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SVEIR modeling for forecasting Covid -19 projection in India

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Abstract : Deterministic simulation model such as SIR, SEIR for epidemic diseases like SARS, Covid-19 provides the helpful information about the trends of the diseases progression and information about their rate of transmission and other vital parameters. With introduction of vaccination compartment for SVEIR model we try to find out more important parameters with vaccine efficacy for the transmission of the disease. More importantly this paper focuses on the vaccination coverage importance for eliminating the Covid-19 disease situation in India. With current effective reproduction rate Re or Rev (Basic reproduction number after vaccination or threshold quantity)= 1.64 with vaccine efficacy =0.71 .Contact rate (β) = 0.16063. Latency rate (α) = 0.19268. Recovery rate = (γ) = 0.09794, estimated the value as 40 % to 45 % vaccination coverage needed for disease endemic at continuous phases. This paper also attempts to find out way of calculating transmission rate at different periodic situation before and after vaccination battling against disease transmission as per the vaccine characteristics and its durability for immunization.

Key Words :- SVEIR; Effective reproduction number; Recovery rate; Transmission rate; Latency rate; Efficacy; Herd immunity.

Introduction

Epidemic mathematical modeling always considered being helpful tool for forecasting disease simulation over the years. Deterministic and stochastic models over the years derived, formulated, structured many mathematical equations for modeling to find trends and important parameters over disease progression. The immense affecting scenario of Covid-19 over the health issues of every individual around the world and its influence on every aspect of human life needs to predict disease spread or trends with at most power that can give vital information over the disease for its transmission. Tools needs to approach with continuous adoptability for dealing with the situation like Covid-19. Many deterministic models are in application for the epidemic disease scenario like compartmental model SEIR (Suspected-Exposed-Infected- Recovered). With vaccination drive introduced and in implementation against the transmitted infection of Covid-19 virus, models are proving to be the immense powerful weapon with capabilities to predict the trend of the disease spread. However situation is still imminence for the episodes specially, with the past history of pandemic phase transformation of virus by its nature.

History of mathematical modeling

Bernoulli [1] for his seminal presentation formulated the first mathematical modeling on infectious disease smallpox explaining the inoculation against smallpox virus can increase the life expectancy by 3 years at birth. Ross [2] presented a benchmark paper for establishing the modern mathematical epidemiology in a systematic way. Kermack and McKendrick [3,4,5] published three seminal papers using deterministic compartmental epidemic modeling for SIR (suspected- infected- recovered) Model. Heester beek & Dietz [6] explained the importance of R0 Basic Reproduction number the most basic fundamental unit used for study of infectious disease in epidemic theory. Driessche[7] illustrated various mathematical model such as SIR, SEIR, Cholera model, West Niel Model, Random Network Model. Model for anthrax transmission, Zika transmission Model for various infectious diseases and explained the method for calculating basic reproduction number such as next generation operator to calculate R0 , R0 in a periodic environment. Survival function method to compute R0,Calculation of R0 for discrete time systems, Stochastic models for estimating R0 [7].

Basic Reproduction Number (R0) and Effective Reproduction Number (Re and Rt)

Basic Reproduction Number (R0) value estimated as a parametric function over three entities 1) Time duration of contagiousness once person becomes

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infected 2) Likelihood possibility of spread of infection per contact between susceptible & infectious individual and the 3) contact rate. At the time of zero immunity in the population [8], Vaccination aims to reduce this contact and transmission over disease by reducing $R_0 < 1$ for the event. For the instance effective reproduction number is calculated and used in the modeling. Effective Reproduction Number R_e also called as R_t, Reproduction Number at time event t is the population number infected through individual specific pathogen at any point of an event. We consider this as R_e^v for vaccination model. However Viceconte [9] in his study based on the parameters factors affecting estimating Covid -19 spread found that Reproduction number R_0 is not the only factor to consider when estimating the burden of the epidemic. Given model for its application was also used in past for assessing the potential impact of an imperfect ANTI-SARS vaccine [10].

Vaccination Compartment: Vaccination mathematical modeling along with the knowledge of key transmission parameters of the virus can provide useful information for the disease and its trends in nature. This paper effort the view on the assumptions imputed with vaccination element for its application over SEIR model eventually derived as SVEIR modeling for the simulation of Covid-19 and its futuristic progress.

Model formulation and assumptions:

Model is divided into 5 groups S-V-E-I-R (Suspected –Vaccinated –Exposed –infected – Recovered), considering all the population under suspected category for threat for Covid-19, S (t) over time period (t). Vaccination element is imputed V(t). Exposed Population derived with time E(t). Infected population derived for time period I(t). Recovered population calculated for R(t).

Assumption:

Population size (N) remains large and homogeneous with constant birth and death rate.

Equations Derived

SIR MODEL (Suspected-Infected- Recovered Model).

Fraction over the total population is measured over each compartment with function of time resulted over predicted variable.

Let

s (t) = S(t)/N fraction of susceptible individual population.

i (t) = I(t)/N fraction of infected individual population.

r (t) = I(t)/N fraction of recovered individual population.

Thus , We have

$$S(t) + I(t) + R(t) = N \rightarrow s(t) + i(t) + r(t) = 1 \ldots\ldots\ldots\ldots\ldots (1).$$

Let β be the contact per day γ be the fixed fractions recovers at every day depending on average days of infection period disease have. Therefore the susceptible equation becomes

Susceptible Equation

$$\frac{dS}{dt} = -\beta \frac{S(t)}{N} I(t) \ldots\ldots\ldots\ldots\ldots\ldots (2).$$

The rate of change in the size of S(t) for time (t) depending on number of already infected population I(t), amount of contact per day β between susceptible and infected population and the number of already susceptible fraction of s(t) in contact with infected people.

Infected population fraction over time (t) covers remaining population after removed or recovered from total infected population having recovery rate γ for the disease.

Equation becomes,

Infected equations

$$\frac{dI}{dt} = \beta \frac{S(t)}{N} I(t) - \gamma I(t) \ldots\ldots\ldots\ldots\ldots\ldots (3)$$

Recovered equation

$$\frac{dR}{dt} = \gamma I(t) \ldots\ldots\ldots\ldots\ldots\ldots (4).$$

Thus, Equation formulated as

$$\frac{dS}{dt} = -\beta \frac{S}{N} I \text{.....(5)}$$

$$\frac{dI}{dt} = \beta \frac{S}{N} I - \gamma I \text{.....(6)}$$

$$\frac{dR}{dt} = \gamma I \text{.....(7)}$$

SEIR MODEL

Many epidemic infectious diseases have latency period for which they don't spread diseases after acquisition of infection in exposed phase and time delays between exposed situations to infectious state can be measured by incubation parameter. Model works at the situation known as SEIR model.

SEIR model equation becomes,

SEIR MODEL

$$\frac{dS}{dt} = -\beta \frac{S}{N} I \text{.....(8)}$$

$$\frac{dE}{dt} = \beta \frac{S}{N} I - \alpha E \text{.....(9)}$$

$$\frac{dI}{dt} = \alpha E - \gamma I \text{.....(10)}$$

$$\frac{dR}{dt} = \gamma I \text{.....(11)}$$

It is easy to understand latency period was missing in SIR model. While in SEIR model due to delay in latency period or start of secondary infection, eventually will result in slower initial growth of the outbreak.

Here we assume a situation of constant birth and death rates parameter $\prod$ and natural mortality rate μ with other vital dynamics models can be represented by,

$$\frac{dS}{dt} = \prod - \frac{\beta SI}{N} - \varepsilon S - \mu S \text{.....(12)}$$

$$\frac{dV}{dt} = \varepsilon S - (1-\tau)\beta VI - \mu V \text{.....(13)}$$

$$\frac{dE}{dt} = \beta SI + (1-\tau)\beta VI - \alpha E - \mu E \text{.....(14)}$$

$$\frac{dE}{dt} = \alpha E - \gamma I - \omega I - \mu I \text{.....(15)}$$

$$\frac{dR}{dt} = \gamma I - \mu R \text{.....(16)}$$

Where,

Π: *−Flow rate birth rate /immigrants of susceptible population.*

ε : *− Vaccination Coverage rate.*

μ : *− Natural mortality rate*

β :- *Contact Rate or Transmission Rate*

γ:- *Recovery Rate per day*

α: *−Latency Rate per day.*

τ : *− Vaccine Efficacy*

ω: *−Disease induced Mortality rate.*

Methodology : Initial value of R_o was estimated from earlier research part over the period 30 th January 2020 to 30 th June 2020 for SEIR model. Secondary data for vaccination model been collected for calculating R_e^V from period 1st December to 31st December 2021 from various government online information sites. Database used from https://www.COVID19india.org [11] and https :// https://www.icmr.gov.in/ [12] for vaccination coverage data. Vaccination data recorded from as secondary source on database https://ourworldindata.org.[13] vaccine efficacy considered to be 0.71 as per the secondary information available by drug manufacturing company Covieshield and Covaxin. Equilibrium population without disease assumed to be constant.

Analysis Method: Rate of development of clinical symptoms exposed becoming infected Latency rate (α) ,(incubation period reciprocal = 1/k) on SAS programming software version 9.3 using secondary data. After getting the values over α other parametric values were calculated for differential equations.

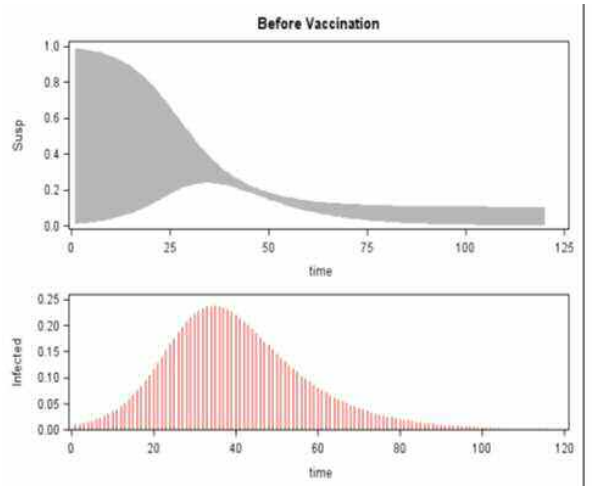

Fig :1- Suspected – infected before vaccination

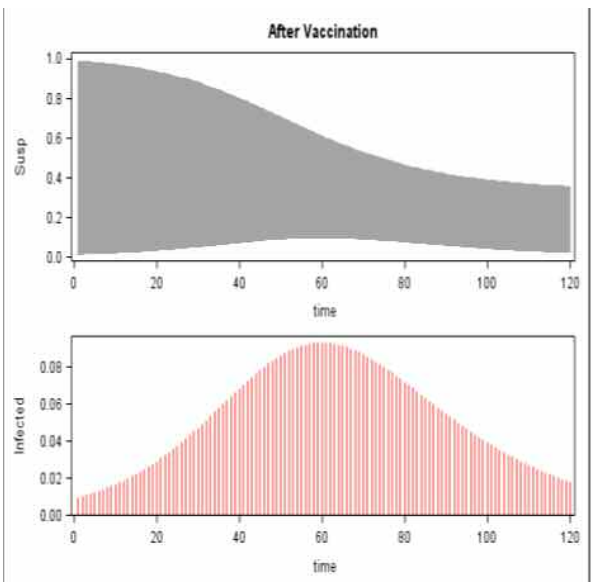

Fig:-2 Suspected -infected after vaccination

Result: - With current effective reproduction rate R^E_0 or R^v_0 (Basic reproduction number after vaccination or threshold quantity) =1.64 with vaccine efficacy (τ) =0.71. Contact rate (β) =0.16063. Latency rate (α) = 0.19268 per day .Recovery rate = 0.09794 .

Discussion

At initial report R_0 was estimated with its value from 1.4 to 2.4 by WHO using ordinary differential equation(14).

Results on modeling estimates the R_e (or R_e^v Reproduction Number after vaccination) at 1.64 with vaccine efficacy (τ) =0.71 .Which was initially estimated at R_0 = 2.51 at the beginning in India to form the base of our study [15] . Its spread was reported over different values for Basic Reproduction Number R_0 .The Imperial College Of London in its report over Covid pandemic estimated R_0 at 2.4 [16]. Vaccination coverage in India reported as 45% till the date for immunity built up against Covid-19 for disease endemic with current efficacy 0.71 ((τ). At the moment contact rate (β) has drop down to (β) 0.16063 which was earlier recorded for 1st phase 0.24560 in our study .Vaccination thus proving a highly effective measure over the battle against disease pandemic. Flow rate considered as constant considering equal birth & death rate ratio with natural mortality rate and birth rate. However this assumption violates the situation as in India, natural mortality rate μ = 73787 per day and according to world bank collection of development crude death rate per 1000 population reported with 7.301 compared to 17.64 birth rate per 1000 population [17]. For modeling the equation with values we consider the equilibrium situation with N_0 =135 crores population all considered as suspected. Fig:1 shows nearly 25% of the population was in a infected mode compared to 9% in Fig 2, considering the average data of 120 days for comparison with before and after vaccination situation, with this to be lowered down much further for endemic, the current vaccination coverage with 45% up to 31 st December 2021, India needs to have 40% to 45% its coverage at consistent basic till the vaccine immunity last and needs continuation for its recycling ,to get the basic reproduction rate under one for endemic. Zhang et al.[18] theoretically estimated R_0 value evaluated at 2.28 in 1st week of February 2020 and estimated that if gets reduced to 50% with initial value the number of cases might reduced by half and if not decreases to 25 to 50% then it will drastically increase by time. This provides the proof to our conclusion. For achieving the herd immunity among susceptible group of population, basic reproduction number (R_o) can estimates proportion among susceptible population, the extent of immunization which needs to be implemented with vaccination at rate > 1 -1/ R_o thus vaccination campaign helps to control on epidemical flow of the disease and eventually helps to practice on disease endemic R_o< 1, depending on immunization period

Conclusion:- Vaccination proves to be immense powerful tool for battling against covid-19 for the situation needed in India .With current epidemic situation and transmission rate of pathogen and

proven efficacy of covid-19 vaccine. India needs to cover its vaccination coverage over 40% populations at every immunization phase over for disease endemic.

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