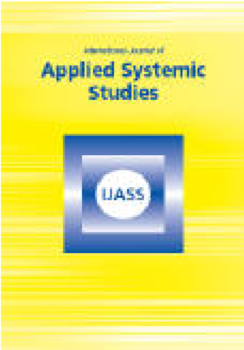


International Journal of Applied Systemic Studies

ISSN online: 1751-0597 - ISSN print: 1751-0589
https://www.inderscience.com/ijass

Transmission of COVID-19 through asymptomatic individuals

Nita H. Shah, Ankush H. Suthar, Purvi M. Pandya

DOI: 10.1504/IJASS.2021.10039858

Article History:

Received:	23 December 2020
Accepted:	23 February 2021
Published online:	17 February 2023

Transmission of COVID-19 through asymptomatic individuals

Nita H. Shah*, Ankush H. Suthar and
Purvi M. Pandya

Department of Mathematics,
Gujarat University,
Ahmedabad-380009, Gujarat, India
Email: nitahshah@gmail.com
Email: ankush.suthar1070@gmail.com
Email: pandya091@gmail.com
*Corresponding author

Abstract: The rapid emergence of the coronavirus disease 2019 (COVID-19) has already taken on pandemic proportions, resulting thousands of deaths around the world. In the present manuscript, a mathematical model is proposed to investigate the current outbreak of the COVID-19. The model includes multiple transmission pathways and emphasises the role of asymptomatic and symptomatic infected population in the spread of this disease. To predict upcoming situation and a detail analysis of the spread of COVID-19 outbreak, basic reproduction number is calculated using publicly reported data from three different countries, where the outbreak is at its peak (USA), initial level (India) and controlled up to certain level (Japan). Analytical and numerical results of the model indicate that current on-going outbreak of COVID-19 would remain endemic if we do not proceed with extreme vigilance due to the serious risk it poses around the globe.

Keywords: COVID-19; asymptomatic transmission; mathematical model; basic reproduction number; numerical simulation.

Reference to this paper should be made as follows: Shah, N.H., Suthar, A.H. and Pandya, P.M. (2023) 'Transmission of COVID-19 through asymptomatic individuals', *Int. J. Applied Systemic Studies*, Vol. 10, No. 1, pp.1–15.

Biographical notes: Nita H. Shah is a Professor in the Department of Mathematics, Gujarat University, Ahmedabad-380009, Gujarat, India. She has 25 years of research experience in inventory management, forecasting and information technology and information systems. She has published 400+ articles in international journals, including *APJOR* (Singapore), *International Journal of Production Economics*, *OMEGA, CCERO* (Belgium), *ECPE* (Romania), *Measuring, Control & Simulation* (France), *JIOS* (India), *IJOMS* (India), *Industrial Engineering* (India), *European Journal of Operational Research, IJIR, IJOR, IJMOR, IJBPSCM*, etc.

Ankush H. Suthar is a research scholar in the Department of Mathematics, Gujarat University, Ahmedabad-380009, Gujarat, India. His research interest is modelling of dynamical systems of infectious diseases. He has eight publications in his credit.

Purvi M. Pandya is a research scholar in the Department of Mathematics, Gujarat University, Ahmedabad-380009, Gujarat, India. Her research interest is modelling of dynamical systems. She has six publications in her credit.

1 Introduction

The pandemic outbreak of a novel coronavirus (COVID-19), broke out in the Chinese province of Wuhan and rapidly infected hundreds of thousands people worldwide since December 2019 (Rothan and Byrareddy, 2020). As on 19 April 2020, 05:30 GMT, the virus has affected 213 countries and territories globally with 2,350,058 confirmed cases, of which 161,268 have passed away and 55,141 cases are in critical condition (worldometers.info). Due to lake of appropriate vaccination and its highly contagious nature, there is still a possibility that the outbreak could become more intense and cause high mortality around the world. There is no doubt that the pandemic has profound effects on world economy and our private and professional lives (Driessche and Watmough, 2002; Fernandes, 2020). To avoid the risk of worst condition of this pandemic outbreak, the central government and local governments of all the infected countries had tightened preventive measures and large-scale movement of population is strictly prohibited (Tahir and Masood, 2020). As the outbreak grows to a greater extent, severally infected areas are imposing a more massive quarantine.

Nowadays, all the health organisations around the world frequently monitors the evidence and information about the preventive measures and spread of COVID-19. Recent analysis by The World Health Organization (WHO) suggest that out of total infected cases, 80% of infected patients are asymptomatic or at an initial stage, 15% are severely infected, suffering from dyspnea and 5% are requiring ventilation as they are at critical stage (Harries et al., 2020). The main clinical manifestations of the infection are dry coughing, fever, dyspnea and desaturation (Jin et al., 2020). Mainly two type of human to human virus transmission are reported, symptomatic, pre-symptomatic transmission. Symptomatic transmission occurs while exposed individuals come in contact with the infected respiratory droplets spread through coughing or sneezing by symptomatic individuals (Huang et al., 2020). The incubation period for COVID-19 is on usual 5–6 days and can be extend up to 14 days, which makes it is hard to find and quarantine infected individuals before symptom onset. The duration of this pre-symptomatic period which is more hazardous, since some infected persons can be contagious in this duration and they can infect others unknowingly (Hatipoğlu, 2020; Zhai et al., 2020).

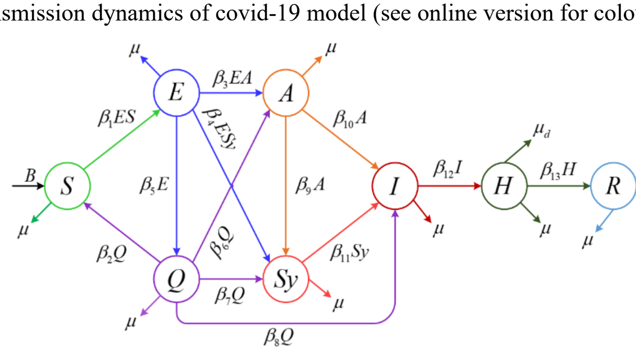
Pandemic outbreak of COVID-19 has turn out to be an unexpected severe problem on public health internationally, several dynamic models have been constructed to give estimations and peak prediction on the transmission dynamics for making epidemic preventing strategies (Katul et al., 2020, Zhou et al., 2020). In our previous study, we have proposed a generalised SEIR model of COVID-19 and optimal control theory is applied to pretend the behaviour of its transmission under various intervention strategies (Shah et al., 2020). Tang et al. (2020a) proposed a compartmental model in which each group is divided into the quarantined and unquarantined subpopulation. To compute the evolution in better way, they redesign and re-estimated the reproduction ratio of the model by introducing diagnose and time-dependent contact rates (Tang et al., 2020a, 2020b). Chen et al. (2020b) constructing a dynamical model to presented the behaviour of incubation period of the infection on local outbreak of COVID-19 (Chen et al., 2020b). Khan and Atangana (2020) have formulated the mathematical results for a fractional ordered model which includes details of interaction among the bats, unknown hosts, humans and the infections reservoir (Khan and Atangana, 2020). In the same way, Chen et al. (2020a) have also constructed a transmission network model for simulating the possible transmission of COVID-19 among bats, hosts, reservoir and people (Chen et al., 2020a). Zhao et al. (2020) divided people from Wuhan City into subclass of different age groups and established a SEIARW-model including market to person and person to person transmission of COVID-19 (Zhao et al., 2020). Zhong et al. (2020) have examined characteristics of the past epidemics of COVID-19 and constructed a mathematical model using epidemiological data to make quick prediction of the outbreak in China (Zhong et al., 2020). Yang and Wang (2020) have formed a mathematical model after studying the multiple transmission pathways that describes the role of the environmental reservoir in the transmission and spread of COVID-19 (Yang and Wang, 2020).

In this work, a compartmental model is constructed to study the asymptomatic and symptomatic transmission of the COVID-19 infection in Section 2. Moreover, its basic reproduction number is also formulated and calculated using real world data. Numerical simulation is carried out in Section 3, which describe the variation in compartments of the model with time and relation between them.

2 Mathematical modelling

In this Section, a mathematical model is formulated where both asymptotically and symptomatically infected class are included separately to analyse asymptomatic as well as symptomatic transmission of COVID-19. In this model, total population of humans are divided in eight compartments, class of susceptible individuals (S), class of exposed individuals (E) where, exposed individuals are those who are surrounded by infection but yet not infected, class of quarantine individuals (Q), class of individuals infected with COVID-19 who does not develop symptoms of disease i.e. class of asymptomatically infected individuals (A), class of symptomatically infected individuals (Sy) this individual has developed signs and symptoms compatible with COVID-19 virus infection, class of all the individuals who are infected by COVID-19 (I), class of hospitalised individuals (H) and last is class of recovered individuals (R). Note that, infected cases are seen in almost every region of the countries because of the highly contagious nature of the virus. Hence in this situation, all the people who regularly stay outside like, doctors, police man, security guard, grocery shop keeper etc. are also considered to be an exposed by COVID-19. To avoid risk factor of COVID-19 spread, whenever infected people caught, all the individuals who came in contact with this infected people in last few days are also kept in quarantine class. The transmission dynamics and flow is shown in following Figure 1.

Figure 1 Transmission dynamics of covid-19 model (see online version for colours)



The population of the all compartments is govern by the following system of non-linear differential equations:

$$\begin{aligned} S' &= B - \beta_1 ES + \beta_2 Q - \mu S \\ E' &= \beta_1 ES - \beta_3 EA - \beta_4 ESy - \beta_5 E - \mu E \\ Q' &= \beta_5 E - \beta_2 Q - \beta_7 Q - \beta_8 Q - \beta_6 Q - \mu Q \\ A' &= \beta_3 EA + \beta_6 Q - \beta_9 A - \beta_{10} A - \mu A \\ Sy' &= \beta_7 Q + \beta_4 ESy + \beta_9 A - \beta_{11} Sy - \mu Sy \\ I' &= \beta_{10} A + \beta_{11} Sy + \beta_8 Q - \beta_{12} I - \mu I \\ H' &= \beta_{12} I - \beta_{13} H - \mu_d H - \mu H \\ R' &= \beta_{13} H - \mu R \end{aligned} \tag{1}$$

The parameters and its value for three different countries used in the model are given in following Table 1.

Table 1 Parameters and its values used in the model. Data for total number of infected cases, critical cases, hospitalised cases and deaths due to COVID-19 for these three countries

Parameters		*USA*	*India*	*Japan*
B	Birth rate	0.0120	0.0182	0.0074
μ	Natural mortality rate	0.0088	0.0073	0.0099
μ_d	Mortality rate due to COVID-19	0.0325	0.0299	0.0218
β_1	Rate by which susceptible individuals get exposed	0.0035	0.0015	0.0016
β_2	Rate by which quarantined individuals become susceptible	0.8076	0.9606	0.9230
β_3	Rate at which exposed individuals become asymptomatically infected	0.2913	0.0012	0.0172
β_4	Rate at which exposed individuals become symptomatically infected	0.0124	0.00053	0.0043
β_5	Rate at which exposed individuals get quarantined	0.8395	0.0684	0.2791
β_6	Rate at which quarantined individuals are moving to asymptomatic class	0.0952	0.0313	0.0616
β_7	Rate at which quarantined individuals are moving to symptomatic class	0.0384	0.0078	0.0154
β_8	Rate at which quarantined individuals get infected by COVID-19	0.1923	0.0391	0.07700
β_9	Rate at which asymptomatic individuals become symptomatic	0.2499	0.2500	0.2499
β_{10}	Transmission rate from asymptomatic class to infected class	0.2000	0.2	0.2
β_{11}	Transmission rate from symptomatic class to infected class	0.8000	0.8	0.8
β_{12}	Rate at which infected individuals get hospitalised	0.9136	0.8846	0.8320
β_{13}	Recovery rate	0.0593	0.0962	0.1756

Notes: That, all the parameters used in this COVID-19 model are non-negative. Consider the feasible region.

Source: Woldometer (https://www.worldometers.info/coronavirus/) (accessed 8 April 2020)

$$\Lambda = \left\{ (S, E, Q, A, Sy, I, H, R,) \in R_+^8 : S + E + Q + A + Sy + I + H + R \leq \frac{B}{\mu} \text{ and } H \leq \frac{B}{\mu_d} \right\} \quad (2)$$

The region is positively invariant, all the solutions of the system (1) are remain in the feasible region (2).

2.1 Endemic equilibrium

The solution of system (1) is an endemic equilibrium point of the model which is given by: $E_p^* = (S^*, E^*, Q^*, A^*, Sy^*, I^*, H^*, R^*)$ where,

$$S^* = \frac{\beta_3\beta_4\beta_5 k_5 r^2(\beta_6 + \beta_7) - \beta_4\beta_5\beta_7 k_3 r + (\beta_4 k_3 r - k_4)(k_1 k_3 - \beta_3 k_1 k_2 r) - \beta_5\beta_6 r(\beta_3\beta_4 + \beta_4\beta_9)}{\beta_1(\beta_4 k_2 r - k_4)(\beta_3 k_2 r - k_3)},$$

$$E^* = k_2 r,\ Q^* = \beta_5 r,\ A^* = -\frac{\beta_6\beta_5 r}{\beta_3 k_2 r - k_3},\ Sy^* = -\frac{\beta_5 r(\beta_3\beta_7 k_2 r - \beta_6\beta_9 - \beta_7 k_3)}{(\beta_4 k_2 r - k_4)(\beta_3 k_2 r - k_3)},$$

$$I^* = -\frac{p\beta_5}{qk_5},\ H^* = -\frac{p\beta_{12}\beta_5}{qk_5 k_6} \text{ and } R^* = \frac{p\beta_{13}\beta_{12}\beta_5}{qk_5 k_6 \mu}$$

The terms used in the expression of compartments of the endemic point are:

$$p = B\beta_1\beta_8(\beta_4 k_2 r - k_4)(\beta_3 - k_3) + \beta_1\beta_5 r(\beta_2 + \beta_6)(\beta_{10}\beta_4\beta_6 k_2 r + \beta_{11}\beta_3\beta_7 k_2 r - \beta_{10}\beta_6 k_4) + (\beta_5\beta_7 - k_1 k_2)(\beta_1\beta_{10}\beta_4\beta_6 k_2 r^2 + \beta_1\beta_{11}\beta_3\beta_7 k_2 r^2 - \beta_1\beta_{10}\beta_6 k_4 r - \beta_4\beta_8 k_3 \mu r)$$

$$q = (\beta_5(\beta_2 + \beta_6 + \beta_7) - k_2 k_1)\beta_1(\beta_4 k_2 r - k_4)(\beta_3 k_2 r - k_3),$$

$$k_1 = \beta_5 + \mu, \quad k_2 = \beta_2 + \beta_7 + \beta_8 + \beta_6 + \mu, \quad k_3 = \beta_9 + \beta_{10} + \mu,$$

$$k_4 = \beta_{11} + \mu, \quad k_5 = \beta_{12} + \mu,\ k_6 = \beta_{13} + \mu_d + \mu$$

Here, r is the highest root of the polynomial, given by $p(x) = b_0 + b_1 z + b_2 z^2 + b_3 z^3 = 0$ and its coefficients are: $b_0 = k_4(\mathrm{B}\beta_1 k_3 - k_1 k_3 \mu)$,

$$b_1 = -B\beta_1 k_2(\beta_3 k_4 - \beta_4 k_3) + \beta_3 k_4 \mu(k_2 k_1 - k_5\beta_6) + k_1 k_2 k_3(\beta_4\mu - \beta_1 k_4) - \beta_4\beta_5\mu(\beta_6\beta_9 + \beta_7 k_3) + \beta_1\beta_2\beta_5 k_3 k_4$$

$$b_2 = -\beta_1\beta_3\beta_5 k_2 k_4(\beta_2 + \beta_6) + \beta_1 k_1 k_2^2(\beta_1 \mathrm{k}_4 + \beta_4 \mathrm{k}_3) + \beta_4\beta_5\beta_6 k_2(\beta_3\mu - \beta_1\beta_9) - \beta_1\beta_4\beta_5 k_2 k_3(\beta_2 + \beta_7) + \beta_3\beta_4 k_2\mu(\beta_5\beta_7 - \mathrm{k}_1\mathrm{k}_2) + \mathrm{B}\beta_1\beta_3\beta_4 k_2^2 \text{ and}$$

$$b_3 = \beta_1\beta_3\beta_4 k_2^2(\beta_2 + \beta_5\beta_6) + \beta_1\beta_3\beta_4 k_2^2(\beta_5\beta_7 - k_1 k_2)$$

2.2 Basic reproduction number

To get threshold value of the COVID-19 transformation, basic reproduction number is formulated using next generation matrix algorithm (Diekmann et al., 1990; Driessche and Watmough, 2002). The basic reproduction number for of system (1) is obtained as the spectral radius of matrix $\left(FV^{-1}\right)$ at an endemic equilibrium point. F and V are obtain from Jacobian matrix of matrices f and v respectively,

$$f=\begin{bmatrix}\beta_1 ES\\ \beta_3 EA\\ \beta_4 ESy\\ 0\\ 0\\ 0\\ 0\\ 0\end{bmatrix} \text{ and } v=\begin{bmatrix}\beta_3 EA+\beta_4 ESy+\beta_5 E+\mu E\\ -\beta_6 Q+\beta_9 A+\beta_{10} A+\mu A\\ -\beta_7 Q-\beta_9 A+\beta_{11} Sy+\mu Sy\\ -B+\beta_1 ES-\beta_2 Q+\mu S\\ -\beta_5 E+\beta_2 Q+\beta_7 Q+\beta_8 Q+\beta_6 Q+\mu Q\\ -\beta_{10} A-\beta_{11} Sy-\beta_8 Q+\beta_{12} I+\mu I\\ -\beta_{12} I+\beta_{13} H+\mu_d H+\mu H\\ -\beta_{13} H+\mu R\end{bmatrix}$$

$$FV^{-1}=\begin{bmatrix}a_1 & a_2 & a_3 & a_4 & a_5 & 0 & 0 & 0\\ a_6 & a_7 & a_8 & a_9 & a_{10} & 0 & 0 & 0\\ a_{11} & a_{12} & a_{13} & a_{14} & a_{15} & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\end{bmatrix}$$

The formulated basic reproduction numberis:

$$R_0=\frac{m^{\frac{1}{3}}}{6}-\frac{2}{m^{\frac{1}{3}}}\left(\frac{1}{3}a_1(a_{13}+a_7)-a_{11}a_3-a_{12}a_8+\frac{1}{3}a_{13}a_7-a_6a_2-\frac{1}{3}\left(a_1^2+a_{13}^2+a_7^2\right)\right)+\frac{1}{3}(a_{13}+a_7+a_1) \tag{3}$$

$$\begin{aligned} m={}&12(a_{13}+a_7)(3a_{12}a_8-a_{13}a_7)-12(a_1+a_{13})(3a_{11}a_3-a_1a_{13})\\ &+12(a_1+a_7)(3a_2a_6-a_1a_7)+108a_{12}(a_3a_6+a_{11}a_8)+8(a_{13}^3+a_7^3)\\ &+a_1^3-72a_{11}(a_3a_7+a_{12}a_8)-72a_{13}a_2a_6+48a_1a_{13}a_7\\ &+12\Big((a_7-a_{13})\big(3a_1^4(a_{13}-a_7)-6a_1^3(a_{11}a_3-a_2a_6+a_7^2)+6\mathrm{a}_1 a_{13}a_7(a_{13}^2+a_7^2)\\ &+30a_1a_{13}a_2a_6a_7\big)+(a_{13}+a_7)\big(6a_1^2a_{12}(4a_8+a_3a_6)-18a_{11}a_2a_8(a_1^2-3a_{12}a_8)\\ &+54a_{12}^2a_3a_6a_8\big)+(a_{13}-6a_7)a_1^3a_{13}^2-6a_1^2a_{11}a_3(a_7^2+a_2a_6)\\ &+30\,\mathrm{a}_1^2\,a_{13}a_7(a_1a_{11}a_3-a_1a_2a_6)+12a_1^3a_8(a_{11}a_2-a_1a_{12})\\ &+30a_1a_{11}a_{13}a_3(a_{13}a_7+a_{11}a_3)-3a_1^2a_{11}a_3(a_{11}a_3+8a_{13})-6a_1^2a_{12}a_8(a_{13}^2+a_2a_6)\\ &-6(a_{13}a_7+a_2a_6)(a_1^2(a_{13}^2+a_{12}a_8)+a_{11}a_{13}a_2a_8)+12a_1^2a_{12}a_3(a_1a_6-5a_{11}a_8)\\ &-3a_1^2a_7^3(a_7+2a_{13})-3a_1^2a_2a_6(a_2a_6-8a_7^2)+2a_1a_{11}^2a_3(27a_2a_8-17a_3a_7)\\ &+6a_1a_{11}a_{12}a_8(a_{13}a_3-18a_2a_8)+2a_1a_{11}a_{12}a_3(27a_3a_6+57a_7a_8)\\ &+6a_1a_{11}a_{13}^2(a_{13}a_3-a_2a_8)+6a_1a_{11}a_{13}a_2(a_3a_6+12a_7a_8)\end{aligned}$$

$$
\begin{aligned}
&-6a_1a_{11}a_3a_7(a_{13}a_7-a_2a_6)+6a_1\,\mathrm{a}_8(a_2a_6-a_7^2)(3a_{11}a_2+a_{12}a_7)\\
&+24a_1a_{12}^2a_8^2(a_1-a_7)-6a_1a_{12}a_{13}(a_{13}a_8+3a_{13}a_3a_6)-a_1a_{12}^2a_{13}a_8(a_8+108a_6)\\
&+30a_{12}a_{13}a_7a_8(a_{13}+a_1a_7)+a_1a_{12}a_{13}a_6(a_2a_8+72a_3a_7)\\
&+18a_1a_{12}a_3a_6(3a_2a_6-a_7^2)+24a_1a_{13}a_2a_6(a_{13}-a_2a_6)\\
&+6a_1a_2a_6a_7(a_7^2-5a_2a_6)-12a_{11}^2a_3^2(a_{11}a_3+3a_{12}a_8)-3a_{11}^2a_{13}a_3^2(a_{13}+8a_7)\\
&+12a_{11}^2a_3^2(2a_7^2-3a_2a_6)-6a_{11}a_{13}^3(a_3a_7-2a_2a_8)-6a_{12}a_2a_6a_8(a_7^2+6a_2a_6)\\
&+27a_{11}^2a_2a_8(2a_{13}a_3+3a_2a_8)+9a_{11}a_2a_3a_8(a_{12}a_6-12a_{11}a_7)\\
&-6a_{11}a_{12}a_3a_8(a_{12}^2+6a_{12}a_8)+3(18a_{11}a_{12}a_3^2a_6+a_{13}^2a_7^2+4a_{13}^3a_2a_6)(a_{13}-2a_7)\\
&+6a_{11}a_{12}a_7a_8a_3(a_{13}-10a_7)-3a_{12}^2a_8^2(a_{13}^2+a_7^2)+6a_{12}a_{13}a_7^2(a_7a_8-a_3a_6a_7)\\
&+6a_{12}a_2a_6a_8(a_{13}a_7-6a_{12}a_8)-6a_{11}a_{13}^2a_3(a_7^2+10a_2a_6)\\
&+6a_{11}a_{13}a_3a_7(4a_7^2+19a_2a_6)-18a_{11}a_{13}a_2a_8(a_7^2+5a_2a_6)\\
&-12a_{11}a_2a_3a_6(3a_2a_6+5a_7^2)+6a_{11}a_2a_7a_8(a_7+9a_2a_6)+12a_{11}a_7^3(a_2a_8-a_7a_3)\\
&-3a_{12}^2a_3^2(4a_{12}a_3-27a_6^2)+6a_{12}a_{13}a_7a_8(a_{13}+5a_{12}a_8)-12a_{12}a_{13}^2a_8(2a_7^2+5a_2a_6)\\
&+12a_{13}a_{12}a_3a_6(a_{13}-9a_2a_6)+6a_{12}a_3a_6a_7(2a_7^2+9a_2a_6)-6a_{13}^2a_2a_6(a_7^2-4a_2a_6)\\
&-3a_2\,\mathrm{a}_6(a_7^2+4a_2a_6)(2a_{13}a_7+a_2a_6)-3a_7^3(a_7a_{13}^2-8a_1a_{11}a_3)\\
&+6a_{12}a_{13}a_7^2(a_7a_8-a_3a_6a_7)
\end{aligned}
$$

The value of the basic reproduction number (R_0) also called the threshold value, depends on the incubation period of the infection, the possibility of infecting exposed individual during one contact and the number of new susceptible individuals communicated per unit of time and environmental factors that govern pathogen transmission. Hence, magnitude of R_0 varies by places and communities. Using current real value data the estimated value of R_0 for three different countries, USA, India and Japan is 6.9026, 5.7880 and 4.7983 respectively.

3 Numerical simulation

This section attempts to describe the model with graphical representation.

Figure 2 (a), (b) and (c) represents the variation in each compartment with time for three different set of parametric values taken from current COVID-19 outbreak in USA, India and Japan respectively. It is found that the population in the class of exposed individual is highest in India which represents very serious scenario of high infected case in upcoming days in India. While in USA exposed individuals are converted into infected cases hence in in Figure 2(a) the population in exposed class is minimum and the population in infected class shows at maximum level. It can be observed that, in India, the population in quarantine class is significant which indicates that Indian government is getting public support to fight against this outbreak. Observing the asymptomatic as well as the symptomatic infected cases from all three figures, we can assume that the current pandemic outbreak is at peak level in USA, while the outbreak is at progressing stage in India and progression in recovered class suggests that the outbreak is controlled up to certain level in Japan. Figure 2(a) and 2(b) shows that in USA and India, the hospitalisation cases are increases exponentially during first week of the outbreak, while in Figure 2(c) we can observe that in Japan it starts to decrease after 4–5 days.

Figure 2 Variation in all the compartments with time (see online version for colours)

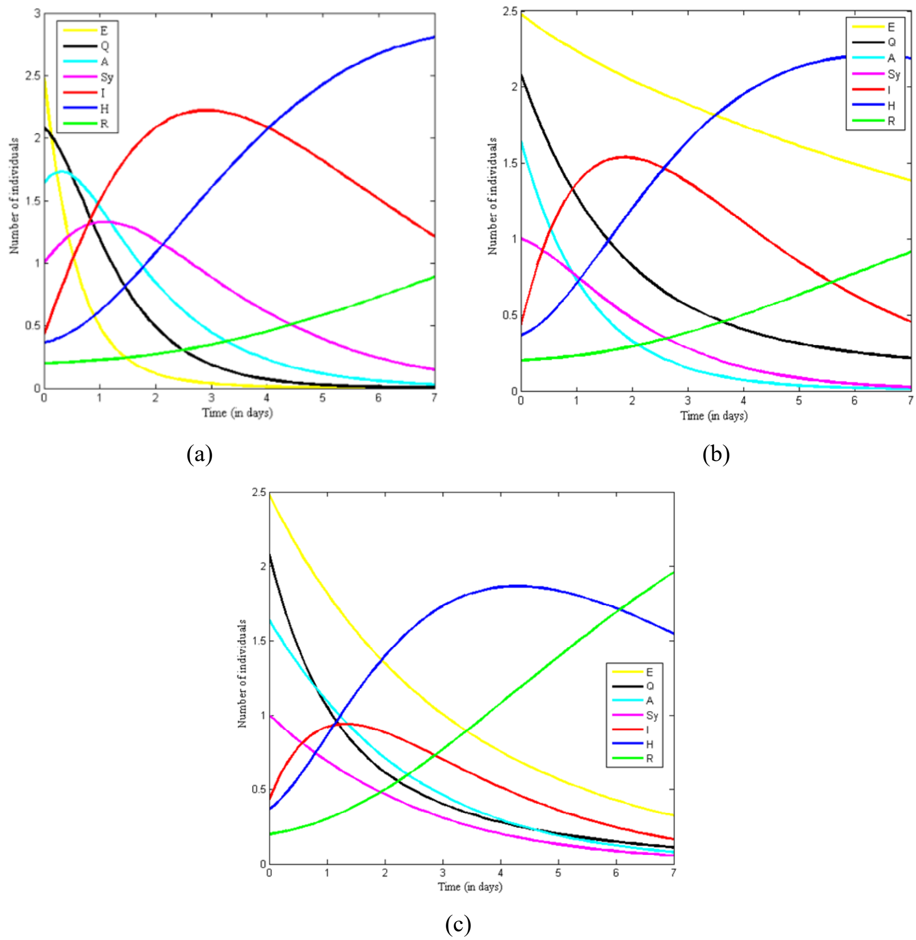


Figure 3 Intensity of virus transmission under asymptomatic and symptomatic infected class in USA (see online version for colours)

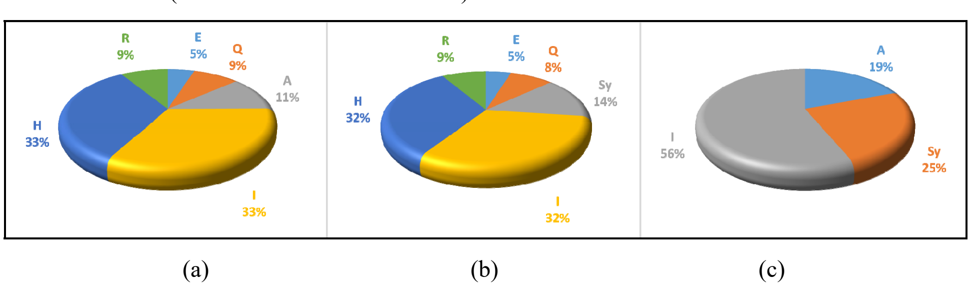
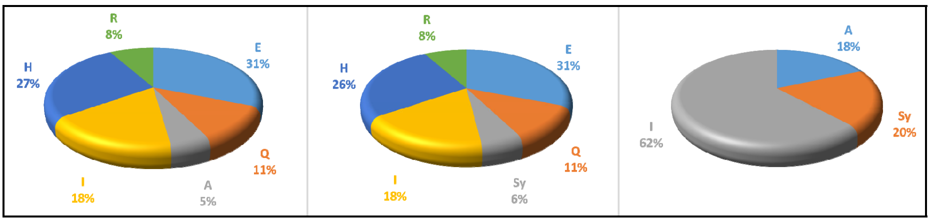


Figure 3(a-b) shows intensity of asymptomatic and symptomatic transmission of COVID-19 individually in highly infected country, USA. It is observed that 11% asymptomatic and 14% symptomatic result into 33% and 32% infected respectively. Out of the infected individuals 33% and 32% needs hospitalisation. The recovered rate is same for both the categories; i.e., 9%. Figure 3(c) depicts that 19% asymptomatic and 25% symptomatic results 56% infected in USA.

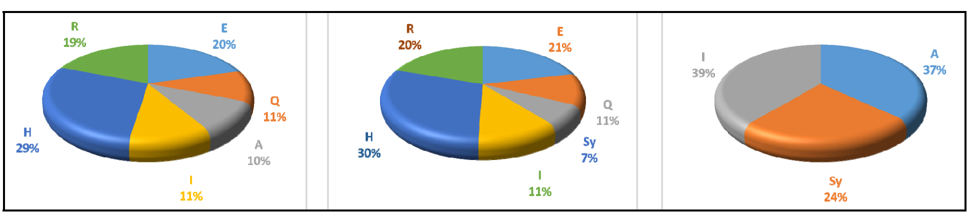
Figure 4 Intensity of virus transmission under asymptomatic and symptomatic infected class in India (see online version for colours)



(a) (b) (c)

Figure 4(a–b) shows intensity of asymptomatic and symptomatic transmission of COVID-19 individually in Japan. It is observed that 5% asymptomatic and 6% symptomatic result into 18% infected. Out of the infected individuals 27% and 26% needs hospitalisation. The recovered rate is same for both the categories; i.e., 8%. Figure 4(c) depicts that 18% asymptomatic and 20% symptomatic results 62% infected in USA. This suggests that Japan government imposed preventive steps at earliest.

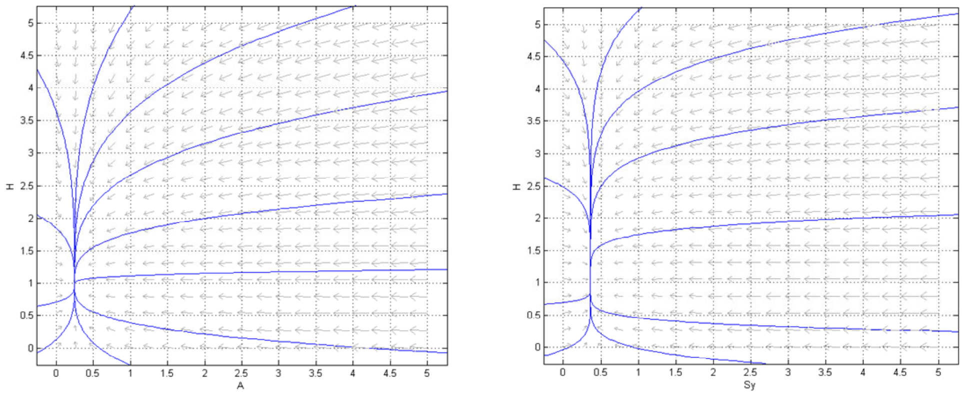
Figure 5 Intensity of virus transmission under asymptomatic and symptomatic infected class in Japan (see online version for colours)



(a) (b) (c)

Figure 5(a–b) shows intensity of asymptomatic and symptomatic transmission of COVID-19 individually in India. It is observed that 10% asymptomatic and 9% symptomatic result into 11% infected. The early steps of lockdown have restricted transmission of COVID-19. Out of the infected individuals 29% and 30% needs hospitalisation. The recovered rate is almost same for both the categories, i.e., 19% and 20% respectively. Figure 5(c) depicts that 37% asymptomatic and 24% symptomatic results 39% infected in India. The government can restrict infected to travel because of social distancing and lockdown of air traffic, road and rail traffics.

Figure 6 Intensity of hospitalisation w.r.t asymptomatic and symptomatic individuals (see online version for colours)



(a) (b)

Figure 6(a) and 6(b) shows the intensity in hospitalisation class under the influence of asymptomatically and symptomatically infected individuals respectively. It can be observed from the figure that the intensity of symptomatic individuals is more and long-term compared to that of the asymptomatic individuals. Moreover Figure 6(a) suggests that recovery rate of the asymptomatic individuals is quite higher than symptomatic individuals.

Figure 7 Intensity of hospitalisation of infected individuals by COVID-19 (see online version for colours)

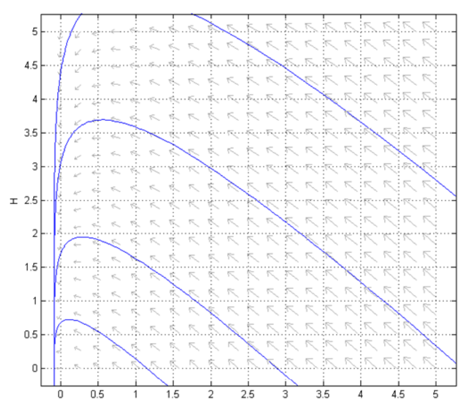
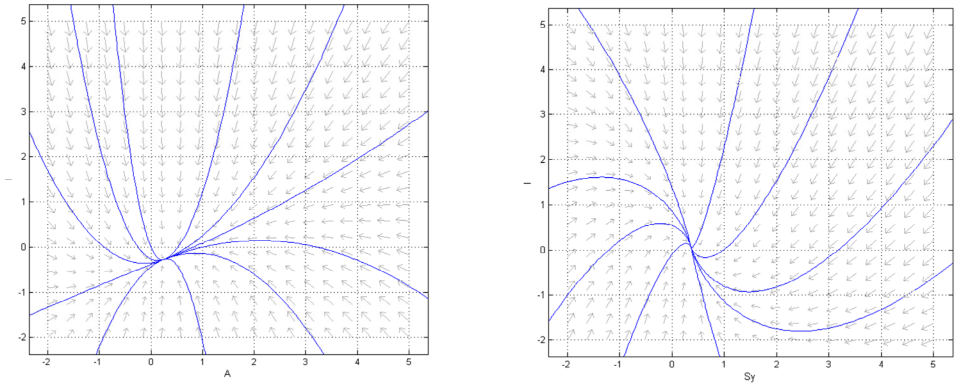


Figure 7 shows that progressively more infected people go towards hospitalisation, but after some point of time it gets stable and hospitalisation cases decrease up to certain level.

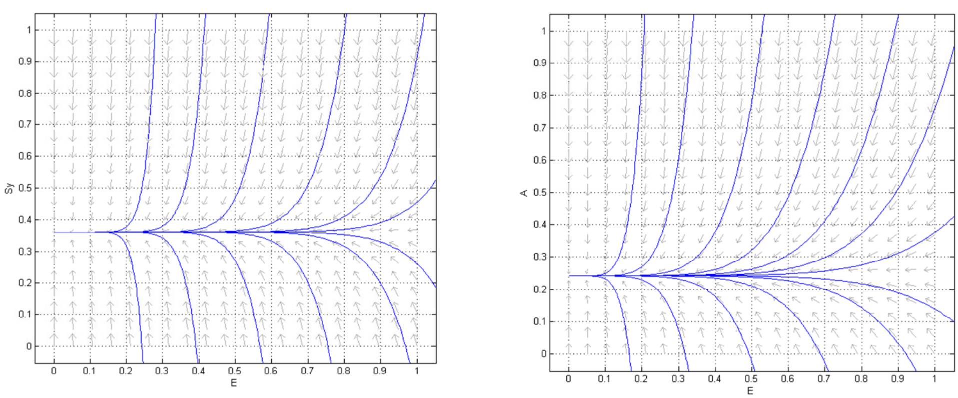
Figure 8 Intensity of asymptomatic and symptomatic individuals in class of infected individuals (see online version for colours)



(a) (b)

Figure 8(a) and 8(b) shows the intensity of asymptomatic and symptomatic individuals in the class of infected individuals by COVID-19 respectively. Comparison of these two figures suggests that intensity of symptomatically infected individuals is more in infected class compared to asymptomatic individuals. From a close observation of directional dynamics, we can say that the infected individuals moves to symptomatic stage with time, or we can say that the asymptomatic individuals become symptomatic over time.

Figure 9 Effect of symptomatic and asymptomatic individuals on exposed class (see online version for colours)



(a) (b)

Figure 9(a) and 9(b) shows the effect of symptomatically and asymptomatically infected individuals on class of exposed individuals respectively. It can be observed from the figures that compare to the asymptomatic individuals, the exposed individuals get infected by COVID-19 at higher intensity by the symptomatically infected individuals.

Figure 10 Variations in susceptible and exposed class (see online version for colours)

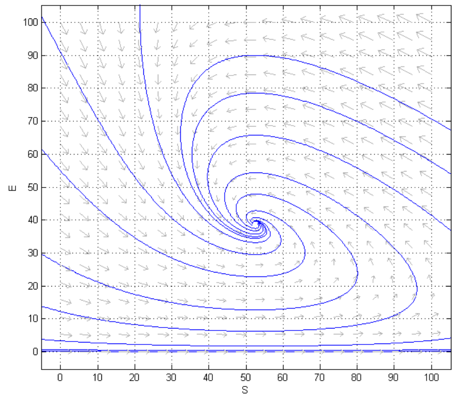
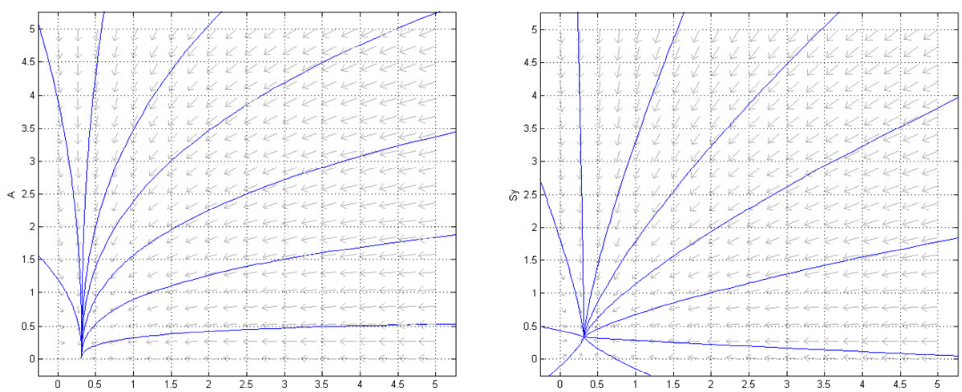


Figure 10 shows that the susceptible individuals quickly get exposed as well as the exposed individuals are become susceptible after some time.

Figure 11 Intensity of asymptomatic and symptomatic individuals in quarantine class (see online version for colours)

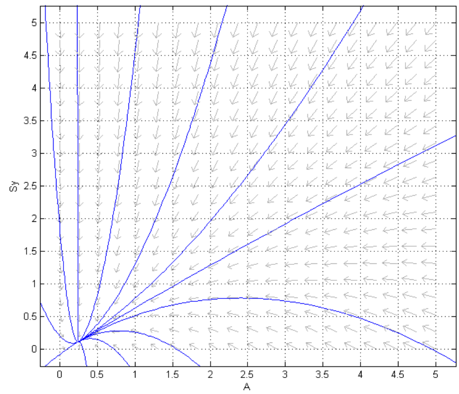


(a) (b)

Comparison of Figures 11(a) and 11(b) suggests that, as the symptomatically infected individuals are more contagious than the asymptomatic individuals and they should be quarantined as soon as possible.

Figure 12 shows that most of the asymptomatic individuals become symptomatic after incubation period of COVID-19.

Figure 12 Transmission between asymptomatic and symptomatic class (see online version for colours)



4 Conclusions

A compartmental model is constructed to study the contagiousness or transmissibility of COVID-19 through two possible human to human transmission ways: symptomatic and asymptomatic. To analyse the re-emerging infectious agents during three different stages of the COVID-19 outbreak, the threshold value of the model is estimated using parametric values taken from three countries with different situations (stage) of the running outbreak:

1 outbreak is at initial stage

2 outbreak is at peak stage

3 outbreak is at partially controlled stage.

From the comparison of these three values of basic reproduction number one can predict the possible upcoming situation and different strategies can be developed to prevent the epidemic of COVID-19. Numerical simulation of the model imitates the risk factor of pre-symptomatic transmission of the virus. The study recommends that it is very crucial to save susceptible as well as exposed individuals from pre-symptomatic transmission to control the epidemic of COVID-19.

Data availability

The data used to support the findings of this study are included within the article.

Acknowledgements

Authors thank reviewers for their positive reviews. Second author (AHS) is funded by a Junior Research Fellowship from the Council of Scientific and Industrial Research (file no.-09/070(0061)/2019-EMR-I) and all the authors are thankful to DST-FIST file # MSI-097 for technical support to the Department of Mathematics, Gujarat University.

Conflict of interest: the authors do not have conflict of interest.

References

Chen, T., Rui, J., Wang, Q., Zhao, Z., Cui, J.A. and Yin, L. (2020a) *A Mathematical Model for Simulating the Transmission of Wuhan Novel Coronavirus*, Vol. 9, No. 24, https://doi.org/10.1186/s40249-020-00640-3.

Chen, Y., Cheng, J., Jiang, Y. and Liu, K. (2020b) 'A time delay dynamic system with external source for the local outbreak of 2019-nCoV', *Applicable Analysis*, pp.1–12, DOI: 10.1080/00036811.2020.1732357.

Diekmann, O., Heesterbeek, J.A.P. and Metz, J.A. (1990) 'On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations', *Journal of Mathematical Biology*, Vol. 28, No. 4, pp.365–382.

Driessche, P. and Watmough, J. (2002) 'Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission', *Mathematical Biosciences*, Vol. 180, No. 1, pp.29–48.

Fernandes, N. (2020) *Economic Effects of Coronavirus Outbreak (COVID-19) on the World Economy*, SSRN: 3557504.

Harries, A., Martinez, L. and Chakaya, J. (2020) 'Monitoring the COVID-19 pandemic in sub-Saharan Africa: focusing on health facility admissions and deaths', *Int. J. Tuberc. Lung Dis*., Vol. 24, No. 5, pp.550–552.

Hatipoğlu, N. (2020) 'The 'new' problem of humanity: new Coronavirus (2019-nCoV/COVID-19) disease', *Medical Journal of Bakirkoy*, Vol. 16, No. 1, pp.1–8.

Huang, C., Wang, Y., Li, X., Ren, L., Zhao, J., Hu, Y., Zhang, L., Fan, G., Xu, J., Gu, X. and Cheng, Z. (2020) 'Clinical features of patients infected with 2019 Novel Coronavirus in Wuhan, China', *The Lancet*, Vol. 395, No. 10223, pp.497–506.

Jin, Y.H., Cai, L., Cheng, Z.S., Cheng, H., Deng, T., Fan, Y.P., Fang, C., Huang, D., Huang, L.Q., Huang, Q. and Han, Y. (2020) 'A rapid advice guideline for the diagnosis and treatment of 2019 novel coronavirus (2019-nCoV) infected pneumonia (standard version)', *Military Medical Research*, Vol. 7, No. 1, p.4.

Katul, G.G., Mrad, A., Bonetti, S., Manoli, G. and Parolari, A.J. (2020) 'Global convergence of COVID-19 basic reproduction number and estimation from early-time SIR dynamics', *Plos One*, Vol. 15, No. 9, e0239800.

Khan, M.A. and Atangana, A. (2020) 'Modelling the dynamics of novel coronavirus (2019-nCov) with fractional derivative', *Alexandria Engineering Journal*, Vol. 59, No. 4, pp.2379–2389.

Rothan, H.A. and Byrareddy, S.N. (2020) 'The epidemiology and pathogenesis of Coronavirus disease (COVID-19) outbreak', *Journal of Autoimmunity*, Vol. 109, Article no. 102433.

Shah, N.H., Suthar, A.H. and Jayswal, E.N. (2020) *Control Strategies to Curtail Transmission of COVID-19*, medRxiv, DOI: 10.1155/2020/2649514.

Sohrabi, C., Alsafi, Z., O'Neill, N., Khan, M., Kerwan, A., Al-Jabir, A., Iosifidis, C. and Agha, R. (2020) 'World Health Organization declares global emergency: a review of the 2019 Novel Coronavirus (COVID-19)', *International Journal of Surgery*, Vol. 76, pp.71–76.

Tahir, M.B. and Masood, A. (2020) *The COVID-19 Outbreak: Other Parallel Problems*, SSRN: 3572258.

Tang, B., Bragazzi, N.L., Li, Q., Tang, S., Xiao, Y. and Wu, J. (2020a) 'An updated estimation of the risk of transmission of the Novel Coronavirus (2019-nCov)', *Infectious Disease Modelling*, Vol. 5, pp.248–255.

Tang, B., Wang, X., Li, Q., Bragazzi, N.L., Tang, S., Xiao, Y. and Wu, J. (2020b) 'Estimation of the transmission risk of the 2019-nCoV and its implication for public health interventions', *Journal of Clinical Medicine*, Vol. 9, No. 2, p.462.

Yang, C. and Wang, J. (2020) 'A mathematical model for the Novel Coronavirus epidemic in Wuhan, China', *Mathematical Biosciences and Engineering*, Vol. 17, No. 3, pp.2708–2724.

Zhai, P., Ding, Y., Wu, X., Long, J., Zhong, Y. and Li, Y. (2020) 'The epidemiology, diagnosis and treatment of COVID-19', *International Journal of Antimicrobial Agents*, Vol. 55, No. 5, Article no. 105955.

Zhao, Z., Zhu, Y.Z., Xu, J.W., Hu, Q.Q., Lei, Z., Rui, J., Liu, X., Wang, Y., Luo, L., Yu, S.S. and Li, J. (2020) *A Mathematical Model for Estimating the Age-Specific Transmissibility of a Novel Coronavirus*, medRxiv, https://doi.org/10.1101/2020.03.05.20031849.

Zhong, L., Mu, L., Li, J., Wang, J., Yin, Z. and Liu, D. (2020) 'Early prediction of the 2019 Novel Coronavirus outbreak in the mainland China based on simple mathematical model', *IEEE Access*, Vol. 8, pp.51761–51769.

Zhou, X., Ma, X., Hong, N., Su, L., Ma, Y., He, J., Jiang, H., Liu, C., Shan, G., Zhu, W. and Zhang, S. (2020) *Forecasting the Worldwide Spread of COVID-19 based on Logistic Model and SEIR Model,* medRxiv, https://doi.org/10.1101/2020.03.26.20044289.