from Phase 1(a low risk) to Phase 6(a full pandemic):

- Phase 1:A virus in animals has caused no known infections in humans.
- Phase 2:An animal virus has caused infection in humans.

- Phase 3:There are scattered cases of small clusters of disease in hu- mans.If the illness is spreading from human to human,it's not broad enough to cause community- level outbreaks.
- Phase 4:The disease is spreading from person to person with confirmed outbreaks at the community level.
- Phase 5:The disease is spreading between humans in more than one country of one of the WHO regions.
- Phase 6:At least one more country,in a different region from Phase 5,has community-level outbreaks.

This work discusses the Phase 6 type spreading disease with awareness.

2 Model description

A complex network with 1000 nodes is used to represent the population. The population is divided into six categories as.

S- Susceptible, people who are healthy and capable to get infection.

A- Awareness, people who get aware about the infection and capable to get infection.

E- Exposed, people who are having infection in the initial and spread infec- tion to other.

AI- Asymptomatic Infection, people who get infection without symptoms and spread infection via indirect contact.

I- Infected, people who have infection with symptoms and spread infection to others.

T- Treatment, people who are taking treatment.

R- The person who got Recovery from the disease. D- dead, people are died to the disease.

M=(m_{ij}) -represents the contacts among the population.

Probability of unaware individual not being infected by any of its neighbours is $r_i^U\ (t)\ = \prod_{j=1}^{n}(1\ - \sigma(AI_j\ +\ I_j)m_{ji})$,Probability of aware individual being informed by any of its neighbours is $r_i^A\ (t)\ = \prod_{j=1}^{n}(1\ - \sigma\zeta(AI_j\ +\ I_j)m_{ji})$.

Hence, totally there are eight possible states in the population, namely S_i, A_i, E_i, I_i, AI_i, T_i, R_i, D_i.

3 Microscopic Markov Chain Approach

Table 1: Parameters and their description

Parameters	Description
m_{ij}	adjacency matrix which represent the contacts among the peoples.
σ	Probability of getting infection of a healthy person.
$(1-\epsilon)_\eta$	transmission rate from exposed state to infected state(Testing).
ϵη	transmission rate from exposed state to asymptomatic state.
δ	recovery rate for an Asymptomatic infected individual through immunity.
κβ	death rate to infection for a person in treatment.
ω	rate of infected individual getting treatment.
γ	infected rate of getting awareness.
r_i^A	probability of an aware person i not being infected.

r_i^U probability of an unaware person i not being infected.
ζ infection reduction factor.
β death rate due to infection for an infected person.
ρ recovery rate for a person in treatment.

The possible transmission flow among the eight states are shown in fig(1).

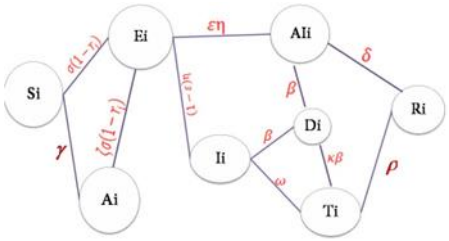


Figure 1: Transmission flow among the states

$X_i(t)$ denotes probability that the i^{th} person is in the state X, $X = S_1, A_1, E_1, AI_1, I_1, T_1, R_1, D_1$. The mathematical equations representing the probability of i^{th} node in various states at time $t + 1$ are given by

$$S_i(t+1) = A + S_i(t)(1 - \sigma(1 - r_i^U(t)) - \gamma) \quad (1)$$

$$A_i(t+1) = S_i(t)\gamma + A_i(t)(1 - \zeta\sigma(1 - r_i^A)) \quad (2)$$

$$E_i(t+1) = S_i(t)[\sigma(1 - r_i^U)] + A_i(t)[\zeta\sigma(1 - r_i^A)] + E_i(t)(1 - \eta) \quad (3)$$

$$AI_i(t+1) = E_i(t)\epsilon\eta + AI_i(t)(1 - \delta - \beta) \quad (4)$$

$$I_i(t+1) = E_i(t)(1 - \epsilon)\eta + I_i(t)(1 - \omega - \beta) \quad (5)$$

$$T_i(t+1) = I_i(t)\omega + T_i(t)(1 - \kappa\beta - \rho) \quad (6)$$

$$R_i(t+1) = T_i(t)\rho + AI_i(t)\delta + R_i(t) \quad (7)$$

$$D_i(t+1) = [AI_i(t) + I_i(t) + \kappa T_i(t)]\beta + D_i(t) \quad (8)$$

$$S_i(t) + A_i(t) + E_i(t) + AI_i(t) + I_i(t) + T_i(t) + R_i = 1 \forall t, \quad \forall i = 1, 2 \ldots N. \quad (9)$$

Solving the system of equations (1 to 9) iteratively, the time evolution of the system for any initial condition can be found.

3.1 Continuous time Markov chain approach

Linearising r_i^U and $r_i^A, r_i^U \approx 1 - \sum_j[\sigma(AI_j + I_j]m_{ji}$ and $r_i^A \approx 1 - \sum_j[\zeta\sigma(AI_j + I_j)m_{ji}$. The continuous time linearised mathematical

$$\frac{dS_i}{dt} = \left(\left(1 - \sigma - \sigma r_i^U\right) - \gamma - 1\right) S_i$$

$$\frac{dA_i}{dt} = \gamma S_i + \left(\left(1 - \zeta\sigma - \zeta\sigma r_i^A\right) - 1\right) A_i$$

$$\frac{dE_i}{dt} = S_i\left(\sigma\left(1 - r_i^U\right)\right) + A_i\left(\zeta\sigma\left(1 - r_i^A\right)\right) + E_i\left((1-\eta) - 1\right)$$

$$\frac{dAI_i}{dt} = E_i\epsilon\eta + AI_i\left((1 - \delta - \beta) - 1\right)$$

$$\frac{dI_i}{dt} = E_i(1-\epsilon)\eta + I_i\left((1 - \omega - \beta) - 1\right)$$

$$\frac{dT_i}{dt} = I_i\omega + T_i\left((1 - \kappa\beta - \rho) - 1\right)$$

$$\frac{dR_i}{dt} = T_i\rho + AI_i\delta - R_i$$

$$\frac{dD_i}{dt} = \left(AI_i + I_i + \kappa T_i(t)\right)\beta - D_i \qquad (10)$$

Definition 1.

The feasible region Γ is defined as

$$\Gamma = \{(S_1, A_1, E_1, AI_1, I_1, T_1, R_1, D_1, S_2, A_2, E_2\ AI_2, I_2, T_2, R_2, D_2, \ldots\ldots S_N, A_N, E_N\ AI_N, I_N, T_N, R_N, D_N)$$

$$*\ \epsilon R^{8N} / \sum_{I=1}^{n} S_1 + A_1 + E_1 + AI_1 + I_1 + T_1 + R_1 + D_1)N\}$$

The feasible region Γ is positively invariant with respect to(1) to (9) and the disease free equilibrium(DFE)

$P_0 = (S_1^0, 0, 0, 0, 0, 0, 0, S_2^0, 0, 0, 0, 0, 0, \ldots\ldots\ldots S_n^0, 0, 0, 0, 0, 0)$ with S_i^0= 1 always exists in Γ next generation matrix.

Theorem 1 finds the basic reproduction number R_0 using NGM.

Theorem 1 The basic reproduction number R0 of the system is given by $\Lambda_{\max}$(H), where h_{ij} =$\left(\frac{C_i}{\zeta+\delta}\right) m_{ij}$, $C_i = \sigma^2(S_i + \zeta^2 A_i)$.

Proof

The equations corresponding to exposed,asymptomatic and infected states are

$$\frac{dE_i}{dt} = S_i\sigma + A_i\zeta\sigma - S_i\sigma\left[1 - \sum \sigma\ (AI_i + I_i)m_{ji}\right] - A_i\zeta\sigma\ \left[1 - \sum \zeta\sigma\ (AI_i + I_i)m_{ji}\right] - E_i\eta$$

$$\frac{dAI_i}{dt} = E_i\epsilon\eta - AI_i\ (\delta + \beta)$$

$$\frac{dI_i}{dt} = E_i(1-\epsilon)\eta - I_i(\omega + \beta) \qquad (11)$$

Take $C_i = \sigma^2(S_i + \zeta^2 A_i)$, i=1,2,....N.

The above equation can be written as

$$\frac{dE_i}{dt} = (C_i \sum_j (AI_j + I_j) m_{ji}) - E_i \eta$$

$$\frac{dAI_i}{dt} = \epsilon \eta E_i - (\delta + \beta) AI_i$$

$$\frac{dI_i}{dt} = (1 - \epsilon) \eta E_i - (\omega + \beta) I_i$$

Let $X = (E_1, E_2, \ldots E_N, AI_1, AI_2, \ldots AI_N, I_1, I_2, \ldots I_N)^T$.

The above equations can be written as

$$\frac{dx}{dt}(F - V)X.$$

Where

$$F = \begin{pmatrix} 0 & C_1 m_{11} & 0 & C_1 m_{21} & 0 & C_1 m_{31} & \cdots & 0 & C_1 m_{N1} \\ 0 & C_2 m_{12} & 0 & C_2 m_{22} & 0 & C_2 m_{32} & \cdots & 0 & C_2 m_{N2} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \\ 0 & C_N m_{1N} & 0 & C_N m_{2N} & 0 & C_N m_{3N} & \cdots & 0 & C_N m_{NN} \\ 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \\ 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \\ 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 \end{pmatrix}_{(3N \times 3N)}$$

$$V = \begin{pmatrix}
\eta & 0 & 0 & \cdots & 0 & 0 & 0 & 0 & \cdots & 0 \\
0 & 0 & 0 & 0 & \cdots & 0 & & & & \\
0 & \eta & 0 & \cdots & 0 & 0 & 0 & 0 & \cdots & 0 \\
 & 0 & 0 & 0 & \cdots & 0 & & & & \\
\vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\
 & \vdots & \vdots & \vdots & \ddots & \vdots & & & & \\
0 & 0 & 0 & \cdots & \eta & 0 & 0 & 0 & \cdots & 0 \\
 & 0 & 0 & 0 & \cdots & 0 & & & & \\
-\epsilon\eta & 0 & 0 & \cdots & 0 & \delta+\beta & 0 & 0 & \cdots & 0 \\
 & 0 & 0 & 0 & \cdots & 0 & & & & \\
0 & -\epsilon\eta & 0 & \cdots & 0 & 0 & \delta+\beta & 0 & \cdots & 0 \\
 & 0 & 0 & 0 & \cdots & 0 & & & & \\
\vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\
 & \vdots & \vdots & \vdots & \ddots & \vdots & & & & \\
0 & 0 & 0 & \cdots & -\epsilon\eta & 0 & 0 & 0 & \cdots & \delta+\beta \\
 & 0 & 0 & 0 & \cdots & 0 & & & & \\
-(1-\epsilon) & 0 & 0 & \cdots & 0 & 0 & 0 & 0 & \cdots & 0 \\
 & \omega+\beta & 0 & 0 & \cdots & 0 & & & & \\
0 & -(1-\epsilon) & 0 & \cdots & 0 & 0 & 0 & 0 & \cdots & 0 \\
 & 0 & \omega+\beta & 0 & \cdots & 0 & & & & \\
\vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\
 & \vdots & \vdots & \vdots & \ddots & \vdots & & & & \\
0 & 0 & 0 & \cdots & -(1-\epsilon) & 0 & 0 & 0 & \cdots & 0 \\
 & 0 & 0 & 0 & \cdots & \omega+\beta & & & &
\end{pmatrix}_{3N\times 3N)}$$

$$= \begin{pmatrix} D(\eta)_{N\times N} & 0_{N\times N} & 0_{N\times N} \\ D(\epsilon\eta)_{N\times N} & D(\delta+\beta)_{N\times N} & 0_{N\times N} \\ D(-(1-\epsilon)\eta)_{N\times N} & 0_{N\times N} & D(\omega+\beta)_{N\times N} \end{pmatrix}.$$

$$R_0 = \Lambda_{max}(FV^{-1})$$

$$V^{-1} = \begin{pmatrix} D(\frac{1}{\eta})_{N\times N} & 0_{N\times N} & 0_{N\times N} \\ D(\frac{\epsilon}{\delta+\beta})_{N\times N} & D(\frac{1}{\delta+\beta})_{N\times N} & 0_{N\times N} \\ D(\frac{1-\epsilon}{\delta+\beta})_{N\times N} & 0_{N\times N} & D(\frac{1}{\omega+\beta})_{N\times N} \end{pmatrix}$$

Hence,

$$FV^{-1} = \begin{pmatrix} \frac{\epsilon c_1 m_{11}}{\delta+\beta} + \frac{(1-\epsilon)c_1 m_{11}}{\delta+\beta} & \frac{\epsilon c_1 m_{21}}{\delta+\beta} + \frac{(1-\epsilon)c_1 m_{21}}{\delta+\beta} & \cdots & \frac{\epsilon c_1 m_{N1}}{\delta+\beta} + \frac{(1-\epsilon)c_1 m_{N1}}{\delta+\beta} & \frac{c_1 m_{11}}{\delta+\beta} & \frac{c_1 m_{21}}{\delta+\beta} \\ & \frac{c_1 m_{11}}{\omega+\beta} & \frac{c_1 m_{21}}{\omega+\beta} & & \frac{c_1 m_{N1}}{\omega+\beta} & \\ \frac{\epsilon c_2 m_{12}}{\delta+\beta} + \frac{(1-\epsilon)c_2 m_{12}}{\delta+\beta} & \frac{\epsilon c_2 m_{22}}{\delta+\beta} + \frac{(1-\epsilon)c_2 m_{22}}{\delta+\beta} & \cdots & \frac{\epsilon c_2 m_{N2}}{\delta+\beta} + \frac{(1-\epsilon)c_2 m_{N2}}{\delta+\beta} & \frac{c_2 m_{12}}{\delta+\beta} & \frac{c_2 m_{22}}{\delta+\beta} \\ & \frac{c_2 m_{12}}{\omega+\beta} & \frac{c_2 m_{22}}{\omega+\beta} & & \frac{c_N m_{N2}}{\omega+\beta} & \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ & \vdots & \vdots & \ddots & \vdots & \\ \frac{\epsilon c_N m_{1N}}{\delta+\beta} + \frac{(1-\epsilon)c_N m_{1N}}{\delta+\beta} & \frac{\epsilon c_N m_{2N}}{\delta+\beta} + \frac{(1-\epsilon)c_N m_{2N}}{\delta+\beta} & \cdots & \frac{\epsilon c_N m_{NN}}{\delta+\beta} + \frac{(1-\epsilon)c_N m_{NN}}{\delta+\beta} & \frac{c_N m_{1N}}{\delta+\beta} & \frac{c_N m_{2N}}{\delta+\beta} \\ & \frac{c_N m_{1N}}{\omega+\beta} & \frac{c_N m_{2N}}{\omega+\beta} & & \frac{c_N m_{NN}}{\omega+\beta} & \\ 0 & 0 & \cdots & 0 & 0 & 0 \\ & 0 & 0 & \cdots & 0 & \\ 0 & 0 & \cdots & 0 & 0 & 0 \\ & 0 & 0 & \cdots & 0 & \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ & \vdots & \vdots & \ddots & \vdots & \\ 0 & 0 & \cdots & 0 & 0 & 0 \\ & 0 & 0 & \cdots & 0 & \\ 0 & 0 & \cdots & 0 & 0 & 0 \\ & 0 & 0 & \cdots & 0 & \\ 0 & 0 & \cdots & 0 & 0 & 0 \\ & 0 & 0 & \cdots & 0 & \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ & \vdots & \vdots & \ddots & \vdots & \\ 0 & 0 & \cdots & 0 & 0 & 0 \\ & 0 & 0 & \cdots & 0 & \end{pmatrix}$$

$$R_0 = \Lambda_{max}(FV^{-1}) = \lambda_{max}(H),$$

where

$$H = \begin{pmatrix} \frac{\epsilon(1-\epsilon)c_1 m_{11}}{\delta+\beta} & \frac{\epsilon(1-\epsilon)c_1 m_{21}}{\delta+\beta} & \cdots & \frac{\epsilon(1-\epsilon)c_1 m_{N1}}{\delta+\beta} \\ \frac{\epsilon(1-\epsilon)c_2 m_{21}}{\delta+\beta} & \frac{\epsilon(1-\epsilon)c_2 m_{22}}{\delta+\beta} & \cdots & \frac{\epsilon(1-\epsilon)c_2 m_{2N}}{\delta+\beta} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\epsilon(1-\epsilon)c_N m_{N1}}{\delta+\beta} & \frac{\epsilon(1-\epsilon)c_N m_{N2}}{\delta+\beta} & \cdots & \frac{\epsilon(1-\epsilon)c_N m_{NN}}{\delta+\beta} \end{pmatrix}_{N\times N}$$

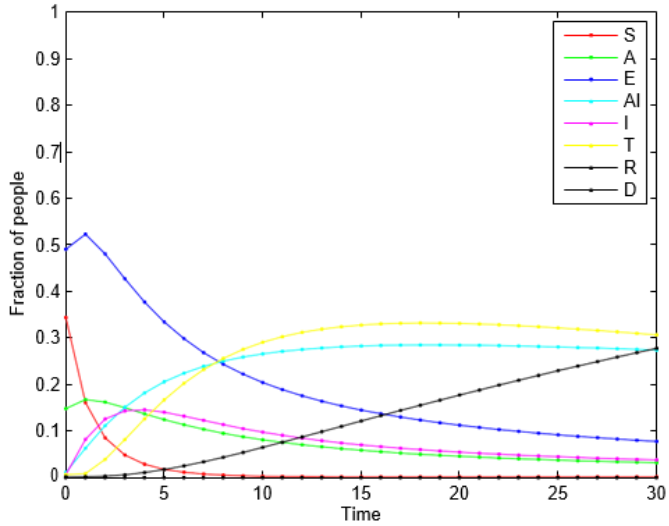


Figure 1: (a) Propagation of various states

The epidemic threshold is given by

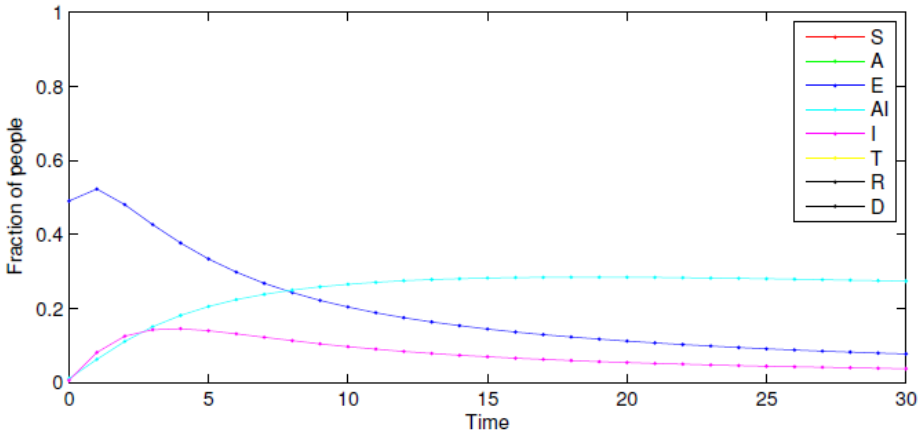
$$R_0 < 1 \Rightarrow \lambda_{max}\,(H) < 1, hv = \left(\frac{C_i}{\delta + \beta}\right) m_{ji}.$$

4 Result and discussion

A complex network, with 100 nodes is taken for numerical simulation. A scale free network is used to represent the direct contacts among the people. The fraction of people in various states at each time step is calculated using MATLAB and it is shown in fig (2). Propagation of Exposed, Infection and Asymptomatic Infection are shown in fig(4).

5 Conclusion

Most of the spreading diseases have both symptomatic and asymptomatic cases in their spreading dynamics. In this paper the spreading dynamics of SAE(AI)ITRD type disease over the complex network is framed. The mathematical model corresponding to the model is framed using microscopic Markov chain approach. The basic reproduction number R_0 is found using the Next-generation matrix. Numerical simulations corresponding to the model is verified.



(b) The propagation of E,I,AI

Figure 2: The impact of awareness reduction factor a) η b) ϵ

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