COVID-19 : An Epidemic to Pandemic Mathematical Analysis of India

Akshaya L*, Alagu Prakalya P[†], Krithika V[‡], Nivetha B[§] and Amelia B A K[¶]

Applied Mathematics and Computational Sciences, PSG College Of Technology

Coimbatore

Email: *19pd04@psgtech.ac.in, [†]19pd05@psgtech.ac.in, [‡]19pd19@psgtech.ac.in, [§]19pd24@psgtech.ac.in, [¶]19pd42@psgtech.ac.in

Abstract—Coronavirus disease 2019 (COVID-19) is a contagious respiratory and vascular disease[1] , caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). First reported in Wuhan, the largest urban in China's Hubei province on December 31, 2019, to the WHO Country Office in China. The spread thus began across the countreis. Due to the high population density, human to human social contact rate is very high in India, which sequentially can spread within a very short period. This paper aims to study the impact of Covid-19 in India through mathematical and graphical analysis. The exponential growth of the projected virus by the day-to-day base is captured in two-dimensional plots to foretell its progress and identify the need to regulate its spread on humanity. Moreover, the implementation of eigenvalues, sparse matrices and eigenvector centrality in the SEQIR model[2] is considered to present some interesting consequences. The dynamics of the SEQIR model is presented by basic reproduction number R_0 and the stability analysis[2]. Numerical inferences are depicted through apt graphical appearances using the data of India[3].

Index Terms—COVID-19, SEQIR, Eigenvalue, Eigenvector centrality, Sparse matrices, Mathematical analysis

I. Introduction

From 2002 to 2003, the severe acute respiratory syndrome coronavirus (SARS-CoV) spiked an epidemic to more than 24 countries dawning from China, which lead to nearly 8000 cases. In 2009 H1F1 influenza was reported, followed by Middle East respiratory syndrome coronavirus (MERS-CoV) in 2012 which was first detected in Saudi Arabia which provoked about 2,500 cases. Based on the history of these epidemics, WHO defined the novel coronavirus as a family of viruses that ranges from the common cold to the MERS-CoV and the SARS-CoV[2].

This novel virus spreads from person to person, principally through the respiratory route. Whenever an infected individual coughs, sneezes, talks, or breaths the transfer happens.New infection occurs when virus-containing particles are exhaled by the infected individual as aerosols and are inhaled, even through eyes by the other who are in close contact[4,5] .Initially, as there was not much awareness of the spread of the virus, gathering in public places took its normal stance all over the world. Only after February 28, 2020, the number of cases was notable and was reported. After April 5, 2020, the spread saw an exponential growth in countries like China, the USA, France, Germany, UK, India, and Italy.

On March 08, 2020, Tedros Adhamon Ghebreyesus, director-general of WHO, declared that the intimidation of a pandemic is becoming a reality, and WHO decided to call the outbreak a "pandemic", and declared Coronavirus disease 2019 (COVID-19) as a global pandemic on March 11, 2020. WHO initially assumed that this will be the first-ever controlled pandemic, which unfortunately was not the case.

A COVID-19 vaccine is not expected until 2021 at the earliest[6]. Some early studies [7,8] suggest between 1 in 5 and 1 in 10 people with COVID-19 will experience symptoms lasting longer than a month.One of the major issues of the outbreak is that the ratio of a large number of infected cases versus the number of medical aid available.

In India, the disease was first detected on 30 January 2020 in Kerala in a student who returned from Wuhan [9,10].To control the spread by maintain social distancing, the China Government adopted the lock down policy and it did control the spreading of the disease. Following this policy, most of the countries adopted it. In this context, some preventive measures such as maintaining social distance, wearing masks, frequently washing the hands with soap and water, etc., were employed to protect humans from this infection.

On 22 March, India observed a 14-hour voluntary public curfew at the insistence of the Prime Minister. It was followed by mandatory lockdowns in COVID-19 hotspots and all major cities. Further, on 24 March, the Prime Minister ordered a nationwide lock down for 21 days, affecting the entire 1.3 billion population of India. On 14 April, India extended the nationwide lock down till 3 May which was followed by two-week extensions starting 3 and 17 May with substantial relaxations. During this phase a Sikh preacher who had traveled across Italy and Germany turned into a super-spreader in villages in Punjab, a Tablighi Jamaat religious congregation event in Delhi emerged as another super-spreader event and in Punjab nearly 4,000 pilgrims who returned from Hazur Sahib in Nanded, Maharashtra most of them tested positive. From 1 June, the government started "unlocking" the country (barring "containment zones") in three unlock phases.[11,12]

Our main goal of this work is to analyze and infer upon the implementation of the graph, sparse matrices and its storage, eigenvalue and eigenvector centrality using the SEQIR model [2] which divides the Indian population (during the pandemic) into five sub populations, and thus drawing the inferences from

the data set of India statistically.

II. REVIEW OF LITERATURE

The following section presents the works of authors towards the pandemic modeling of India and few theorems reflected on it;

D. Pal, D. Ghosh, P.K. Santra and G.S. Mahapatra in their research "Mathematical Analysis of a COVID-19 Epidemic Model by using Data-Driven Epidemiological Parameters of Diseases Spread in India" [2] had proposed a model system where the Indian population *(N(t))* was divided into five mutually exclusive sub populations on the basis of the disease spread, (which will be assumed as the primary graph in this paper) namely susceptible population *(S(t))*, infected but not detected by testing population *(E(t))*, quarantined population *(Q(t))*, confirmed infected population who are in under treatment in isolation word *(I(t))*, and the population who lived in the secured zone and are not affected by COVID-19 virus *(R(t))*.
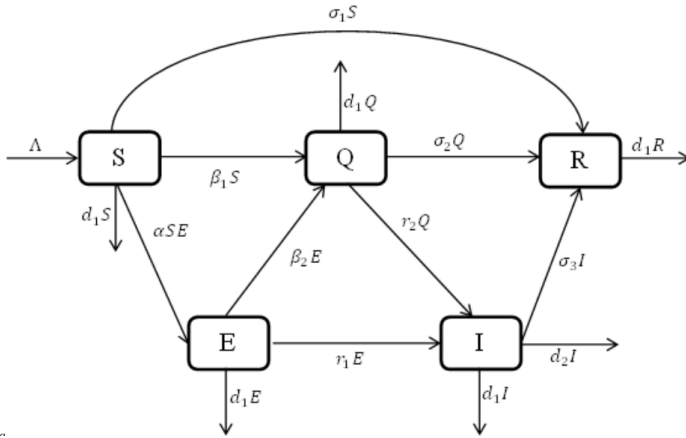

Fig. 1. Transfer diagram of the SEQIR Covid-19 model

Fig.1 represents the proposed SEQIR model with natural death rate $d_1 > 0$ in each of the sub populations and a net inflow of susceptible Indian individuals into the county (India) at a rate $\Lambda > 0$ per unit time is assumed.

A. Model Derivation of Disease

From the graph SEQIR,differentiating the parameters with respect to time we have

TABLE I
EXPLANATION OF PARAMETERS EXPLOITED IN SEQIR MODEL

Parameter	Meaning
Λ	The recruitment rate at which new individuals enter India
α	The transmission rate from susceptible population to infected but not detected by testing population
β_1	The transmission rate from susceptible population to quarantine population
β_2	The transmission rate from infected but not detected by testing population to quarantine population
σ_1	The transmission rate from susceptible population to secured zone
σ_2	The transmission rate from infected but not detected by testing population to secured zone
σ_3	The transmission rate from quarantine population to secured zone
r_1	The transmission rate from infected but not detected by testing population to infected population
r_2	The transmission rate from quarantine population to infected population for treatment
d_1	Natural death rate of all five sub populations
d_2	Death rate of Infected population due to Covid-19

$$\frac{dS}{dt} = \Lambda - \alpha SE - \beta_1 S - \sigma_1 S - d_1 S$$

$$\frac{dE}{dt} = \alpha SE - r_1 E - \beta_2 E - d_1 E$$

$$\frac{dQ}{dt} = \beta_1 S + \beta_2 E - r_2 Q - \sigma_2 S - d_1 Q$$

$$\frac{dI}{dt} = r_1 E + r_2 Q - \sigma_3 I - d_2 I - d_1 I$$

$$\frac{dR}{dt} = \sigma_1 S + \sigma_2 Q + \sigma_3 I - d_1 R$$

where, *S(0) > 0, E(0) ≥ 0, I(0) ≥ 0, Q(0) ≥ 0, R(0) > 0* which can be rewritten as,

$$\frac{dS}{dt} = \Lambda - \alpha SE - AS$$

$$\frac{dE}{dt} = \alpha SE - BE$$

$$\frac{dQ}{dt} = \beta_1 S + \beta_2 E - CQ$$

$$\frac{dI}{dt} = r_1 E + r_2 Q - DI$$

$$\frac{dR}{dt} = \sigma_1 S + \sigma_2 Q + \sigma_3 I - d_1 R$$

where , *A = (β_1 + σ_1 + d_1), B=(r_1 + β_2 + d_1), C = (r_2 + σ_2 + d_1), D = (σ_3 + d_1 + d_2)*

B. Basic Reproduction Number

The basic reproduction number R_0 (BRN) is the number of individuals directly infected by an infectious person in a susceptible population[13]. In order to compute the value

of BRN , the next-generation matrix method is used.[14

Assuming $y = (E, Q, I, R, S)^T$

$$\frac{dy}{dt} = F(y) - v(y)$$

$$\text{where, } F(y) = \begin{bmatrix} \alpha SE \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{ and } v(y) = \begin{bmatrix} BE \\ -\beta_1 - \beta_2 + CQ \\ -r_1 E - r_2 Q + DI \\ -\sigma_1 S - \sigma_2 Q - \sigma_3 I + d_1 R \\ -\Lambda + \alpha SE + AS \end{bmatrix}$$

Having designed the transmission part ($F(y)$, from where new infection originates) and the transition part ($v(y)$), the spectral radius(the largest absolute value of the given square matrix' eigenvalues) of FV^{-1},which are the Jacobian matrices at E gives the BRN[15]. F and V are calculated using the method of the next-generation matrix, thus the calculated spectral radius at $E_0(\frac{\Lambda}{A},0,0,0,0)$ [2] for the SEQIR model is

$$R_0 = \frac{\alpha \Lambda}{AB} > 0$$

Therefore BRN is non-negative.

In the further sections of this paper ,based on the proposed model, few mathematical conclusions will be manifested.

III. DAY-WISE VISUALISATION

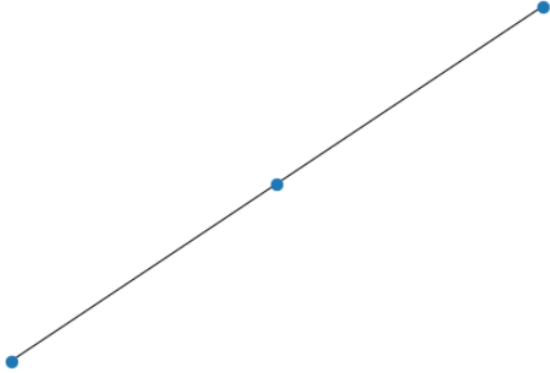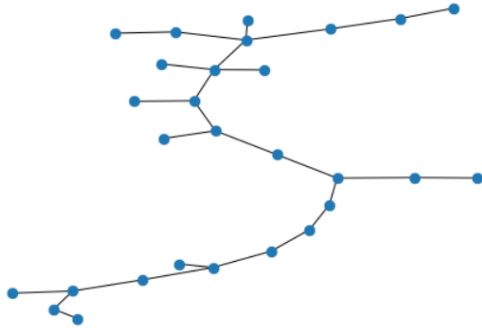Fig. 2. 30 January,2-3 February,2020 spread

Fig. 3. 23, March, 2020 spread

Considering the initial spread in India , from Kerala[16] we have constructed the graph in Fig. 2, Fig. 3, Fig .4 ,where the

Fig. 4. 23, May, 2020 spread

nodes represents the infected individuals and the edges are assumed to be the link of cause of the infection.From this, it is transparent that the graph has no self-loops or parallel-edges between them. Following is the day-wise visualisation based on the dataset of India[3].
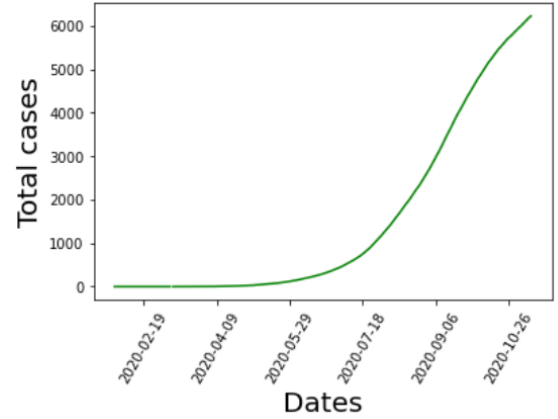

Fig. 5. Day wise visualisation of Covid-19 in India (Total cases - 1e3)

In order to formulate the cause and effect of the spread mathematically, the Indian population during the pandemic is divided into five mutually exclusive compartments on the basis of the disease status namely the SEQIR and is studied.

IV. PROPERTIES OF SEQIR

From the model, it is evident that the graph is directed with no self-loops or parallel-edges between the five sub populations.

A. Sparse Graph

Sparse matrices allows special techniques to take advantage of the large number of zero elements.The adjacency matrix obtained from the graph(SEQIR) is checked for sparsity using a python package named NetworkX[17] and it is sparse

, thus we conclude that the graph is sparse. Since , the obtained sparse matrix's diagonal elements are zero , here it can be stored either using the Compressed Row Storage (CRS) method or the Compressed Column Storage (CCS) method[17]. These storage methods makes no assumptions about the sparsity structure of the matrix, and they efficiently store only the non-zero elements.

B. Stability Analysis

- Since there can be no direct result drawn from the adjacency matrix of the intended model,the Jacobian of the matrix (J)[2] is constructed at $E_0(\frac{\Lambda}{A},0,0,0,0)$ is given by :

$$\begin{bmatrix} -A & -\alpha\frac{\Lambda}{A} & 0 & 0 & 0 \\ 0 & \alpha\frac{\Lambda}{A}-B & 0 & 0 & 0 \\ \beta_1 & \beta_2 & -C & 0 & 0 \\ 0 & r_1 & r_2 & -D & 0 \\ \sigma_1 & 0 & \sigma_2 & \sigma_3 & -d_1 \end{bmatrix}$$

- Now, using the formula *det(J - λI)* = 0. We obtain the respectives eigenvalues and the eigenvectors are computed.
- The eigenvalues from calculations are found to be :

λ_1 = -A < 0, $\lambda_2 = \alpha \frac{\Lambda}{A}$ - B , λ_3 = -C < 0, λ_4 = -D < 0 and $\lambda_5 = -d_1 < 0$

- For the system of the mentioned differential system of linear equations to be asymptotically stable the system must result in having negative eigenvalues, which in this case is true if $\lambda_2 < 0$. If it so then ,

$$\alpha \frac{\Lambda}{A} - B < 0$$
$$\alpha \frac{\Lambda}{AB} < 1$$
$$R_0 < 1 \text{ (BRN)}$$

- The system is thus locally asymptotically stable under the condition $R_0 < 1$.

C. Eigenvector Centrality

In graph theory, eigenvector centrality is a measure of the influence of a node in a given network. The node itself can have a higher eigenvector centrality measure even when it is weakly influential but it's strongly connected to its neighborhood nodes. Relative scores are given to all nodes in the network based on the concept that connections to high-scoring nodes contribute more to the score of the node in question than the equal connections to low-scoring nodes. A high eigenvector score means that a node is connected to many high scoring nodes. The Eigenvector centrality measures are calculated using a python package named NetworkX [18] for the adjacency matrix of the SEQIR model. The node with the highest the above centrality measure is *Q(t)*, with an estimated value of 0.5257.

D. Further Interpretations and Discussions

- Due to high population density, human to human social contact rate is very high in India. Besides, due to the substantial number of infected cases and limited medical capacity, the diagnostic test of the exposed, asymptomatic, and quarantined classes for confirmation of Covid-19 infection is low.
- A susceptible person may be infected by close contact with an infected person. In general, the quarantined and isolated individuals are unable to transmit the virus to other susceptible individuals, but we observe that the staff/laborers, doctors, nurses, ambulance drivers, and much more particularly who is in demand and required during the period of quarantine in isolation centers have also been infected by such individuals.
- On the other hand, an asymptomatic infected human has no symptoms, but he/ she will be able to transmit the virus to other susceptible humans. So susceptible humans may (once the diagnostic test is done) or may not be preventive (when the diagnostic test is not done) to avoid the virus transmission from an asymptomatic infected person.
- The rural health care system lacks resources but rural areas are not as compact and dense as urban areas. Notably, the lack of awareness about social distancing in rural areas and low testing rates have contributed significantly to the *E(t)*.
- 'Herd immunity', also known as 'population immunity', is a concept used for vaccination, in which a population can be protected from a certain virus if the threshold of the vaccination is reached. Many countries call for a return to normal life for people at lower risk of severe COVID-19, to allow SARS-CoV-2 to spread to a sufficient level to give herd immunity. However, herd immunity can cause unwanted deaths and increased severe cases. Even once herd immunity is attained across a population, it's still possible to have large outbreaks in areas where vaccination rates are low.

E. Conclusion

In this research paper, a mathematical model of the Covid-19 virus was studied and it dealt with the spread of Covid-19 along with the day to day databases of India. The main aim is to study the spread of Covid-19 mathematically and graphically ,for which the SEQIR model was considered as the primary model graph for a detailed observation of the effects caused by the virus in India. A directed graph with no loops and no multiple edges representing the five compartments(sub population) was analysed. The sparse matrix is obtained from the graph and then the eigenvalues are found to make the analysis easier. The goal of this work is to analyze and infer the implementation of the graph, sparse matrices, and its storage, eigenvalue, eigenvector centrality using the SEQIR model and how external factors affect the growth of the virus in the sub populations.

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