

511 **5. Supplementary Appendix**

512 *Positivity and boundedness of the solution for the Model (2.2)*

513 This subsection is provided to prove the positivity and boundedness of solutions of  
514 the system (2.2) with initial conditions  $(S(0), L(0), E(0), A(0), I(0), C(0), R(0))^T \in \mathbb{R}_{+0}^7$ .

515 We first state the following lemma.

**Lemma 5.1.** *Suppose  $\Omega \subset \mathbb{R} \times \mathbb{C}^n$  is open,  $f_i \in C(\Omega, \mathbb{R}), i = 1, 2, 3, \dots, n$ . If  $f_i|_{x_i(t)=0, X_t \in \mathbb{C}_{+0}^n} \geq 0$ ,  $X_t = (x_{1t}, x_{2t}, \dots, x_{1n})^T, i = 1, 2, 3, \dots, n$ , then  $\mathbb{C}_{+0}^n \{ \phi = (\phi_1, \dots, \phi_n) : \phi \in \mathbb{C}([-\tau, 0], \mathbb{R}_{+0}^n) \}$  is the invariant domain of the following equations*

$$\frac{dx_i(t)}{dt} = f_i(t, X_t), t \geq \sigma, i = 1, 2, 3, \dots, n.$$

516 where  $\mathbb{R}_{+0}^n = \{(x_1, \dots, x_n) : x_i \geq 0, i = 1, \dots, n\}$  [39].

517 **Proposition 5.1.** *The system (2.2) is invariant in  $\mathbb{R}_{+0}^7$ .*

518 *Proof.* By re-writing the system (2.2) we have:

$$\frac{dX}{dt} = B(X(t)), X(0) = X_0 \geq 0 \tag{S-1}$$

$$B(X(t)) = (B_1(X), B_1(X), \dots, B_7(X))^T$$

We note that

$$\begin{aligned} \frac{dS}{dt}|_{S=0} &= \Pi_H + \omega L > 0, \quad \frac{dL}{dt}|_{L=0} = lS \geq 0, \quad \frac{dE}{dt}|_{E=0} = \frac{\beta_1 S(I + \rho A)}{N - C} \geq 0, \\ \frac{dA}{dt}|_{A=0} &= (1 - \kappa)\sigma E \geq 0, \quad \frac{dI}{dt}|_{I=0} = \kappa\sigma E \geq 0, \quad \frac{dC}{dt}|_{C=0} = \tau I \geq 0, \\ \frac{dR}{dt}|_{R=0} &= \gamma_1 A + \gamma_2 I + \gamma_3 C \geq 0. \end{aligned}$$

519 Then it follows from the Lemma 5.1 that  $\mathbb{R}_{+0}^7$  is an invariant set for the COVID-19  
520 system (2.2) with lockdown. □

521 **Corollary 5.1.** *The system (2.1) is invariant in  $\mathbb{R}_{+0}^6$ .*

522 *Proof.* Proceeding as proposition 5.1, we can easily show that  $\mathbb{R}_{+0}^6$  is an invariant set for  
523 the COVID-19 system (2.1) without lockdown. □

524 **Lemma 5.2.** *The system (2.2) is bounded in the region*

525  $\Omega = \{(S, L, E, A, I, C, R) \in \mathbb{R}_{+0}^7 | S + L + E + A + I + C + R \leq \frac{\Pi_H}{\mu}\}$

*Proof.* We have from the system (2.2):

$$\begin{aligned} \frac{dN}{dt} &= \Pi_H - \mu N - \delta C \leq \Pi_H - \mu N \\ \implies \lim_{t \rightarrow \infty} \sup N(t) &\leq \frac{\Pi_H}{\mu} \end{aligned}$$

526 Hence the system (2.2) is bounded. □

527 **Corollary 5.2.** *The system (2.1) is bounded in the region*  
 528  $\Omega^* = \{(S, E, A, I, C, R) \in \mathbb{R}_{+0}^6 | S + E + A + I + C + R \leq \frac{\Pi_H}{\mu}\}$

529 *Proof.* proceeding same as lemma 5.2, we can easily show that the system (2.1) is bounded  
 530 in  $\Omega^*$ .  $\square$

531 *Local stability of disease-free equilibrium (DFE)*

The DFE of the model (2.2) is provided as follows:

$$\begin{aligned} \varepsilon_0 &= (S^0, L^0, E^0, A^0, I^0, C^0, R^0) \\ &= \left( \frac{\Pi_H(\mu + \omega)}{\mu(\mu + \omega + l)}, \frac{\Pi_H l}{\mu(\mu + \omega + l)}, 0, 0, 0, 0, 0 \right) \end{aligned}$$

The local stability of  $\varepsilon_0$  can be established for the COVID-19 system (2.2) by using the next generation operator method. Using the notation in [32], the matrices  $F$  for the new infection and  $V$  for the transition terms are given, respectively, by

$$F = \begin{pmatrix} 0 & \rho\beta_1 & \beta_1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \mu + \sigma & 0 & 0 & 0 \\ -(1 - \kappa)\sigma & \gamma_1 + \mu & 0 & 0 \\ -\kappa\sigma & 0 & \gamma_2 + \tau + \mu & 0 \\ 0 & 0 & -\tau & \delta + \gamma_3 + \mu \end{pmatrix}.$$

It follows that the basic reproduction number [40], denoted by  $R_0 = \Phi(FV^{-1})$ , where  $\Phi$  is the spectral radius, is given by

$$R_0 = \frac{\beta_1 \kappa \sigma}{(\mu + \sigma)(\gamma_2 + \tau + \mu)} + \frac{\rho \beta_1 (1 - \kappa) \sigma}{(\mu + \sigma)(\gamma_1 + \mu)}$$

532 Using Theorem 2 in [32], the following result is established.

533 **Lemma 5.3.** *The DFE,  $\varepsilon_0$ , of the model (2.2) is locally-asymptotically stable (LAS) if*  
 534  $R_0 < 1$ , *and unstable if  $R_0 > 1$ .*

535 The threshold quantity,  $R_0$  is the basic reproduction number of the disease [40; 41; 42].  
 536 This represent the average number of secondary cases generated by a infected person in  
 537 a fully susceptible population. The epidemiological significance of 5.3 is that when  $R_0$   
 538 is less than unity, a low influx of infected individuals into the population will not cause  
 539 major outbreaks, and the disease would die out in time.

540 *Global stability of DFE*

541 **Theorem 5.1.** *The DFE of the model (2.2) is globally asymptotically stable in  $\Omega$  when-*  
 542 *ever  $R_0 \leq 1$ .*

*Proof.* Consider the following Lyapunov function

$$\mathcal{L} = \left( \frac{\sigma(\kappa k_2 + \rho(1 - \kappa)k_3)}{k_1 k_2} \right) E + \left( \frac{\rho k_3}{k_2} \right) A + I$$

where  $k_1 = \mu + \sigma$ ,  $k_2 = \gamma_1 + \mu$  and  $k_3 = \gamma_2 + \tau + \mu$ .  
 We take the Lyapunov derivative with respect to  $t$ ,

$$\begin{aligned} \dot{\mathcal{L}} &= \left( \frac{\sigma(\kappa k_2 + \rho(1 - \kappa)k_3)}{k_1 k_2} \right) \dot{E} + \left( \frac{\rho k_3}{k_2} \right) \dot{A} + \dot{I} \\ &= \frac{\sigma(\kappa k_2 + \rho(1 - \kappa)k_3)}{k_1 k_2} \left[ \frac{\beta_1 S(I + \rho A)}{N - L - C} - k_1 E \right] + \frac{\rho k_3}{k_2} [(1 - \kappa)\sigma E - k_2 A] + (\kappa\sigma E - k_3 I) \\ &\leq \frac{\beta_1 \sigma(\kappa k_2 + \rho(1 - \kappa)k_3)}{k_1 k_2} (I + \rho A) - \frac{\sigma(\kappa k_2 + \rho(1 - \kappa)k_3)}{k_2} E + \frac{\rho(1 - \kappa)k_3 \sigma}{k_2} E \\ &\quad - \rho k_3 A + \kappa\sigma E - k_3 I \quad (\text{Since } S \leq N - L - C \text{ in } \Omega) \\ &= \frac{\beta_1 \sigma(\kappa k_2 + \rho(1 - \kappa)k_3)}{k_1 k_2} (I + \rho A) - \rho k_3 A - k_3 I \\ &= \frac{\beta_1 \sigma(\kappa k_2 + \rho(1 - \kappa)k_3)}{k_1 k_2 k_3} k_3 (I + \rho A) - \rho k_3 A - k_3 I \\ &\leq k_3 (R_0 - 1)(I + \rho A) \leq 0, \quad \text{whenever } R_0 \leq 1. \end{aligned}$$

543 Since all the variables and parameters of the model (2.2) are non-negative, it follows that  
 544  $\dot{\mathcal{L}} \leq 0$  for  $R_0 \leq 1$  with  $\dot{\mathcal{L}} = 0$  at diseases free equilibrium. Hence,  $\mathcal{L}$  is a Lyapunov  
 545 function on  $\Omega$ . Therefore, followed by LaSalle's Invariance Principle [43], that

$$(E(t), A(t), I(t)) \rightarrow (0, 0, 0) \text{ as } t \rightarrow \infty \quad (\text{S-2})$$

Since  $\lim_{t \rightarrow \infty} \sup I(t) = 0$  (from S-2), it follows that, for sufficiently small  $\epsilon > 0$ , there exist  
 constants  $B_1 > 0$  such that  $\lim_{t \rightarrow \infty} \sup I(t) \leq \epsilon$  for all  $t > B_1$ .

Hence, it follows from the sixth equation of the model (2.2) that, for  $t > B_1$ ,

$$\frac{dC}{dt} \leq \tau\epsilon - k_4 C$$

Therefore using comparison theorem [44]

$$C^\infty = \lim_{t \rightarrow \infty} \sup C(t) \leq \frac{\tau\epsilon}{k_4}$$

So as  $\epsilon \rightarrow 0$ ,  $C^\infty = \lim_{t \rightarrow \infty} \sup C(t) \leq 0$

Similarly by using  $\lim_{t \rightarrow \infty} \inf I(t) = 0$ , it can be shown that

$$C_\infty = \lim_{t \rightarrow \infty} \inf C(t) \geq 0$$

Thus, it follows from above two relations

$$C_\infty \geq 0 \geq C^\infty$$

Hence  $\lim_{t \rightarrow \infty} C(t) = 0$

Similarly, it can be shown that

$$\lim_{t \rightarrow \infty} R(t) = 0, \lim_{t \rightarrow \infty} S(t) = \frac{\Pi_H (\mu + \omega)}{\mu (\mu + \omega + l)}, \text{ and } \lim_{t \rightarrow \infty} L(t) = \frac{\Pi_H l}{\mu (\mu + \omega + l)}.$$

546 Therefore by combining all above equations, it follows that each solution of the model  
547 equations (2.2), with initial conditions  $\in \Omega$ , approaches  $\varepsilon_0$  as  $t \rightarrow \infty$  for  $R_0 \leq 1$ .  $\square$

#### 548 *Existence and stability of endemic equilibria*

In this section, the existence of the endemic equilibrium of the model (2.2) is established. Let us denote

$$M_1 = \frac{\mu + \omega}{\mu + \sigma}, M_2 = \frac{(1 - \kappa) \sigma (\mu + \omega)}{(\mu + \gamma_1) (\mu + \sigma)}, M_3 = \frac{\kappa \sigma (\mu + \omega)}{(\mu + \gamma_2 + \tau) (\mu + \sigma)},$$

$$M_4 = \frac{\kappa \tau \sigma (\mu + \omega)}{(\mu + \gamma_2 + \tau) (\mu + \gamma_3 + \delta) (\mu + \sigma)}.$$

Let  $\varepsilon^* = (S^*, E^*, A^*, I^*, C^*, R^*)$  represents any arbitrary endemic equilibrium point (EEP) of the model (2.2). Further, define

$$\lambda^* = \frac{\beta_1 (I^* + \rho A^*)}{N^* - L^* - C^*} \quad (\text{S-3})$$

It follows, by solving the equations in (2.2) at steady-state, that

$$S^* = \frac{(\mu + \omega) L^*}{l}, L^* = \frac{\Pi_H l}{\lambda^* (\mu + \omega) + \mu (\mu + \omega + l)}, E^* = \frac{M_1 L^* \lambda^*}{l}, \quad (\text{S-4})$$

$$A^* = \frac{M_2 L^* \lambda^*}{l}, I^* = \frac{M_3 L^* \lambda^*}{l}, C^* = \frac{M_4 L^* \lambda^*}{l}$$

$$R^* = \frac{(\gamma_1 M_2 + \gamma_2 M_3 + \gamma_3 M_4) L^* \lambda^*}{l \mu}$$

Substituting the expression in (S-4) into (S-3) shows that the non-zero equilibrium of the model (2.1) satisfy the following linear equation, in terms of  $\lambda^*$ :

$$A\lambda^* = B \tag{S-5}$$

where

$$\begin{aligned} A &= \mu M_1 + M_2(\mu + \gamma_1) + M_3(\mu + \gamma_2) + \gamma_3 M_4 \\ B &= \mu(\mu + \omega)(R_0 - 1) \end{aligned}$$

549 Since,  $M_1 > 0$ ,  $M_2 > 0$ ,  $M_3 > 0$ , and  $M_4 > 0 \implies A > 0$ , it is clear that the  
 550 model (2.2) has an unique endemic equilibrium point (EEP) whenever  $R_0 > 1$  and no  
 551 positive endemic equilibrium point whenever  $R_0 < 1$ . This rules out the possibility of  
 552 the existence of equilibrium other than DFE whenever  $R_0 < 1$ . Therefore, we have the  
 553 following result:

554 **Theorem 5.2.** *The model (2.2) has a unique endemic (positive) equilibrium, given by*  
 555  *$\varepsilon^*$ , whenever  $R_0 > 1$  and has no endemic equilibrium for  $R_0 \leq 1$ .*

556 Now we will prove the local stability of endemic equilibrium.

557 **Theorem 5.3.** *The endemic equilibrium  $\varepsilon^*$  of the COVID-19 system (2.2) with lockdown*  
 558 *is locally asymptotically stable if  $R_0 > 1$ .*

*Proof.* The Jacobian matrix of the system (2.2)  $J_{\varepsilon_0}$  at DFE is given by

$$J_{\varepsilon_0} = \begin{pmatrix} -(\mu + l) & \omega & 0 & -\rho\beta_1 & -\beta_1 & 0 & 0 \\ l & -(\mu + \omega) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\mu + \sigma) & \rho\beta_1 & \beta_1 & 0 & 0 \\ 0 & 0 & (1 - \kappa)\sigma & -(\mu + \gamma_1) & 0 & 0 & 0 \\ 0 & 0 & \kappa\sigma & 0 & -(\mu + \gamma_2 + \tau) & 0 & 0 \\ 0 & 0 & 0 & 0 & \tau & -(\mu + \gamma_3 + \delta) & 0 \\ 0 & 0 & 0 & \gamma_1 & \gamma_2 & \gamma_3 & -\mu \end{pmatrix},$$

559 Here, by taking  $\beta_1$  as a bifurcation parameter, we use the central manifold theory  
 560 method to determine the local stability of the endemic equilibrium [45]. Taking  $\beta_1$  as the  
 561 bifurcation parameter and gives critical value of  $\beta_1$  at  $R_0 = 1$  is given as

$$\beta_1^* = \frac{(\mu + \sigma)(\gamma_1 + \mu)(\gamma_2 + \tau + \mu)}{[\kappa\sigma(\gamma_1 + \mu) + (1 - \kappa)\rho\sigma(\gamma_2 + \tau + \mu)]}$$

The Jacobian of (2.2) at  $\beta = \beta_1^*$ , denoted by  $J_{\varepsilon_0}|_{\beta=\beta_1^*}$  has a right eigenvector (corresponding to the zero eigenvalue) given by  $w = (w_1, w_2, w_3, w_4, w_5, w_6, w_7)^T$ , where

$$\begin{aligned} w_1 &= -\frac{(\mu + \sigma)(\mu + \omega)}{\mu(\mu + \omega + l)}, w_2 = -\frac{(\mu + \sigma)l}{\mu(\mu + \omega + l)}, w_3 = 1, w_4 = \frac{(1 - \kappa)\sigma}{\mu + \gamma_1}, \\ w_5 &= \frac{\kappa\sigma}{\mu + \gamma_2 + \tau}, w_6 = \frac{\kappa\sigma\tau}{(\mu + \gamma_2 + \tau)(\mu + \gamma_3 + \delta)} \\ w_7 &= \frac{\gamma_1(1 - \kappa)\sigma}{\mu(\gamma_1 + \mu)} + \frac{\gamma_2\kappa\sigma}{\mu(\gamma_2 + \tau + \mu)} + \frac{\gamma_3\tau\kappa\sigma}{\mu(\gamma_2 + \tau + \mu)(\delta + \gamma_3 + \mu)} \end{aligned}$$

Similarly, from  $J_{\varepsilon_0}|_{\beta=\beta_1^*}$ , we obtain a left eigenvector  $v = (v_1, v_2, v_3, v_4, v_5, v_6, v_7)$  (corresponding to the zero eigenvalue), where

$$v_1 = 0, v_2 = 0, v_3 = 1, v_4 = \frac{\rho\beta_1^*}{\gamma_1 + \mu}, v_5 = \frac{\beta_1^*}{\gamma_2 + \tau + \mu}, v_6 = 0, v_7 = 0.$$

Selecting the notations  $S = x_1, L = x_2, E = x_3, A = x_4, I = x_5, C = x_6, R = x_7$  and  $\frac{dx_i}{dt} = f_i$ . Now we calculate the following second-order partial derivatives of  $f_i$  at the disease-free equilibrium  $\varepsilon_0$  and obtain

$$\begin{aligned} \frac{\partial^2 f_3}{\partial x_4 \partial x_3} &= -\frac{\rho\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)} = \frac{\partial^2 f_2}{\partial x_3 \partial x_4}, \\ \frac{\partial^2 f_3}{\partial x_5 \partial x_3} &= -\frac{\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)} = \frac{\partial^2 f_3}{\partial x_3 \partial x_5}, \\ \frac{\partial^2 f_3}{\partial x_4^2} &= -\frac{2\rho\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)}, \\ \frac{\partial^2 f_3}{\partial x_5^2} &= -\frac{2\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)}, \\ \frac{\partial^2 f_3}{\partial x_4 \partial x_5} &= -\frac{(1 + \rho)\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)} = \frac{\partial^2 f_3}{\partial x_5 \partial x_4}, \\ \frac{\partial^2 f_3}{\partial x_7 \partial x_4} &= -\frac{\rho\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)} = \frac{\partial^2 f_3}{\partial x_4 \partial x_7}, \\ \frac{\partial^2 f_3}{\partial x_7 \partial x_5} &= -\frac{\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)} = \frac{\partial^2 f_3}{\partial x_5 \partial x_7}. \end{aligned}$$

Now we calculate the coefficients  $a$  and  $b$  defined in Theorem 4.1 [45] of Castillo-Chavez and Song as follow

$$a = \sum_{k,i,j=1}^6 v_k w_i w_j \frac{\partial^2 f_k(0,0)}{\partial x_i \partial x_j}$$

and

$$b = \sum_{k,i=1}^6 v_k w_i \frac{\partial^2 f_k(0,0)}{\partial x_i \partial \beta}$$

Replacing the values of all the second-order derivatives measured at DFE and  $\beta_1 = \beta_1^*$ , we get

$$a = -2(w_3 + w_4 + w_5 + w_7) \left[ \frac{\rho\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)}w_4 + \frac{\beta_1^*\mu(\mu + \omega + l)}{\Pi_H(\mu + \omega)}w_5 \right] < 0$$

and

$$\begin{aligned} b &= \rho w_4 + w_5 \\ &= \frac{(1 - \kappa)\sigma\rho}{(\mu + \gamma_1)} + \frac{\kappa\sigma}{(\mu + \gamma_2 + \tau)} > 0. \end{aligned}$$

562 Since  $a < 0$  and  $b > 0$  at  $\beta = \beta_1^*$ , therefore using the Remark 1 of the Theorem 4.1 stated  
 563 in [45], a transcritical bifurcation occurs at  $R_0 = 1$  and the unique endemic equilibrium of  
 564 the COVID-19 system (2.2) with lockdown is locally asymptotically stable for  $R_0 > 1$ .  $\square$

## Figures

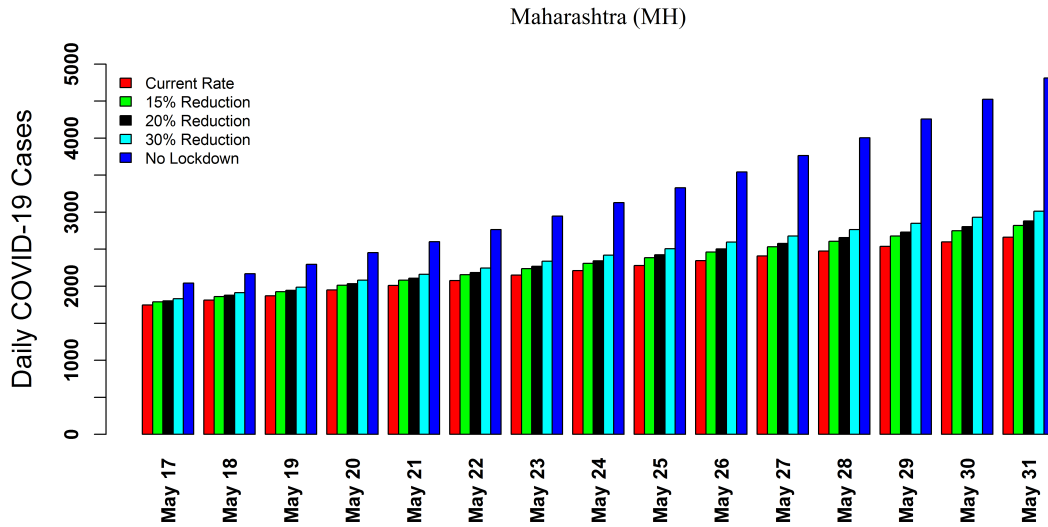


Figure S1: Ensemble model forecast for the daily notified COVID-19 cases in Maharashtra during May 17, 2020 till May 31, 2020, under five different social distancing measure. Various legends are **Current Rate**: daily notified case projection using the estimated value of the lockdown rate (see Table 4 main text), **15% Reduction**: daily notified case projection using 15% reduction in the estimated value of the lockdown rate (see Table 4 main text), **20% Reduction**: daily notified case projection using 20% reduction in the estimated value of the lockdown rate (see Table 4 main text), **30% Reduction**: daily notified case projection using 30% reduction in the estimated value of the lockdown rate (see Table 4 main text), and **No lockdown**: daily notified case projection based on no lockdown scenario, respectively.



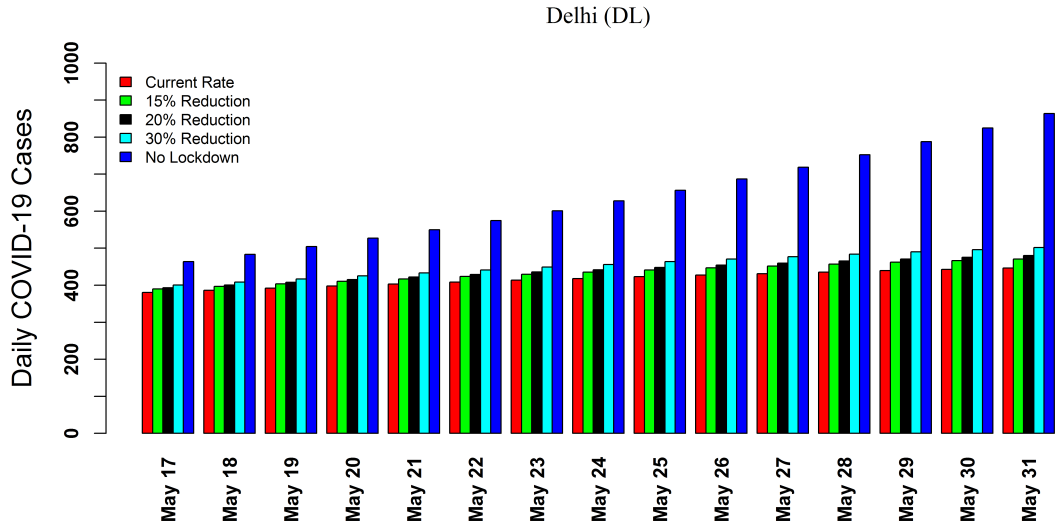


Figure S2: Ensemble model forecast for the daily notified COVID-19 cases in Delhi during May 17, 2020 till May 31, 2020, under five different social distancing measure. Various legends are same as Fig S1.

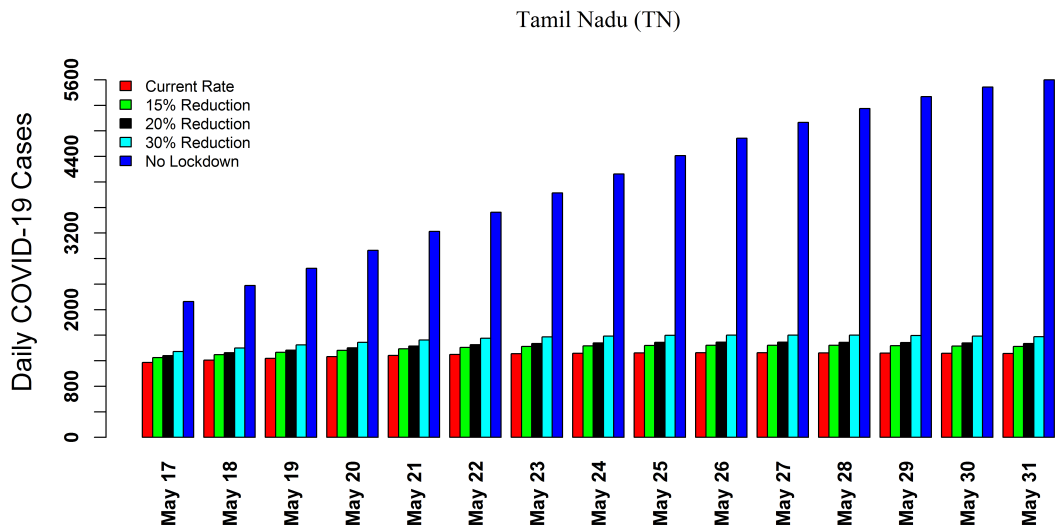


Figure S3: Ensemble model forecast for the daily notified COVID-19 cases in Tamil Nadu during May 17, 2020 till May 31, 2020, under five different social distancing measure. Various legends are same as Fig S1.

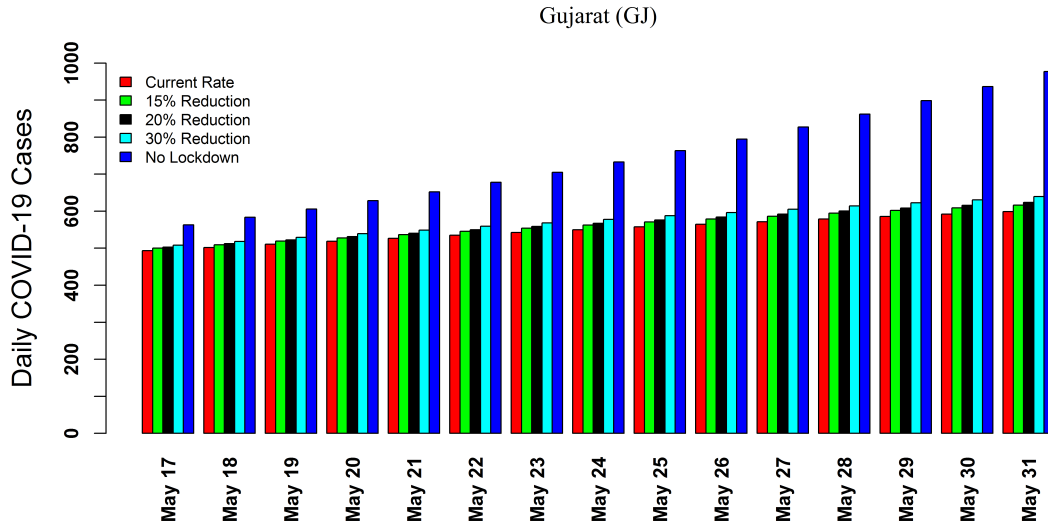


Figure S4: Ensemble model forecast for the daily notified COVID-19 cases in Gujarat during May 17, 2020 till May 31, 2020, under five different social distancing measure. Various legends are same as Fig S1.

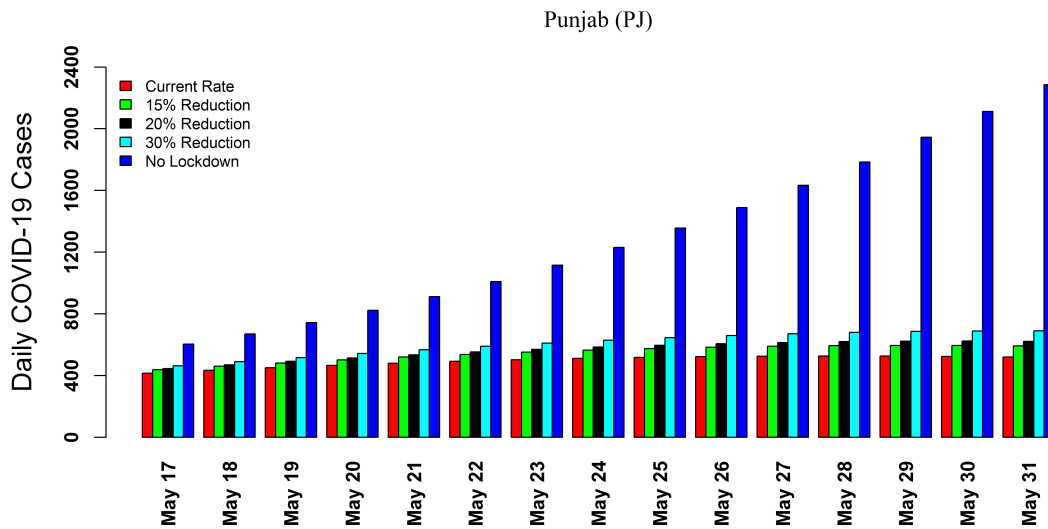


Figure S5: Ensemble model forecast for the daily notified COVID-19 cases in Punjab during May 17, 2020 till May 31, 2020, under five different social distancing measure. Various legends are same as Fig S1.

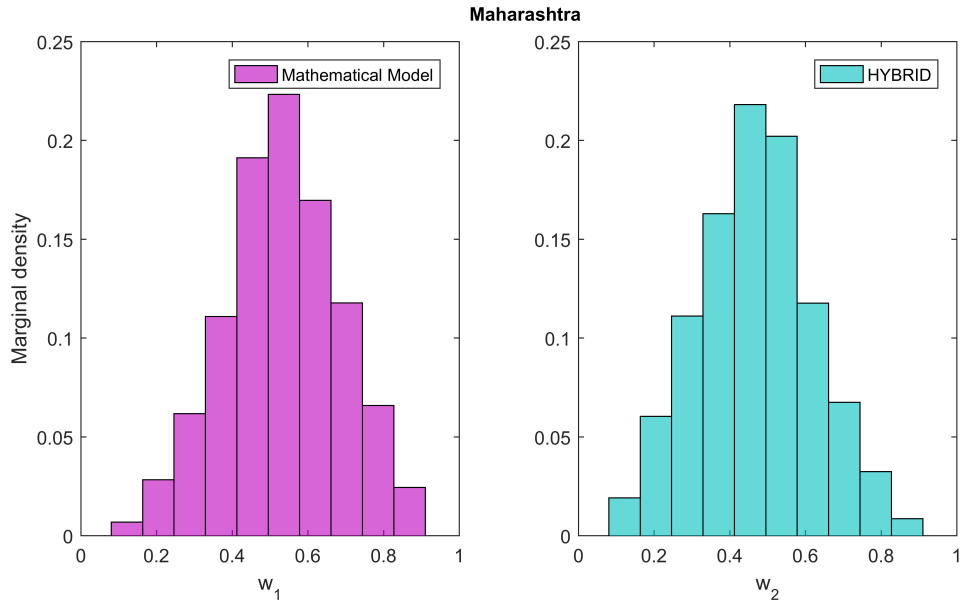


Figure S6: Posterior density of the weights for the mechanistic mathematical model (2.1 & 2.2) and the best statistical forecast model (HYBRID), respectively for Maharashtra.

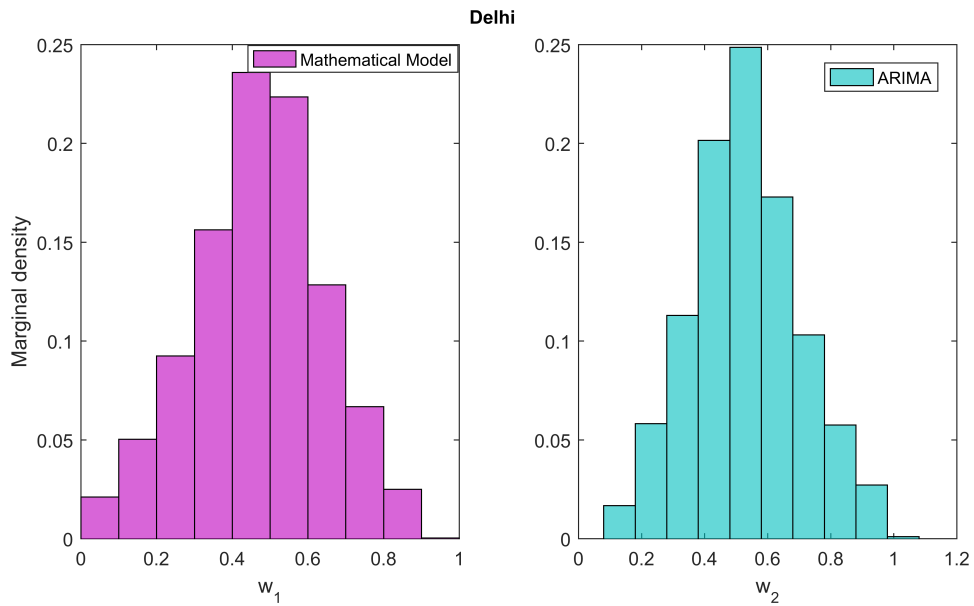


Figure S7: Posterior density of the weights for the mechanistic mathematical model (2.1 & 2.2) and the best statistical forecast model (ARIMA), respectively for Delhi

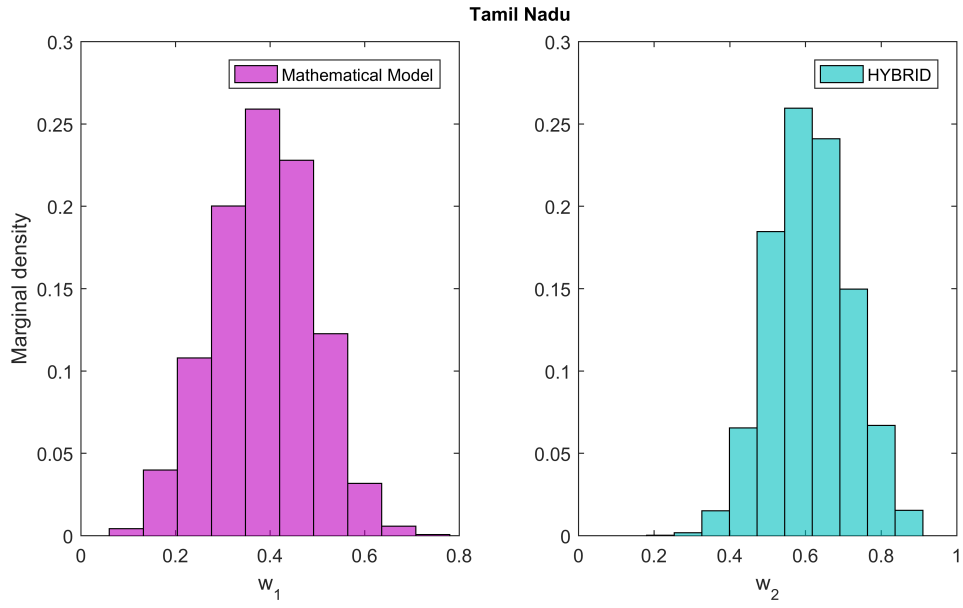


Figure S8: Posterior density of the weights for the mechanistic mathematical model (2.1 & 2.2) and the best statistical forecast model (HYBRID), respectively for Tamil Nadu.

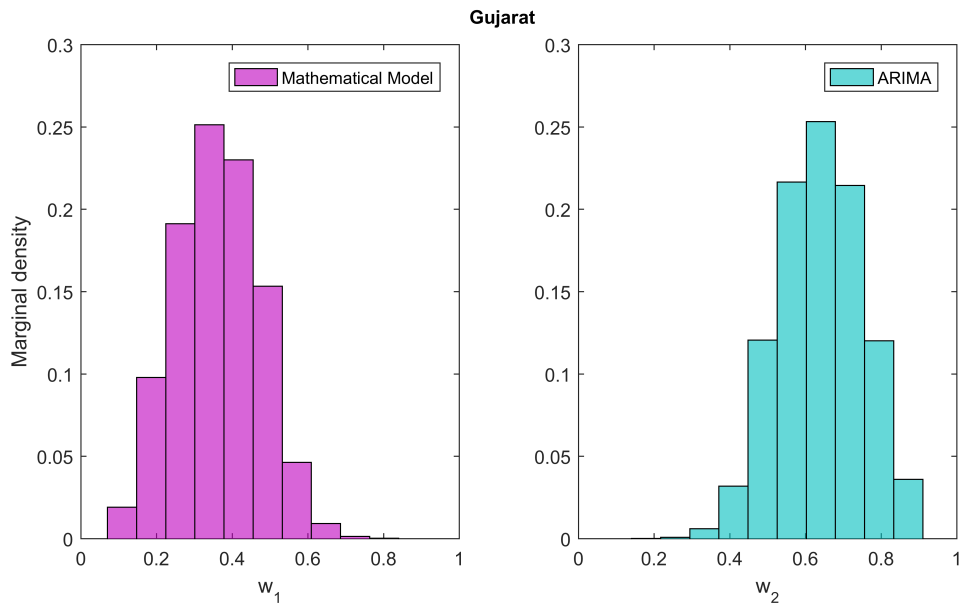


Figure S9: Posterior density of the weights for the mechanistic mathematical model (2.1 & 2.2) and the best statistical forecast model (ARIMA), respectively for Gujarat.

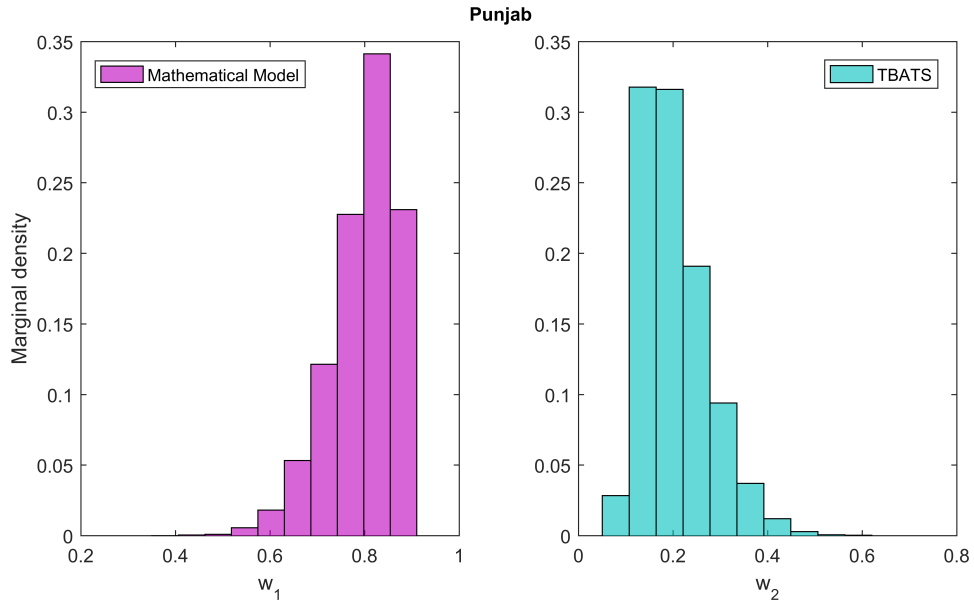


Figure S10: Posterior density of the weights for the mechanistic mathematical model (2.1 & 2.2) and the best statistical forecast model (TBATS), respectively for Punjab.

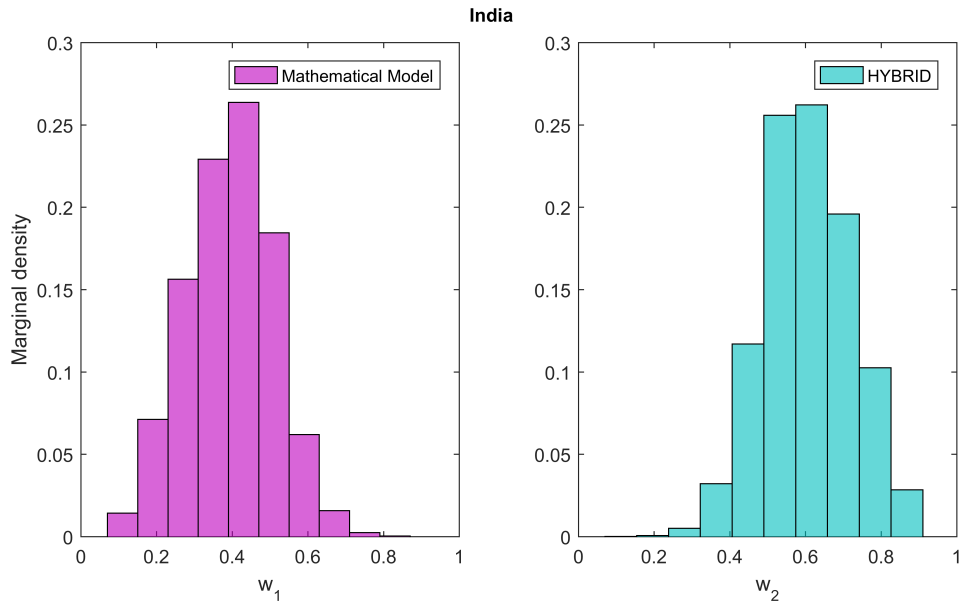


Figure S11: Posterior density of the weights for the mechanistic mathematical model (2.1 & 2.2) and the best statistical forecast model (HYBRID), respectively for India.

## Tables

Table S1: Estimated initial state variables of the mathematical model (2.1). All data are given in the format **Estimate (95% CI)**.

<b>Location</b>	<b><math>S(0)</math></b>	<b><math>E(0)</math></b>	<b><math>A(0)</math></b>	<b><math>I(0)</math></b>
<b>Maharashtra</b>	123243118 (114977907–124511349)	27.27 (0.51–35.06)	9531 (9483–9989)	24.76 (14.17–30.26)
<b>Delhi</b>	16070717 (10346593–19737264)	14.74 (0.05–14.97)	437 (92.38–4017)	282 (7.82–325)
<b>Tamil Nadu</b>	75367306 (70335585–79738740)	4.80 (0.05–4.73)	0.40 (0.03–2.52)	7.61 (1.96–10.88)
<b>Gujarat</b>	66848292 (60218205–69744037)	7630 (2622–9775)	26.10 (1.26–28.70)	14.01 (0.02–20.54)
<b>Punjab</b>	26433551 (26433543–26433556)	7.83 (0.20–13.81)	19.26 (0.29–29.54)	8 (1.08–15.96)
<b>India</b>	1226841787 (1219848614–1297276832)	221104 (21136–279521)	462997 (27541–642484)	36043 (3601–84059)

Table S2: Goodness of fit (RMSE) for the three statistical forecast model (ARIMA, TBATS and HYBRID), respectively. RMSE for different locations are calculated only for the test period data (May 4, 2020 till May 8, 2020). RMSE values of the best performed statistical forecast model in different locations are shown in red.

Location	ARIMA	TBATS	HYBRID
Maharashtra	179.84368	110.57237	<b>90.04999</b>
Delhi	<b>92.17782</b>	96.11452	94.14085
Tamil Nadu	182.5897	244.8254	<b>119.9740</b>
Gujarat	<b>28.16381</b>	37.36576	30.92572
Punjab	292.5078	<b>188.9780</b>	238.9491
India	457.7622	438.1160	<b>368.0725</b>

Table S3: Weight estimates for the mechanistic mathematical model (2.1 & 2.2) and the best statistical forecast model, respectively. Respective subscript are MH: Maharashtra, DL: Delhi, TN: Tamil Nadu, GJ: Gujarat, PJ: Punjab, and IND: India.  $w_1$  and  $w_2$  denote the weights of the COVID-19 mathematical model (2.1 & 2.2) and the best statistical forecast model, respectively for a region. All data are provided in the format **Estimate (95% CI)**.

Weights	MH	DL	TN	GJ	PJ	IND
$w_1$	0.48 (0.2243–0.8262)	0.5186 (0.1112–0.8004)	0.6158 (0.1801–0.5848)	0.2009 (0.1554–0.5737)	0.8331 (0.6291–0.8942)	0.3131 (0.1695–0.6149)
$w_2$	0.52 (0.1738–0.7757)	0.4814 (0.1996–0.8888)	0.3842 (0.4152–0.8199)	0.7991 (0.4263–0.8446)	0.1669 (0.1058–0.3709)	0.6869 (0.3851–0.8305)

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