Epidemiology Modelling and Network Analysis Based on Queueing Theory for Predicting the Transmission and Control of COVID-19

By

Nandita Suresh Kamath

ID No. 2018B4A20868P

Under the supervision of

Dr Rakhee Kulshrestha, Associate Professor

BIRLA INSTITUTE OF TECHNOLOGY AND SCIENCE,

PILANI CAMPUS

20th December, 2022

List of Symbols and Abbreviations Used

Symbol	Meaning
λ	Rate of Infection
μ	Rate of Removal (Recovery/Death)
ρ	Service Utilization
L	Average Number of Customers in the System
W	Average Delay per Customer
L_q	Average Number of Customers in the Queue
W_q	Average Waiting Time
T_d	Total Delay in the System
T_m	Average Time an Individual that is Infected Spends in the System
T_r	Recovery Time
N	Number of Infected Individuals in the System
S	Susceptible Class
E	Exposed Class
I	Infected Class
R	Recovered/Removed Class
m	Total Number of Exposed Persons
n	Total Number of Infected Persons
π_k	QSD for Total Number of Infectious Persons
Ω	State Space for QSD
Φ	Probability that Specific Person is in Infectious State
E_a	Exposed with comorbidities
E_b	Exposed without comorbidities
I_S	Infected-Symptomatic
I_A	Infected-Asymptomatic
R_0	Reproduction number
T	Transmissibility
T_c	Epidemic threshold
c	Mean Degree
c^2	Mean Square Degree

Abstract

Since 2019, COVID-19 continues to decimate the world population and cause harm to human life and the economy. Given the random and non-sequential pattern of its transmission, the study aims to conduct a comparative analysis of the queueing theory-based approach and epidemic modelling-based approach to help determine the transmission patterns and find effective control measures to prevent its spread. The study combines the statistical nature of M/M/1 queues and networks and the deterministic nature of SEIR epidemic models to determine the optimum rate of infection of the disease in three states across six months. The reproduction numbers are calculated before and after intervention and are validated against the transmissibility of the disease.

Table of Contents

Chapter 1 - Queueing Model for COVID-19 Transmission and Control

1.1 Introduction

This chapter models the transmission of COVID-19 as an M/M/1 queue and calculates the basic queueing properties from COVID-19 data of three states In India, Maharashtra, Karnataka and Rajasthan ranging from March to August 2020. The values are plotted to determine the optimum value for the probability of infection.

1.2 Literature Review on Advances in Queueing Theory in Epidemic Research

A detailed literature review of the available published literature showed that several researchers have proposed different models to explain transmission dynamics and the control measures of epidemics using queueing concepts.

Kendall implemented Imbedded Markov Chain and other stochastic processes to build a GI/M/S queue to indicate the application of BDP in M/G/1 queues. This paper was one of the first to extend a single-server queue to a multiple server queue for epidemic application. *Kitaev* created an M/G/1 queue by utilising the logic of Processor Sharing Service Discipline and proved a relation between BDP and M/G/1 with processor sharing. He also delivered an expression for the number of jobs present at a specific time. *Ball and Donnelly* calculated the cost of an epidemic by implementing branching process on M/G/1 queue. *Trapman and Bootsman* worked on a basic SIR model to build a M/G/1 model. *Hernandez-Suarez* worked on SIS and SEIS models to build a M/G/N queue where each individual was considered to be a server that was busy or idle. *Okoro* reviewed fundamental of Markovian Queueing model as BDP and applied its results on M/M/1, M/M/S, M/M/1/K and M/M/s/K queues. Most recently, Chinyere Dike worked on M/M/1 models to compute optimum transmission metrics and applied those to a compartmental model for Ebola Virus. This thesis applies the results found in the series of papers published by Chineyere Dike and applied on the COVID-19 disease.

1.3 Introduction to M/M/1 Queues (∞/FIFO)

The M/M/1 queue is a model with a Poisson arrival process, exponentially dispersed service times, and a single server. The system's queue capacity is limitless with first in, first out mode. The first M in the notation represents Poisson input, the second M represents Poisson output, 1 represents the number of servers, and ∞ represents an unlimited system capacity. Figure 1 depicts this visually.

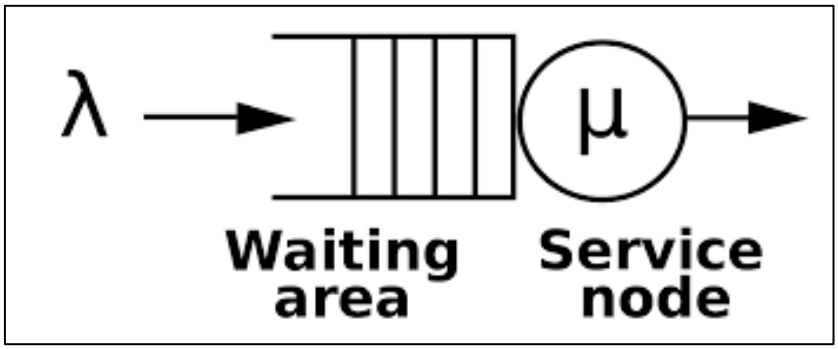


Figure 1 – Visual Representation of M/M/1 Queue

1.4 COVID-19 Data for Maharashtra. Rajasthan and Karnataka

COVDI-19 data of six months is obtained for 3 states from March 2020 to August 2020. Table 1 to 3 displays the cumulative raw data collected for the 3 states.

Table 1 - COVID-19 Data for Maharashtra

Month-Year	Mar-20	Apr-20	May-20	Jun-20	Jul-20	Aug-20
Cumulative Time (hrs)	744	1464	2208	2928	3672	4416
No. of Infected Persons	168	7722	27000	38423	75141	45435

Table 2 - COVID-19 Data for Karnataka

Month-Year	Mar-20	Apr-20	May-20	Jun-20	Jul-20	Aug-20
Cumulative Time (hrs)	744	1464	2208	2928	3672	4416
No. of Infected Persons	75	223	1579	4491	63322	18402

Table 3 - COVID-19 Data for Rajasthan

Month-Year	Mar-20	Apr-20	May-20	Jun-20	Jul-20	Aug-20
Cumulative Time (hrs)	744	1464	2208	2928	3672	4416
No. of Infected Persons	71	1548	1066	952	7460	2994

1.5 Generation of Basic Properties of Queueing Theory

The waiting time stage of every epidemic disease is characterised by system or individual delay of infected individuals. The problem of waiting time in EVD transmission and control analysis could be derived from the delay model. Thus, total delay of infected individual in the system is expressed as

$$T_d = T_m + T_r$$

where T_d is the Total Delay in the System, T_m is the Average or Mean Time an Individual that is Infected Spends in the System and T_r is the Recovery Time. For N Number of Infected Individuals in the System at Time t,

$$E(N) = \lambda E(T)$$

where E(N) is Expectation of Number of Infected Individuals in the System at Time t and E(T) is Expectation of the Total Delay in the System. N(T) is the Number of Individuals Infected in the System at Time t and is expressed as:

$$N(t) = N_A(t) - N_D(t)$$

where $N_A(t)$ is the Number of Individuals Infected that Arrives at the System up to Time t and $N_D(t)$ is the Number of Individuals Infected that Departs from the System up to Time t.

Rate of infection = $\lambda = \frac{\sum_{i=1}^{n} N_i(t)}{T_m}$ and Rate of recovery = $\mu = 1 + \frac{T_m \lambda}{\lambda}$, where T_m is the Mean Time an Infected Spends in the System.

Basic properties of queuing theory versus the formula are given Table 4.

Table 4 - Analogy of Basic Properties of Queueing Theory

Queueing Logic	COVID-19 Model Logic	Abbreviation	Symbol	Formula
Arrival Rate	Rate of infection	RI	λ	
Service Rate	Rate of removal (recovering or dead)	RR	μ	
Service Utilization	Probability of Infection	PI	ρ	$\frac{\lambda}{\mu}$
Average number of customers in the system	Average Number in the System that are infected	ANS	L	$\frac{\lambda}{\mu - \lambda}$
Average delay per customer	Average Waiting Time for a Recovery to occur in the system	AWTR	W	$\frac{1}{\mu - \lambda}$
Average number of customers in the queue	The Expected Number of Person in the System before infection	ENP	L_q	$\frac{\rho^2}{1 - \rho}$
Average waiting time	Average Waiting Time in the System before infection	AWTS	W_q	$\frac{\rho}{\mu - \lambda}$

1.6 Calculation of Metrics from COVID-19 Data Using M/M/1 to M/M/10 Queues

Table 5 – Queueing Metrics for M/M/1-M/M/10 in Maharashtra Population

M/M/c	RI	RR	ANS	ENP	AWTR	AWTS	PI
1	403.9354	404.9354	403.935	402.9375	1	0.9975	0.9975
2	403.9354	404.9354	1.3279	0.3303	0.0033	0.0008	0.4988
3	403.9354	404.9354	1.0425	0.045	0.0026	0.0001	0.3325
4	403.9354	404.9354	1.0043	0.0067	0.0025	0	**0.2494**
5	403.9354	404.9354	0.9985	0.0009	0.0025	0	0.1995
6	403.9354	404.9354	0.9977	0.0001	0.0025	0	0.1663
7	403.9354	404.9354	0.9975	0	0.0025	0	0.1425
8	403.9354	404.9354	0.9975	0	0.0025	0	0.1247
9	403.9354	404.9354	0.9975	0	0.0025	0	0.1108
10	403.9354	404.9354	0.9975	0	0.0025	0	0.0998

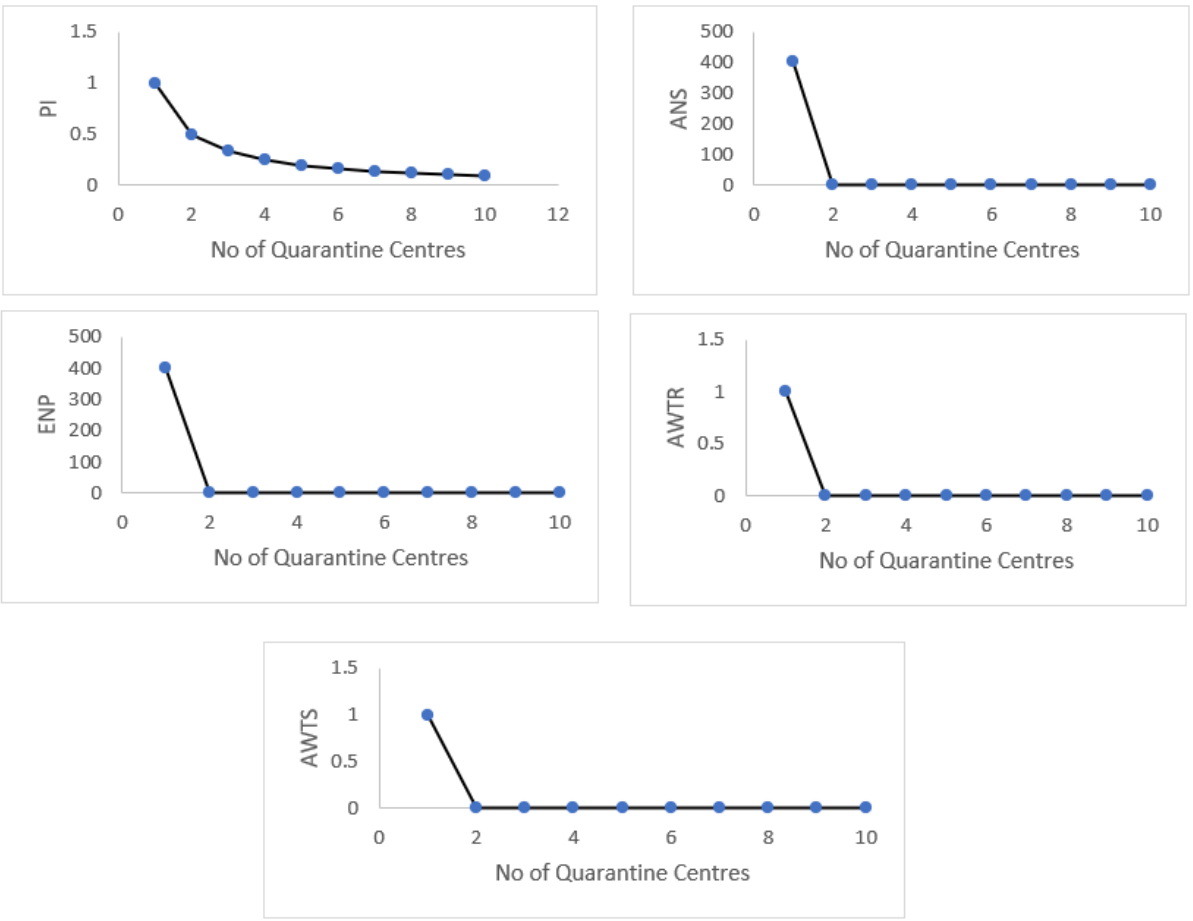


Figure 2 – Graphical Analysis of Queueing Metrics for Maharashtra

Table 6 – Queueing Metrics for M/M/1-M/M/10 in Karnataka Population

M/M/c	RI	RR	ANS	ENP	AWTR	AWTS	PI
1	183.525	184.525	183.525	182.5304	1	0.9946	0.9946
2	183.525	184.525	1.3213	0.3268	0.0072	0.0018	0.4973
3	183.525	184.525	1.0391	0.0445	0.0057	0.0002	0.3315
4	183.525	184.525	1.0012	0.0066	0.0055	0	**0.2486**
5	183.525	184.525	0.9955	0.0009	0.0054	0	0.1989
6	183.525	184.525	0.9947	0.0001	0.0054	0	0.1658
7	183.525	184.525	0.9946	0	0.0054	0	0.1421
8	183.525	184.525	0.9946	0	0.0054	0	0.1243
9	183.525	184.525	0.9946	0	0.0054	0	0.1105
10	183.525	184.525	0.9946	0	0.0054	0	0.0995

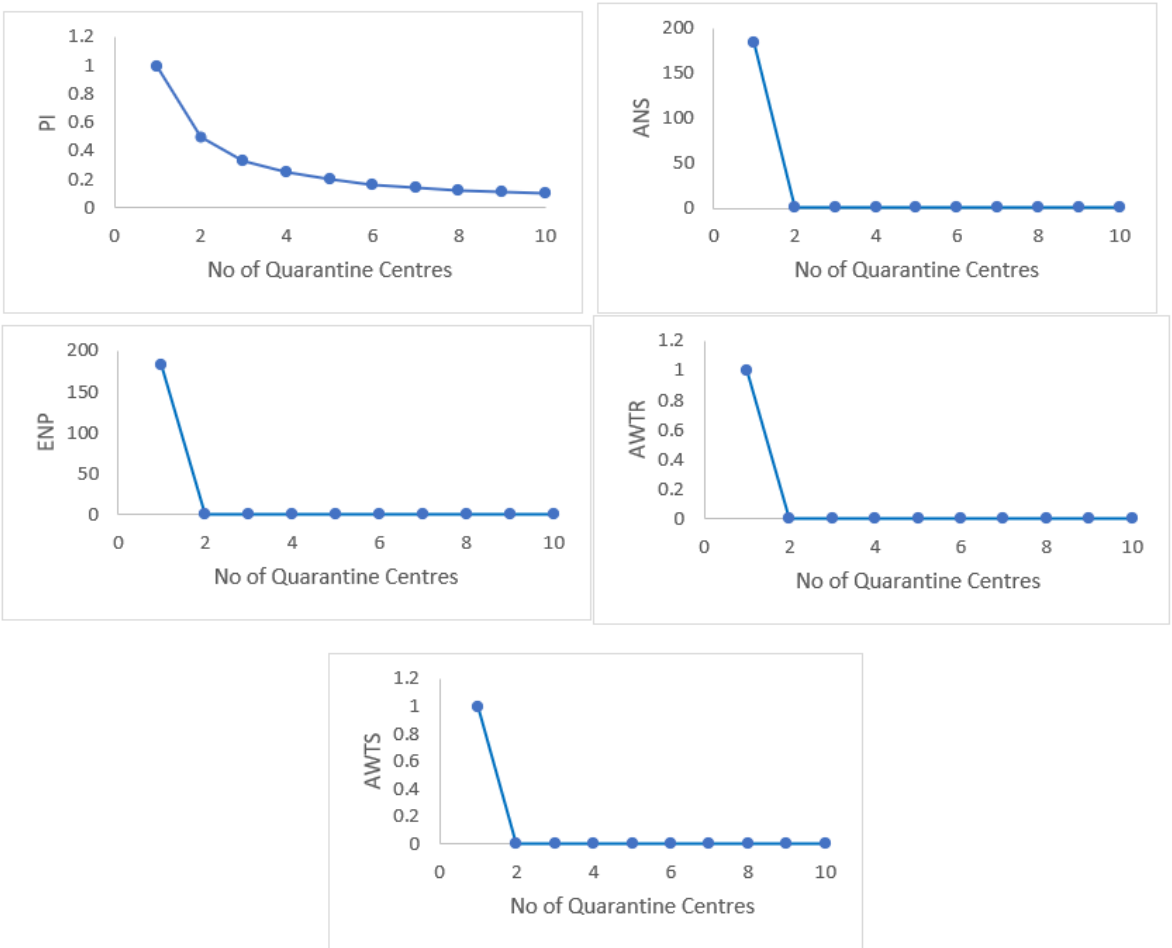


Figure 3 – Graphical Analysis of Queueing Metrics for Karnataka

Table 7 – Queueing Metrics for M/M/1-M/M/10 in Rajasthan Population

QC	RI	RR	ANS	ENP	AWTR	AWTS	PI
1	29.3562	30.3563	29.356	28.3889	1	0.9671	0.9671
2	29.3562	30.3563	1.2621	0.2951	0.043	0.0101	0.4835
3	29.3562	30.3563	1.0069	0.0398	0.0343	0.0014	0.3224
4	29.3562	30.3563	0.9729	0.0058	0.0331	0.0002	0.2418
5	29.3562	30.3563	0.9679	0.0008	0.033	0	**0.1934**
6	29.3562	30.3563	0.9672	0.0001	0.0329	0	0.1612
7	29.3562	30.3563	0.9671	0	0.0329	0	0.1382
8	29.3562	30.3563	0.9671	0	0.0329	0	0.1209
9	29.3562	30.3563	0.9671	0	0.0329	0	0.1075
10	29.3562	30.3563	0.9671	0	0.0329	0	0.0967

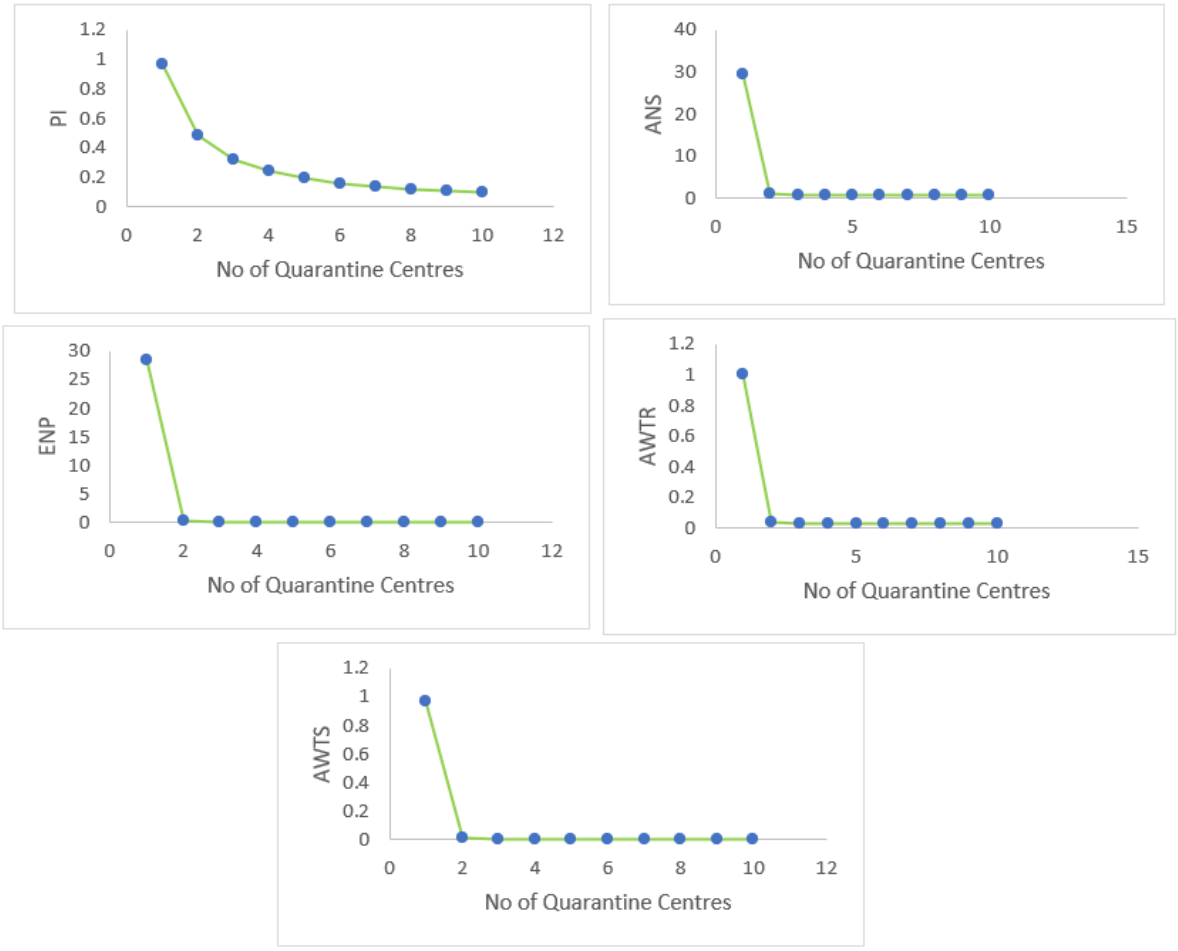


Figure 4 – Graphical Analysis of Queueing Metrics for Rajasthan

Tables 5,6 and 7 calculate the queueing metrics across the three states with increasing number of quarantine centres. It is observed that the probability of infection drastically decreases from 0.9 to 0.09 approximately for queues M/M/1 to M/M/10.

Figures 2,3 and 4 plot the number of servers against the metrics. It is noted that there is a steep curve at QC=4 when rate of infection is approximately 0.2 across the states. This value is taken as optimum rate of infection for further use.

Chapter 2 – Quasi-Stationary Distribution of SEIR Model

2.1 Introduction

This chapter proves the development of a Quasi-Stationary Distribution of a basic SEIR model. The distribution is approximated to a normal curve using COVID-19 data to determine the rate of infection

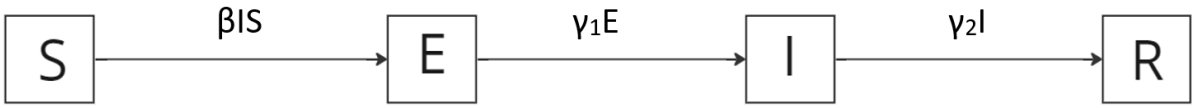
2.2 The SEIR Based Quasi-Stationary Distribution

In an SEIR model, the Exposed and Infected classes together create the Disease Class. These 2 classes are considered infectious and a danger to the rest of the population. Hence, the QSD for this model is a 2-dimensional arrangement; $\pi_{m,n}$where it signifies the minimum ratio of time in which there are $k = m + n$ infectious individuals. Here, m signifies exposed individuals and n signifies infected individuals.

The QSD with respect to k is analyzed and the model's state space is described in terms of the exposed and infected class (E, I) as follows:

$$\Omega = \{(e, i); e + I \leq N;\ e, I \in Z^{+}\}$$

The transitions between the phases of the SEIR model are given below:



Where β represents the transmission rate of COVID-19, γ1 and γ2 represents the rate of removal/recovery of exposed and infected individuals respectively.

The Quasi-Stationary Distribution of the SEIR model is:

$$P_{i,j,k,m}(t, t + \Delta) = P\,[\,E(t + \Delta) = k, I(t + \Delta) = m | E(t) = I, I(t) = j]$$

Evidently, $\{k, m\}, \{i, j\} \in \Omega$ (State Space) causes immediate changes in probabilities. The probabilities stated below describe state changes as time evolves and individuals enter or exit each class of the system.

i. The probability of transition state from k to k+1 due to interaction of exposed or infected individual occurring at time t with susceptible class. This signifies an increase in infectious individual by 1.

$$P_{k,m;k+1,m}(t, t+\Delta) = \beta\Delta\mathrm{m}(\mathrm{N}-\mathrm{k}-\mathrm{m})/\mathrm{N} + \mathrm{o}(\Delta)$$

ii. The probability of transition state from k to k-1 due to recovery or death of exposed or infected individual occurring at time t. This signifies a decrease in system size by 1.

$$P_{k,m;k-1,m+1}(t, t+\Delta) = w\Delta\mathrm{k} + \mathrm{o}(\Delta)$$

iii. The probability of transition state from m to m+1 or m-1 signifies an increase or decrease in the infectious class.

$$P_{k,m;k,m-1}(t, t+\Delta) = \gamma\Delta\mathrm{m} + \mathrm{o}(\Delta)$$

It is important to note that disease transmission happens randomly and is not dependant the model parameters. The QSD is identically distributed as the health and immunity of the susceptible class is assumed to be constant.

For QSD, assume the random variable, $I^T(t) = E(t) + I(t)$ which represents the total number of infectious individuals at time t as a sum of the random variables E(t) and I(t).

Similarly, $P^T_{j,k}(t, t+\Delta) = \lim_{t\to\infty} P[I^T(t+\Delta) = \mathrm{k} | \mathrm{I}^{\mathrm{T}}(t) = j \;\&\; j, k \in \Omega]$

Then P^T_k represent the k^{th}element of infectious individual of QSD.

It is important to note that disease transmission happens randomly and is not dependant the model parameters. The QSD is identically distributed as the health and immunity of the susceptible class is assumed to be constant and the number of exposed and infected individuals can be counted.

By applying renewal theory as proved by Hernandez-Suarez in 2010 and Ross in 2007 as $t \to \infty$ and selecting infected individuals at random; let $\{X_1, X_2, \ldots\}$ be a series of nonnegative, independent, uniformly distributed random variables.

The renewal process $\{N(t), t \geq 0\}$, which is a counting process is therefore defined as $N(t) = \max\{n: S_n \leq t\}$with $\sum_{j=1}^{n} X_j = S_n$

Let $E[X_j] = \gamma$. Using the principle of the strong law of large numbers (SLLN):

$$\frac{S_n}{n} \to \gamma, \text{ as } n \to \infty$$

Hence $S_n \to \infty$ as $n \to \infty$. Thus $S_n \leq t$ for at most a finite number of values of n and thus N(t) needs to be infinite. Although $N(t) < \infty$ for every t, it is true that with probability 1,

$$N(\infty) = \lim_{t \to \infty} N(t) = \infty$$

With probability 1,

$$\frac{N(t)}{t} \to \frac{1}{\gamma} \text{ as } t \to \infty$$

Additionally, $\frac{m(t)}{t} \to \frac{1}{\gamma}$ as $t \to \infty$ where m(t) is the renewal function. The likelihood that an infected individual is in the disease class (E and I) is

$$\Phi = \gamma_2^{-1}(\gamma_1^{-1} + \gamma_2^{-1})^{-1}$$

Note that at a certain time t, the likelihood that one individual is in state E or I do not rely on whether the other individual is in state E or I.

A binomial distribution with parameters k and Φ governs the number of infectious individuals. Hence,

$$\lim_{t \to \infty} P[I(t) = j | I^T(t) = k] = \binom{k}{j} \Phi^{\mathrm{j}} (1 - \Phi)^{\mathrm{k-j}}$$

The immediate transition probabilities are,

$$\lim_{t \to \infty} P[I^T(t + \Delta) = \mathrm{k} + 1 | \mathrm{I^T}(t) = k]$$

$$= \lim_{t \to \infty} \sum_{j=0}^{k} P(infection\ in(t, t + \Delta) | \mathrm{E(t) = k - j, I(t) = j}) \mathrm{P[E(t) = k - j, I(t) = j]}$$

$$= \sum_{j=0}^{k} \beta \Delta_{\mathrm{j}} (\frac{N - k}{N}) \left(\frac{k}{j}\right) \Phi^{\mathrm{j}} (1 - \Phi)^{\mathrm{k-j}} + o(\Delta)$$

$$= \beta \Delta \mathrm{k} \Phi \left(\frac{N-k}{N} \right) + o(\Delta)$$

Also, $\lim_{t \to \infty} P[I^T(t+\Delta) = \mathrm{k}-1 | \mathrm{I^T}(t) = k]$

$$= \lim_{t \to \infty} \sum_{j=0}^{k} P(recovery\ in(t, t+\Delta) | \mathrm{E(t)} = \mathrm{k}-\mathrm{j}, \mathrm{I(t)} = \mathrm{j}) \mathrm{P}[\mathrm{E(t)} = \mathrm{k}-\mathrm{j}, \mathrm{I(t)} = \mathrm{j}]$$

$$= \sum_{j=0}^{k} \gamma_2 \Delta_{\mathrm{j}} (\frac{k}{j}) \Phi^{\mathrm{j}} (1-\Phi)^{\mathrm{k-j}} + o(\Delta)$$

$$= \gamma_2 \Delta \mathrm{k} \Phi + o(\Delta)$$

Once N is sufficiently large and ρ is constant, the QSD of the number of Susceptible persons can be approximated with a Poisson random variable.

Let $Q = \{q_1^{(2)}, q_2^{(2)}, \dots, q_N^{(2)}\}$ be the stationary distribution of the QSD approximation after there are two infectious persons

$$\gamma_j = \gamma(j = 2) \text{ and } \beta_j = \frac{\beta j(N-j)}{N}, j = 1,2,..,N$$

However, from the work of Nasell in 1999, $q_n^{(2)}$ follows the relation,

$$q_k^{(2)} = q_2^{(2)} \frac{\left(\frac{\rho}{N}\right)^{k-1}}{(N-k)!} (N-1)!$$

Where $\rho = \frac{\beta}{\gamma}$ but γ is represented as γ_2 since it involves 2 permanently infected individuals. Kryscio and Lefevre proved that $\sum_{j=1}^{n} q_j \sim \sum_{j=1}^{n} p_j \ for\ n = 1,..,N$. At present, $P_k = q_{N-k}^0$ is defined as the QSD approximation to the number of susceptible.

$$\frac{\rho}{N} = N\gamma_2$$

Hence

$$P_k = q_2^{(2)} \frac{(N\gamma_2)^{N-k-1}}{k!} (N-1)!$$

Meanwhile,

$$\sum_{k=0}^{N-1} P_k = 1$$

Computing for q_1^0 gives

$$q_2^2 = \frac{(N\gamma_2)^N e^{-N\gamma_2}}{N!}$$

Consequently, the approximation to the distribution for the S class in the SEIR model for a general distribution of the duration of the infectious state is a Poisson approximation with parameter $N\gamma_2/\beta$. The epidemiologically significant instance which is when ρ>1 and $N \to \infty$ gives

$$P_k = \frac{\left(\frac{N\gamma_2}{\beta}\right)^k}{k!\left(e^{\left(\frac{N\gamma_2}{\beta}\right)} - 1\right)}$$

QSD for the number of infectious individuals which are the busy servers in an SEIR model is determined by the length of infective time, which is service time. The COVID-19 transmission model SEIR has 2 transmission phases on every server and is also understood as queueing theory based.

Hence, the rate of infection (arrival rate) is $\beta\Phi$ and mean recovery time (service time) is $\gamma_1^{-1} + \gamma_2^{-2}$

Then the Poisson distribution parameters meant for the number of susceptible is

$$\frac{N}{\beta\Phi\mathrm{E(S)}} = \frac{N}{[\beta\Phi(\gamma_1^{-1}+\gamma_2^{-2})]} \text{ where } \Phi = \Phi_1 + \Phi_2 = 1$$

Average number of infected individuals is $\frac{N\gamma_2}{\beta}$.

Average joint QSD for the model becomes

$$[E, I] = [\frac{N\gamma_2(1-\Phi_1)}{\beta}, \frac{N\gamma_2\Phi_1}{\beta}]$$

The new infections rate equates the rate of recovery in equilibria thus the proportion of the number of infected in equilibria is $1 - \frac{\gamma}{\beta}$

An analogy that connects the basic reproduction number in epidemiology, R0 with ρ, probability of infection (the server utilization of the system):

$$(1 - R_0^{-1}) = \rho$$

The number of susceptible is given roughly through a Poisson distribution by approximation with parameter $\frac{N\gamma_2}{\beta}$ once it is large enough. Then, the approximation to $P_{m,n}$ is derived following the assumption that $\frac{N\gamma_2}{\beta}$ is large for the number of exposed and infected individuals respectively. The assumption is appropriate for COVID-19 transmission as the infectious phases are exposed and infected. These two phases make up the two random variables which gave the probability distribution of the phases. The marginal distribution found to determine the effect of each phase while other phases are held constant. The joint distribution is appropriate for our model since the two phases when joined together help to determine the effects of the phases which in turn can be approximated to a normal distribution when n is large.

2.3 Results of QSD for SEIR Model

The number of Exposed, Infected and Total Infectious individuals and their Standard Normal value for Maharashtra, Rajasthan and Karnataka are found across six months from March to August 2020.

These values are used to stochastic SEIR epidemic model for approximation for Maharashtra, Rajasthan and Karnataka

The transmission of an individual into the exposed or infected phase is designed as an exponential distribution. This means that disease transmission occurs continuously and independently at a constant average rate for the period of transmission.
The observed and expected values are plotted in figures 5,6 and 7.

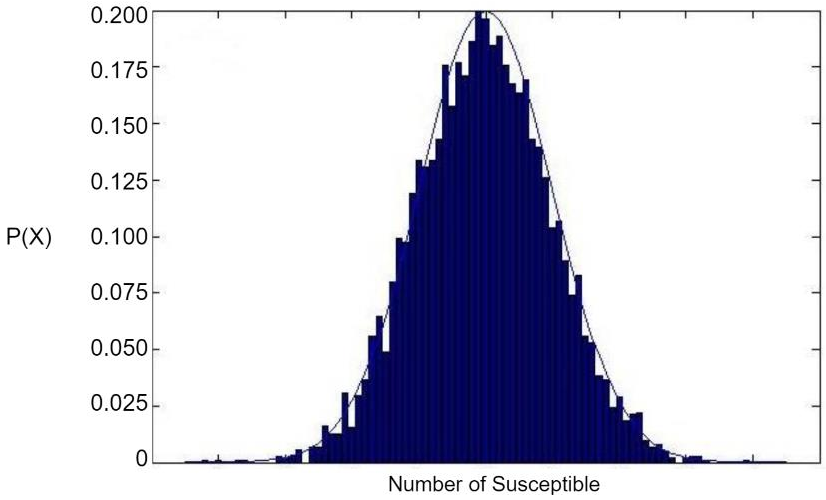


Figure 5 – Maharashtra Stochastic SEIR Epidemic Model (Histogram)

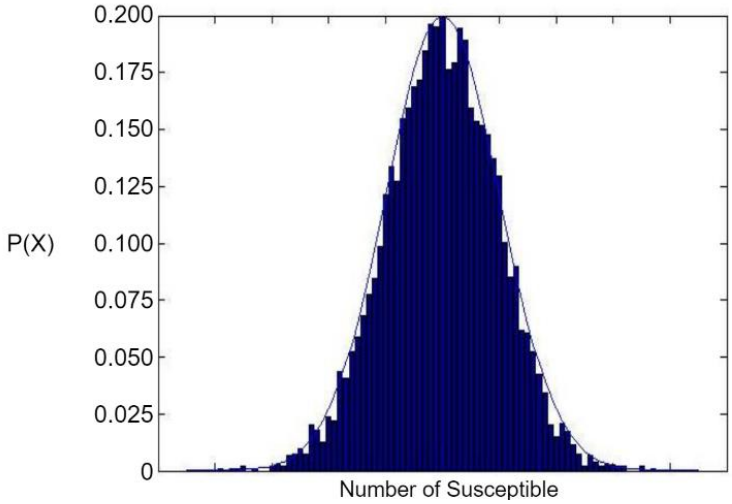


Figure 6 – Rajasthan Stochastic SEIR Epidemic Model (Histogram)

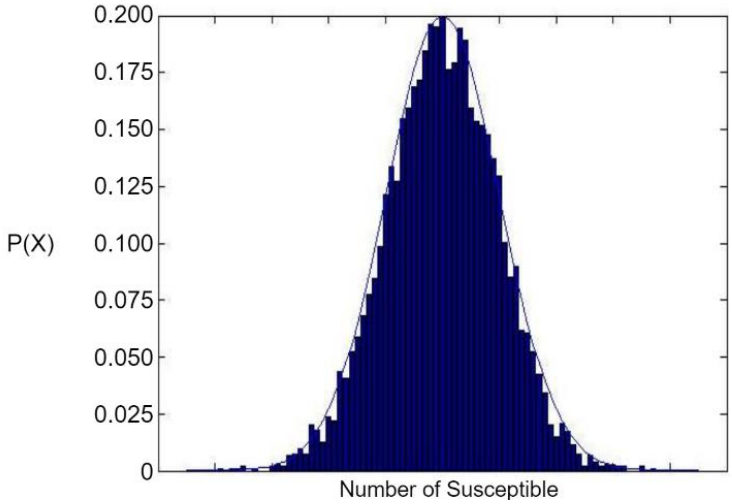


Figure 7 – Rajasthan Stochastic SEIR Epidemic Model (Histogram)

In these figures, the values of the susceptible was standardized to normal distribution. The approximation to the QSD for the total number of susceptible and for the joint distribution in the figures yielded reasonable approximation which means that when the probability is 0.2, the model is at equilibrium.

Chapter 3 – Modified SEIR Compartmental Model and Model Parameters

3.1 Introduction

This chapter modifies a basic SEIR model to incorporate more infectious states to make the model more realistic. The optimum probability of infection derived in chapter 1 is used to calculate the disease-free equilibrium point and the reproduction number.

3.2 Model Formation

A basic SIR model is extended into a six-compartment model to simulate the transmission and spread of COVID-19 disease.

The latency period of the COVID-19 pathogen is considered to make the model accurate as in reality, it takes time for the pathogen in the environment to find a suitable and susceptible host body to replicate and reproduce within. Only after this incubation period does the host become infectious to the surrounding population. As this state of pathogen incubation cannot be categorized as susceptible or Infected, an Exposed Class is created.

This Exposed Class is further split into two, to incorporate the population exposed with and without underlying health comorbidities that are found to increase the chances of contracting COVID-19. These health concerns include Hypertension, Cardiac disease and lung disease.

The infected class is also split into two, to incorporate the population of infected individuals that are symptomatic and asymptomatic. According to epidemic data, both these classes are infectious and are capable to spread the disease amongst the healthy and susceptible population.

A total of six such state variables or classes are considered within the human population of size N at time t denoted as $N(t)$. The classes are Susceptible $S(t)$, Exposed with comorbidities $E_a(t)$, Exposed without comorbidities $E_b(t)$, infected with symptoms $I_S(t)$, Infected without symptoms $I_A(t)$ and the recovered as $R(t)$. Hence the total human population, $N(t)=S(t)+E_a(t)+ E_b(t)+I_S(t)+I_A(t)+R(t)$.

The disease is transmitted when a healthy but susceptible individual comes in close contact with an infected individual. The pathogen begins to incubate in this host body making it exposed to its effects. The incubation period of the pathogen inside an individual with comorbidities is less than that of an individual without. After the period of latency, when the pathogen has multiplied sufficiently, the host moves to the Infected Class and begins to exhibit symptoms and is considered infectious to the rest of the population. A majority of the infectious class show improvement and transition to the Recovered Class recover while the rest perish and exit the population.

The disease transmission flow of the proposed model is sketched in Figure 8.

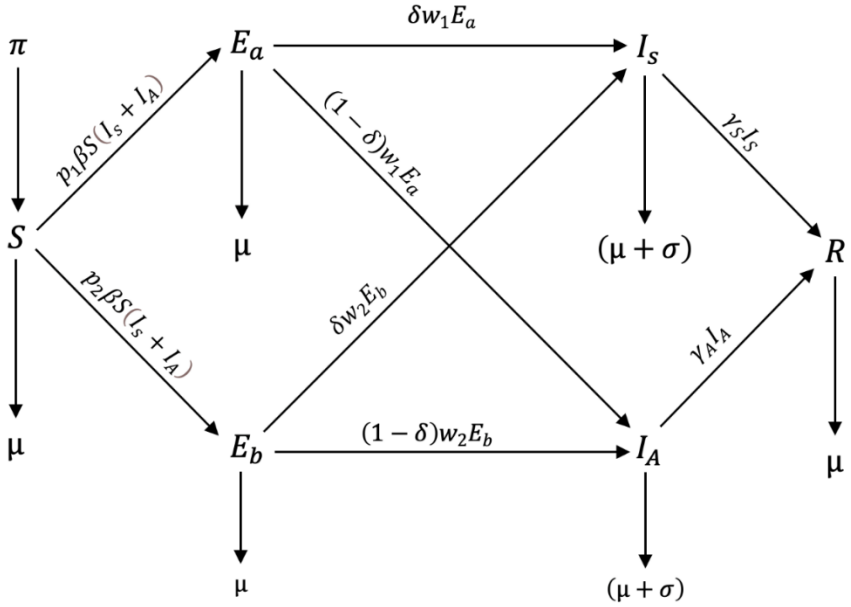


Figure 8 – Flow of Disease through the Compartments

The model system is formed by the following nonlinear ODEs:

$$\frac{dS}{dt} = \pi - p_1\beta S(I_S + I_A) - p_2\beta S(I_S + I_A) - \mu S$$

$$\frac{dE_a}{dt} = p_1\beta S(I_s + I_A) - w_1 E_a - \mu E_a$$

$$\frac{dE_b}{dt} = p_2\beta S(I_S + I_A) - w_2 E_b - \mu E_b$$

$$\frac{dI_S}{dt} = \delta w_1 E_a + \delta w_2 E_b - \gamma_S I_S - (\mu + \sigma) I_p$$

$$\frac{dI_A}{dt} = (1-\delta) w_1 E_a + (1-\delta) w_2 E_b - \gamma_A I_A - (\mu + \sigma) I_A$$

$$\frac{dR}{dt} = \gamma_S I_S + \gamma_A I_A - \mu R$$

By assuming initial conditions to be non-negative:

$S(0) = S_0 > 0$, $E_a(0) = E_a > 0$, $E_b(0) = E_b > 0$, $I_S(0) = I_S > 0$, $I_A(0) = I_A > 0$, $R(0) = R > 0$

All model parameters are assumed to be positive for all time $t > 0$.

The model parameters are explained is Table 8.

Table 8 – Description of model parameters

Parameter	Description
π	Birth rate of population
μ	Death rate of population
σ	Disease induced death rate
β	Transmission rate of disease
p	Ratio of transition from S to E_a/E_b
δ	Ratio of transition from exposed to Infected (Symptomatic) class
w_1	Rate of infection from E_a to infected class
w_2	Rate of infection from E_b to infected class
γ_S	Treatment rate for symptomatic class
γ_A	Treatment rate for asymptomatic class

3.3 Mathematical Model Analysis

Positivity of Solutions - For the COVID-19 infection model system to make epidemiological sense, it is necessary to prove that all the state variables remain positive for all time.

Theorem 1. Let the initial condition for the model be S(t)>0, E_a(t)>0, E_b(t)>0, I_S(t)>0, I_A(t)>0 and R(t)>0. Then the solution of the COVID-19 model with positive initial condition will remain positive for all time t > 0.

Proof. Let t1 = sup {t > 0: S (0)>0, V (0)>0, E_1 (0)>0, E_2 (0)>0, I_p (0)>0, I_{exp} (0)>0, R (0)>0}.

Consider the first equation of the model given below as

$$\frac{dS}{dt} = \pi - p_1\beta S(I_S + I_A) - p_2\beta S(I_S + I_A) - \mu S$$

$$\frac{dS}{dt} = \pi - (p_1\beta(I_S + I_A) - p_2\beta S(I_S + I_A) - \mu)S$$

$$\frac{dS}{dt} \geq -(p_1\beta(I_S + I_A) - p_2\beta S(I_S + I_A) - \mu)S$$

$$\int \frac{dS}{S} \geq -\int (p_1\beta(I_S + I_A) - p_2\beta S(I_S + I_A) - \mu)\ \mathrm{dt}$$

$$S(t) \geq S(0)\exp(-\int (p_1\beta(I_S + I_A) - p_2\beta S(I_S + I_A) - \mu)\ dt\ \geq\ 0$$

Similarly, it can also be shown that, E_a(t)>0, E_b(t)>0, I_S(t)>0, I_A(t)>0 and R(t)>0 for all time t > 0. Hence, we conclude that all solutions of the model system remain positive for all nonnegative initial conditions

3.4 Invariant Region

Theorem 2. For the non-negative initial conditions, the solutions of the system are contained in the region D $\subset R_+^7$, defined by D = $\left\{(S, E_a, E_b, I_S, I_A, R) \in R_+^6 :\ N \leq \frac{\pi}{\mu}\right\}$

Proof. All ODEs of the model system are summed to give

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE_a}{dt} + \frac{dE_b}{dt} + \frac{dI_S}{dt} + \frac{dI_A}{dt} + \frac{dR}{dt}$$

The change in the complete population is defined by

$$\frac{dN}{dt} = \pi - \mu N - \sigma(I_S + I_A)$$

Hence, $\frac{dN}{dt} \leq \pi - \mu N$

Hence, $\frac{dN}{dt} \leq 0$ if $N(t) \geq \frac{\pi}{\mu}$

A standard comparison theorem can be used to show that

$$N(t) \leq N(0)e^{-\mu t} + \frac{\pi}{\mu}(1 - e^{-\mu t})$$

In particular, if $N(0) \leq \frac{\pi}{\mu}$ then $N(t) \leq \frac{\pi}{\mu}$ for all t>0. Hence, the set D is positively invariant. Moreover, if $N(0) \geq \frac{\pi}{\mu}$ then either the solution enters the domain D in finite time or N(t) asymptotically approaches $\frac{\pi}{\mu}$ as t → ∞. Thus, the domain D attracts all solutions in R_+^5. Since the domain D is positively invariant, it suffices to examine the dynamics of the system's orbits in D. Therefore, we conclude that the model is mathematically and epidemiologically sound.

3.5 Analysis of Disease-Free Equilibrium (DFE)

P0, the disease-free equilibrium (DFE) state, is a steady-state solution where there are no infections in the population. The disease class is the population of infected individuals. Taking into account the initial equation of the system, we obtain:

$P_0 = (S, Ea_0, Eb_0, IS_0, IA_0, R_0) = \left(\frac{\pi}{\mu}\ 0,\ 0,\ 0,\ 0,\ 0\right)$

3.6 Calculation of Reproduction Number

Basic reproduction number usually denoted by R0 is the number of secondary cases that one case of infected individual would produce in susceptible population. The Next Generation Matrix Method is used to determine R_0. The ODEs are regrouped into disease classes (E_a, E_b, I_S, I_A) and non-disease classes (S and R) and the disease classes are rearranged in the form, $\frac{dx}{dt}$ = F(x) – V(x) when x = $(E_a, E_b, I_S, I_A)^{T.}$

$$F(x) = \begin{bmatrix} P_1\beta S(I_S + I_A) \\ P_2\beta S(I_S + I_A) \\ 0 \\ 0 \end{bmatrix} \text{ and}$$

$$V(x) = \begin{bmatrix} \mu E_a + w_1 E_a \\ \mu E_b + w_2 E_b \\ -\delta w_1 E_a - \delta w_2 E_b + \gamma_S I_S + (\mu + \sigma) I_S \\ -(1-\delta) w_1 E_a - (1-\delta) w_2 E_b + \gamma_A I_A + (\mu + \sigma) I_A \end{bmatrix}$$

As infected compartments are only E_a, E_b, I_S and I_A, then F and V are the Jacobian matrices of order 4 × 4 at disease free equilibrium are

$$F = \begin{bmatrix} 0 & 0 & \frac{\pi\beta p_1}{\mu} & \frac{\pi\beta p_1}{\mu} \\ 0 & 0 & \frac{\pi\beta p_2}{\mu} & \frac{\pi\beta p_2}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \text{ and}$$

$$V = \begin{bmatrix} \mu + w_1 & 0 & 0 & 0 \\ 0 & \mu + w_2 & 0 & 0 \\ -\delta w_1 & -\delta w_2 & \gamma_S + \mu + \sigma & 0 \\ w_1(\delta - 1) & -w_2(1 - \delta) & 0 & \gamma_A + \mu + \sigma \end{bmatrix}$$

The next generation matrix which is FV^{-1} is calculated for the model and the spectral radius (absolute dominant eigen value) of matrix FV^{-1} is computed. This value is the effective reproduction number.

$$R = \frac{\pi\beta(p_1 w_1 + p_2 w_2)(\delta\gamma_A - \delta\gamma_S + \gamma_S + \mu + \sigma)}{\mu(\mu + w_1)(\gamma_A + \mu + \sigma)(\gamma_S + \mu + \sigma)}$$

3.7 Numerical Simulation

The model parameters are given quantifiable numerical values and the model is simulated on MATLAB to produce a graph to visually depict transmission dynamics of the model as shown in Figure 2.

The optimum Rate of Infection for exposed individuals without comorbidities (w2) are calculated using the queueing model and the rate of infection for exposed individuals with comorbidities are assumed to be more than 30% than that of the former. The remaining model parameters are given appropriate values borrowed from published research. These values are given in Table 9.

Table 9 - Numerical values of model parameters

Parameter	Description	Values ($year^{-1}$)
π	Recruitment rate	0.00018 $days^{-1}$
μ	Natural death rate	$4.563\times10-5$ $days^{-1}$
σ	Disease induced death rate	0.0018
β	Transmission rate of disease	0.017
p_1	Ratio of transition from Susceptible to Exposed (with comorbidities) class	0.4
p_2	Ratio of transition from Susceptible to Exposed (without comorbidities) class	0.6
δ	Ratio of transition from exposed to Infected (with symptoms) class	0.7
w_1	Rate of Infection for Exposed with comorbidities	Maharashtra: 0.3242; Rajasthan: 0.2514; Karnataka: 0.3232
w_2	Rate of Infection for Exposed without comorbidities	Maharashtra: 0.2494; Rajasthan: 0.1934; Karnataka: 0.2486
γ_S	Rate of treatment for Symptomatic Class to Recovery	0.09 $days^{-1}$
γ_A	Rate of treatment for Asymptomatic Class to Recovery	0.00914 $days^{-1}$

The reproduction number at optimum rate of infection (after intervention) for the 3 states are given in table 10:

Table 10 – Reproduction Numbers for the three states

State	Basic Reproduction Number
Maharashtra	2.01790
Karnataka	2.01788
Rajasthan	2.01782

It is observed that the value of R0 is approximately 2.017 across the three states. The difference is negligible however, maximum for Maharashtra and the least for Rajasthan.

The reproduction number before intervention (for 1 quarantine centre) is also calculate and noted to be 2.3423
When R0 is less than 1, the disease is expected to die and when the R0 is more than or equal to 1, the disease will cause an endemic or epidemic respectively. In our calculations, R0 is greater than 1 for all 3 states. This result shows that the endemic system is unstable and urgent intervention is required.

For efficient computing, the ode45 function on MATLAB's standard solver is utilised to implement the 4th order Runge-Kutta technique with a configurable time step. Initial values for the ODE equations of the model are S (0) = 1500, E_a (0) = 1000, E_b (0) = 1000, I_S (0) = 500, I_A (0) = 500, R (0) = 0.

Figures 9,10 and 11 show the transmission of the disease graphically for the three states.

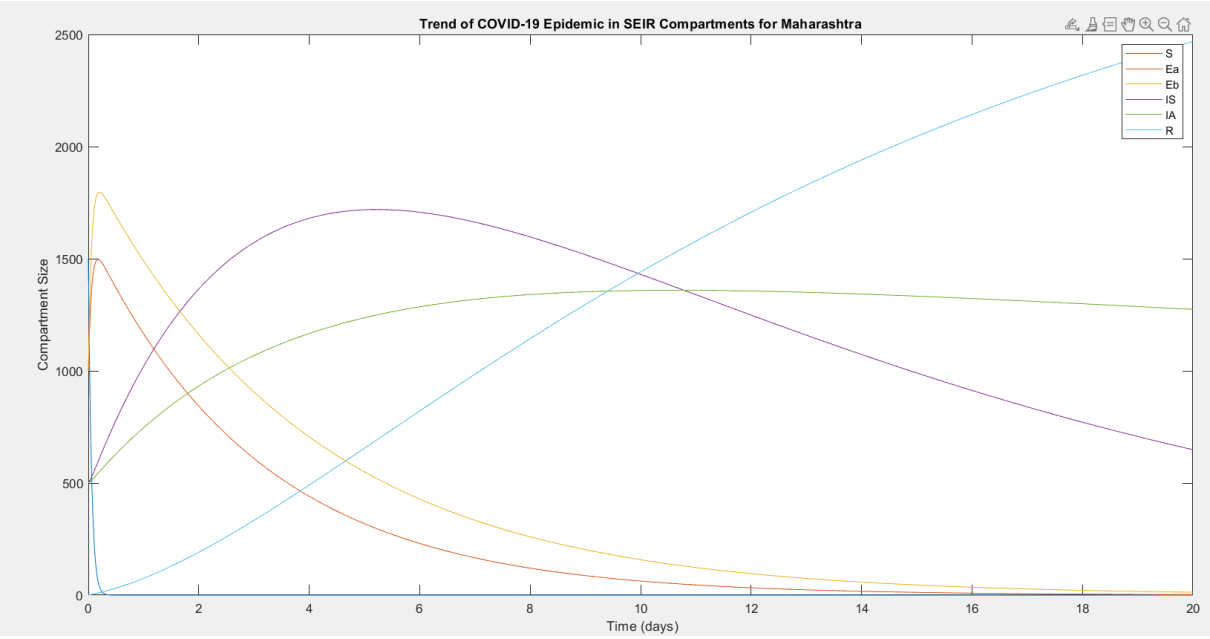


Figure 9 – Spread of COVID-19 in Maharashtra

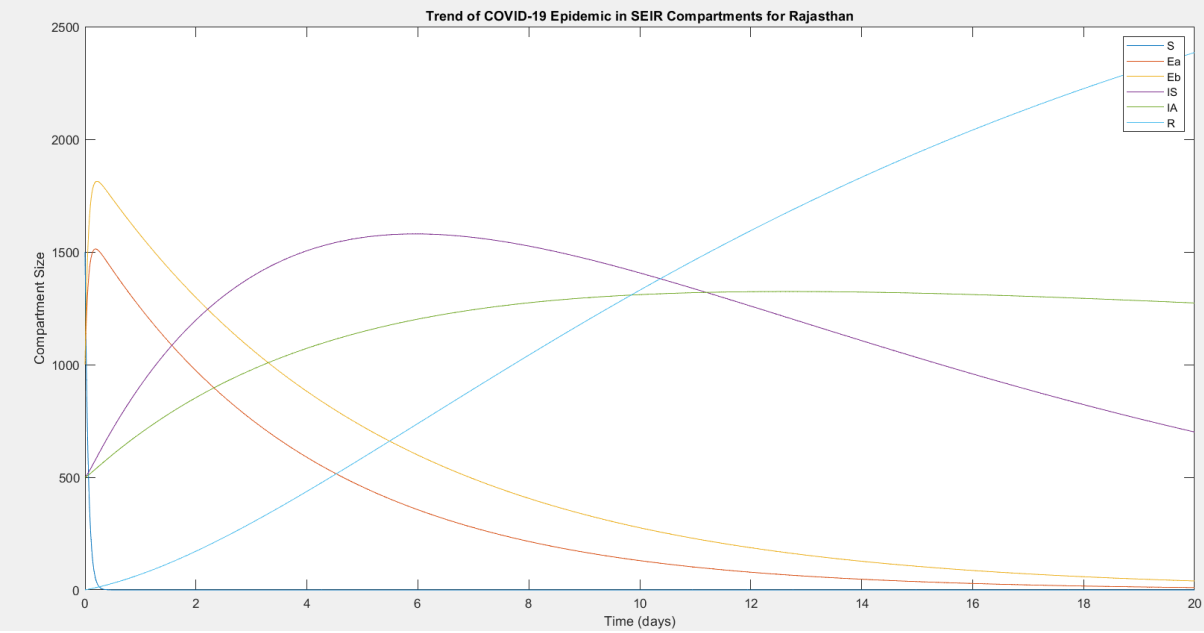


Figure 10 – Spread of COVID-19 in Rajasthan

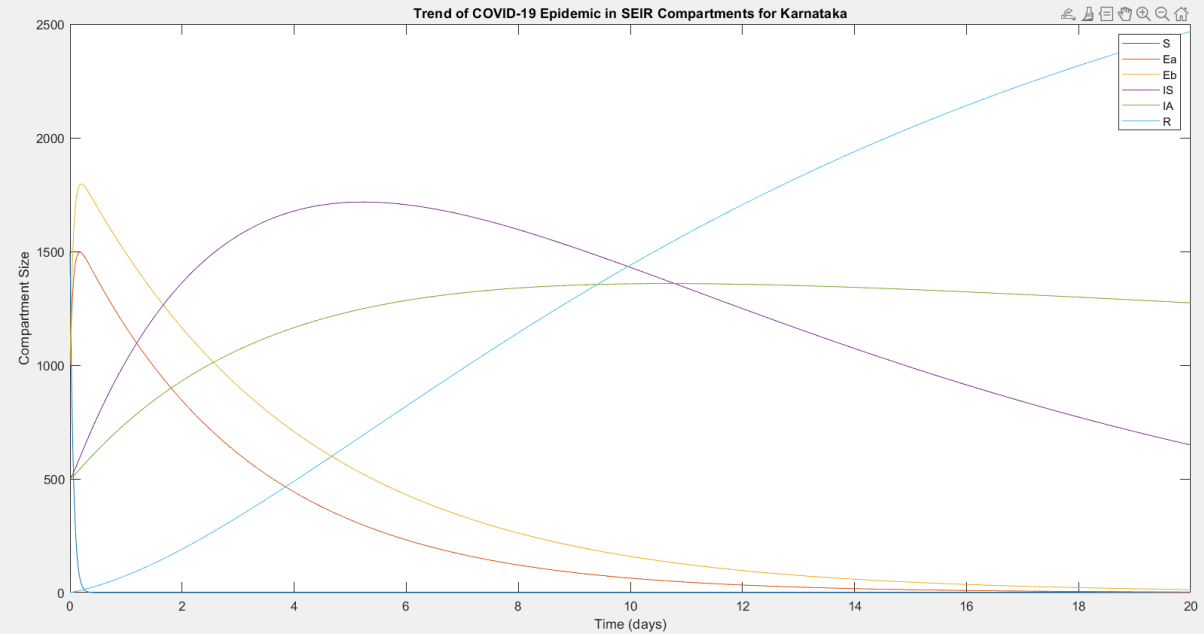


Figure 11 - Spread of COVID-19 in Karnataka

Chapter 4 – Urban Contact Network

4.1 Introduction

COVID-19 being a contagious, communicable and highly transmissible disease displays a very random and non-sequential transmission pattern. To account for this the model is modified to a more realistic approach by developing an SEIR model which is an open queueing network.

These networks are characterised by Poisson arrivals and subsequent transfer to one or more servers until departure. The network involves the multiple servers/contact stations which symbolizes an urban contact network in the population. These offer a high degree of realism, which involves stations like households, shopping centre, religious centre, schools, workplaces, hospitals and so on in a given community. In the community, every individual serves as a node for the network and the edge signifies contact. Figure 12 depicts this concept diagrammatically.

Transmissibility of the disease is calculated to validate the reproduction numbers derived by our epidemic model before and after intervention.

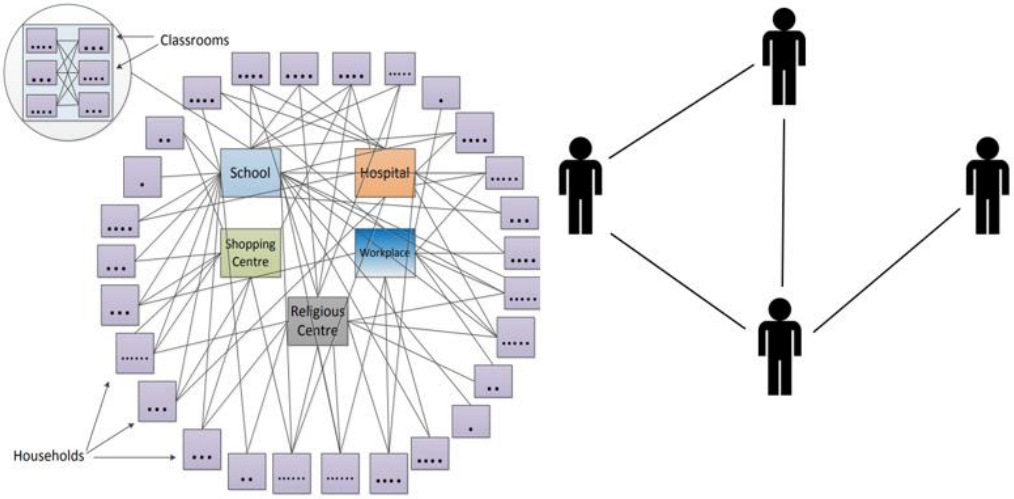


Figure 12 – Urban Contact Network Analysis

4.2 Transmissibility of COVID-19

The Transmissibility of an illness, T is the average probability that an infectious person would transfer the disease to a susceptible person with whom they have come into contact. Transmissibility T reviews key aspects of disease transmission, including the frequency of

interactions between individuals, the likelihood that a contact would result in transmission, the duration of the infectious phase, and the vulnerability of individuals to COVID-19 infection. Critical Transmissibility or epidemic threshold T_c is the degree of transmissibility at which a population is susceptible to large-scale epidemics when R_0 is 1.

Meyers (2005) and Brauer and Castillo-Chávez (2012) showed that the fundamental reproduction number and pandemic threshold are determined by

$$R_0 = T\frac{< c^2 >}{< c > -1}$$

$$T_C = \frac{< c >}{< c^2 > - < c >}$$

Where $< c >$ is the network's mean degree and $< c^2 >$ is the network's mean square degree. T_c is also known as the minimal transmissibility (T) required for an outbreak to become a widespread pandemic.

Cumulative degree distribution versus degree of contact is depicted in Figure 13 for urban contact networks. The line in the illustration depicts the probability, that a randomly selected individual (vertex) holds at least the specified number of contacts (degree). This involves the difference between the number of individuals per household and the sum of the mean degree against the mean degree.

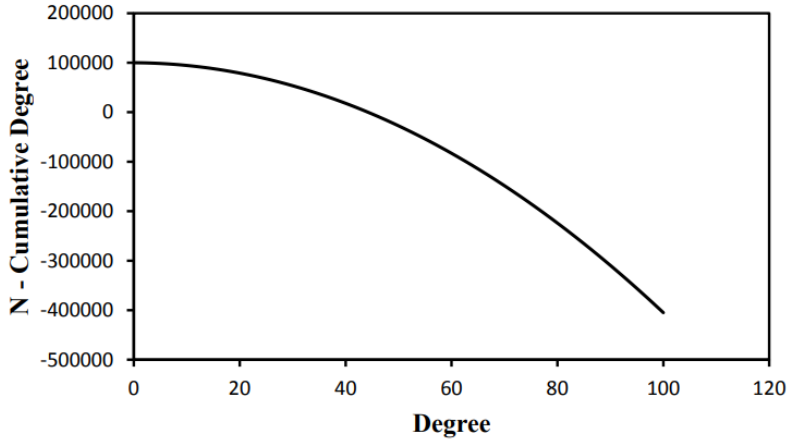


Figure 13 - Cumulative Degree Distribution for Urban Contact Network

By using the value of <c> as 8.7579, the mathematical expressions above are integrated to generate the probability of the network and the value of transmissibility of the disease. These

values are calculated with respect to reproduction number before and after intervention. It was observed that the vulnerability decreased after intervention.

Table 11 – Transmissibility before and after intervention

	Reproduction Number	**Transmissibility**	**Probability of Network Infected**
Before Intervention	2.3423	0.1417	50.53%
After Intervention	2.0178	0.1221	43.62%

Chapter 5 – Conclusion

This research aims to conduct a comparative analysis of the queueing theory based and epidemiology based statistical and mathematical models to determine the probability of infection of COVID-19.

M/M/1 queues are applied to 6-month data of three states to analyse the transmission patterns and effectivity of intervention and control measures through increasing the number of quarantine centres. The basic queueing properties were used to determine the optimum rate of infection for each state which was observed to be decreasing drastically as the number of servers/quarantine centres were increased. The deductions of the queueing theory applications to COVID-19 problem estimated the rate of infection to be approximately 0.2 across the three states.

A basic SEIR epidemic model is applied to the data using queueing theory. A two-dimensional QSD model was constructed and approximated into a normal distribution curve. The curve indicated the rate of infection to be close to 0.2 as well.

The SEIR model is further modified into a 6-phase compartmental model by taking into account exposed individuals with and without comorbidities and infected class with and without symptoms. The disease-free equilibrium points and reproduction numbers are calculated for each state. It is noted the R0 reduces marginally after intervention

Finally, the model is applied to a more realistic urban contact network and the transmissibility of the disease is used as a benchmark to validate the values of R0 derived by the epidemic model.

APPENDIX

1) Reproduction Number – Proof (Python)

```
from sympy import*
init_printing()
p1,p2,beta,delta,w1,w2,gamma_S,gamma_A,mu,S,Ea,Eb,IS,IA,R,sigma=
symbols('p1 p2 beta delta w1 w2 gamma_S gamma_A mu S Ea Eb IS IA R
sigma')

f1=p1*beta*S*(IS+IA)
f2=p2*beta*S*(IS+IA)
f3=0
f4=0

F=Matrix ([f1,f2,f3,f4]).jacobian([Ea,Eb,IS,IA])
F=F.subs(S,pi/mu)
F

v1=(mu*Ea)+(w1*Ea)
v2=(mu*Eb)+(w1*Eb)
v3=(-delta*w1*Ea)-(delta*w2*Eb)+(gamma_S*IS)+((mu+sigma)*IS)
v4=(-(1-delta)*w1*Ea)-((1-delta)*w2*Eb)+(gamma_A*IA)+((mu+sigma)*IA)

V=Matrix ([v1,v2,v3,v4]).jacobian([Ea,Eb,IS,IA])
V

G=F*V.inv()
G

G.eigenvals()
```

2) Transmission of COVID-19 in compartmental model (MATLAB)

i) Maharashtra

```
function Mah
IC = [1500;1000;1000;500;500;0];
tspan = [0 20];
[t,Y] = ode45(@odefun, tspan, IC);
plot(t, Y)

function DYdt = odefun(~,Y)
S = Y(1);
Ea = Y(2);
Eb = Y(3);
IS = Y(4);
IA=Y(5);
R = Y(6);
```

```
pi=0.00018;
mu=0.00004563;
beta=0.017;
delta=0.7;
w1=0.3242;
w2=0.2494;
gammaS=0.09;
gammaA=0.00914;
p1=0.4;
p2=0.6;
sigma=0.0018;

dSdt = pi-(mu*S)-(p1*beta*S*(IS+IA))-(p2*beta*S*(IS+IA));
dEadt = (p1*beta*S*(IS+IA))-(mu*Ea)-(w1*Ea);
dEbdt = (p2*beta*S*(IS+IA)) -  (mu*Eb)-(w2*Eb);
dISdt = (delta*w1*Ea)+(delta*w2*Eb)-((mu+sigma)*IS)-(gammaS*IS);
dIAdt =((1-delta)*w1*Ea)+((1-delta)*w2*Eb)-((mu+sigma)*IA)-
(gammaA*IA)
dRdt = (gammaS*IS)+(gammaA*IA)-(mu*R);

DYdt = [dSdt; dEadt;dEbdt;dISdt; dIAdt;dRdt];
```

ii) Rajasthan

```
function Raj
IC = [1500;1000;1000;500;500;0];
tspan = [0 20];
[t,Y] = ode45(@odefun, tspan, IC);
plot(t, Y)

function DYdt = odefun(~,Y)
S = Y(1);
Ea = Y(2);
Eb = Y(3);
IS = Y(4);
IA=Y(5);
R = Y(6);


pi=0.00018;
mu=0.00004563;
beta=0.017;
delta=0.7;
w1=0.2514;
w2=0.1934;
gammaS=0.09;
gammaA=0.00914;
p1=0.4;
p2=0.6;
```

```
sigma=0.0018;

dSdt = pi-(mu*S)-(p1*beta*S*(IS+IA))-(p2*beta*S*(IS+IA));
dEadt = (p1*beta*S*(IS+IA))-(mu*Ea)-(w1*Ea);
dEbdt = (p2*beta*S*(IS+IA)) -  (mu*Eb)-(w2*Eb);
dISdt = (delta*w1*Ea)+(delta*w2*Eb)-((mu+sigma)*IS)-(gammaS*IS);
dIAdt =((1-delta)*w1*Ea)+((1-delta)*w2*Eb)-((mu+sigma)*IA)-
(gammaA*IA)
dRdt = (gammaS*IS)+(gammaA*IA)-(mu*R);

DYdt = [dSdt; dEadt;dEbdt;dISdt; dIAdt;dRdt];
```

iii) Karnataka

```
function Kar
IC = [1500;1000;1000;500;500;0];
tspan = [0 10];
[t,Y] = ode45(@odefun, tspan, IC);
plot(t, Y)

function DYdt = odefun(~,Y)
S = Y(1);
Ea = Y(2);
Eb = Y(3);
IS = Y(4);
IA=Y(5);
R = Y(6);


pi=0.00018;
mu=0.00004563;
beta=0.017;
delta=0.7;
w1=0.3232;
w2=0.2486;
gammaS=0.09;
gammaA=0.00914;
p1=0.4;
p2=0.6;
sigma=0.0018;

dSdt = pi-(mu*S)-(p1*beta*S*(IS+IA))-(p2*beta*S*(IS+IA));
dEadt = (p1*beta*S*(IS+IA))-(mu*Ea)-(w1*Ea);
dEbdt = (p2*beta*S*(IS+IA)) -  (mu*Eb)-(w2*Eb);
dISdt = (delta*w1*Ea)+(delta*w2*Eb)-((mu+sigma)*IS)-(gammaS*IS);
dIAdt =((1-delta)*w1*Ea)+((1-delta)*w2*Eb)-((mu+sigma)*IA)-
(gammaA*IA)
dRdt = (gammaS*IS)+(gammaA*IA)-(mu*R);

DYdt = [dSdt; dEadt;dEbdt;dISdt; dIAdt;dRdt]
```

REFERENCES

1) Alan, M. (2013). Hunter's Tropical Medicine and Emerging Infectious Diseases. (9th ed). New York: Saunders

2) Anderson, H. and Britton, T. (2000). Stochastic Epidemics in Dynamic Populations: Quasi- Stationarity and Extinction. Journal Mathematical Biology. 41: 559-580

3) Ball, F. and Donnelly, P. (1995). Strong Approximations for Epidemic Models. Stochastic Processes and their Applications. 55: 1-21.

4) Ball, F. and Stefanov, V. T. (2001). Further Approaches to Computing Fundamental Characteristics of Birth-Death Processes. Journal of Applied Probability. 38: 995-1005

5) Blower, S. M., Small, P. M. and Hopewell, P. C. (1996). Control Strategies for Tuberculosis Epidemics: New Models for Old Problems. Science. 273: 497.

6) Bolch, G., Greiner S., De Meer H., Trivedi K. S. (2006). Queueing Networks and Markov Chains. (2nd edition). USA: John Wiley. ISBN 978-0-7923-9650-5.

7) Brauer, F. and Castillo-Chavez, C. (2012). Mathematical Models in Population Biology and Epidemiology. (2nd ed.). London: Springer

8) Driessche, P. V. D and Watmough, J. (2001). Reproduction Numbers and Sub-threshhold Endemic Equilibria for Compartmental Models of Disease Transmission. Mathematical Biosciences. 180: 29-48.

9) Hernandez-Suarez C. M., Castillo-Chavez C., Lopez O. M., and Hernandez-Cuevas K. (2010). An Application of Queueing Theory to SIS and SEIS Epidemic Models. Mathematical Biosciences and Engineering. 7(4): 809-823

10) Kendall, D. (1953). Stochastic Processes Occurring in the Theory of Queues and their Analysis by the Method of the Imbedded Markov Chain. The Annals of Mathematical Statistics. 24: 338-354.

11) Ross, S. M. (2007). Introduction to Probability Models. (9th ed.). USA: Academic Press, Elsevier Inc.