

Table 1: List of variables for the SEIR model

t	Time (days)
N	Total population
S(t)	number of susceptible individuals on day t
E(t)	number of individuals exposed to the disease but are not infectious on day t
I(t)	number of infectious individuals on day t
R(t)	number of individuals who have recovered and are now immune to the disease on day t
s(t)	fraction of susceptible individuals on day t (S(t)/N)
e(t)	Fraction of exposed individuals on day t (E(t)/N)
i(t)	Fraction of infectious individuals on day t (I(t)/N)
r(t)	fraction of recovered individuals on day t (R(t)/N)

Table 2: List of parameters in the SEIR model

d	Number of days it takes to recover from the disease
γ	Recovery rate
x	Number of contacts an infected has per day
y	Fraction of contacts that result in infection
β	Disease transmission rate or rate at which one infectious individual transmits the disease to others per day. It is the products of the number of contacts an infected has per day and the fraction of contacts that result in infection
z	Incubation period
δ	Rate at which exposed individuals become infectious

Equations of Rate of Change

Change in ratio of susceptible individuals over time

$$\beta = xy$$

$$ds/dt = -\beta s(t)i(t)$$

Change in ratio of recovered individuals over time

$$\gamma = 1/d$$

$$dr/dt = \gamma i(t)$$

Change in ratio of exposed individuals over time

$$\delta = 1/z$$

$$de/dt = \beta s(t)i(t) - \delta e(t)$$

Change in ratio of infectious individuals over time

$$di/dt = \delta e(t) - \gamma i(t)$$

Reproductive Number

$$R_0 = \beta/\gamma$$

To account for the differences in the spread of the disease in different regions, the heterogenous host population can be divided into smaller homogenous groups using the mrSEIR model so that more meaningful comparisons can be made.

Defining vectors for each variable (ratio of susceptible, exposed, infectious and recovered) for each region (n):

$$\begin{aligned} \vec{s} &= \begin{bmatrix} s1 \\ \vdots \\ sn \end{bmatrix} & \vec{e} &= \begin{bmatrix} e1 \\ \vdots \\ en \end{bmatrix} & \vec{i} &= \begin{bmatrix} i1 \\ \vdots \\ in \end{bmatrix} & \vec{r} &= \begin{bmatrix} r1 \\ \vdots \\ rn \end{bmatrix} \\ \vec{\beta} &= \begin{bmatrix} \beta1 & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & \beta n \end{bmatrix} \end{aligned}$$

The parameters δ and γ will remain constant as they are pathogen specific. However, a vector is defined for β as it will vary from region to region based on the number of contacts infectious individuals are having in that region. Also β is calculated from R_0 which can vary from region to region.

It should be noted that the Hadamard Product (\odot) is used to allow for element-wise multiplication of the two vectors. Specifically, two vectors of the same dimensions are multiplied to produce another vector of the same dimension. This simplifies the calculation process and allows all the data to be generated simultaneously.

The vectors are substituted into the original 4 differential equations as follows to calculate the change in ratio of susceptible, exposed, infectious and recovered individuals in n regions.

$$\vec{\dot{s}} = -\vec{\beta}(\vec{s} \odot \vec{i})$$

$$\vec{\dot{e}} = \vec{\beta}(\vec{s} \odot \vec{i}) - \delta \vec{e}$$

$$\vec{\dot{i}} = \delta \vec{e} - \gamma \vec{i}$$

$$\vec{\dot{r}} = \gamma \vec{i}$$

The dot on top of the variables denotes time differentials (ds/dt). To demonstrate the use of the Hadamard Product to solve the first differential equation with 3 regions (n=3):

$$\vec{\dot{s}} = - \vec{\beta} (\vec{s} \circ \vec{i})$$

$$\vec{\dot{s}} = - \begin{bmatrix} \beta_1 & 0 & 0 \\ 0 & \beta_2 & 0 \\ 0 & 0 & \beta_3 \end{bmatrix} \begin{bmatrix} s_1 \\ s_2 \\ s_3 \end{bmatrix} \circ \begin{bmatrix} i_1 \\ i_2 \\ i_3 \end{bmatrix}$$

$$\vec{\dot{s}} = - \begin{bmatrix} \beta_1 & 0 & 0 \\ 0 & \beta_2 & 0 \\ 0 & 0 & \beta_3 \end{bmatrix} \begin{bmatrix} s_1 i_1 \\ s_2 i_2 \\ s_3 i_3 \end{bmatrix} = \begin{bmatrix} -\beta_1 s_1 i_1 \\ -\beta_2 s_2 i_2 \\ -\beta_3 s_3 i_3 \end{bmatrix}$$

In this way, the mrSEIR model can be used simultaneously for multiple regions at the same time.

Table 3: Initial values of the variables and parameters for the mrSEIR model for 4 states in India

State	Population density (persons per km ²)	S(0) (in millions)	E(0)	I(0)	R(0)	Average R ₀
Bihar	1102	124	11	4	0	1.88
Uttar Pradesh	828	237	31	38	0	1.70
Haryana	573	29	5	31	0	1.62
Madhya Pradesh	236	85	24	15	0	1.56

The results of the mrSEIR model of COVID19 for the 4 states over a period of 300 days taking 25 March 2020, the first day of the lockdown, as day 0 are illustrated in Fig. 3 – 6. The ratio of infectious individuals for each state is plotted additionally in Figure 7 so that the rate of change of infectious individuals can be seen more clearly.



