



To

Laura Temime, Ph.D.
BMC Infectious Diseases
<https://bmcinfectdis.biomedcentral.com/>

Dear Dr. Temime,

We would like to thank the associate editor and the reviewers for their constructive feedback on our manuscript titled "*A comparison of five epidemiological models for transmission of SARS-CoV-2 in India*" (INFD-D-20-03634) by Soumik Purkayastha, Rupam Bhattacharyya, Ritwik Bhaduri, Ritoban Kundu, Xuelin Gu, Maxwell Salvatore, **Debashree Ray**, Swapnil Mishra, Bhramar Mukherjee and for giving us an opportunity to address the concerns through a revision. We would like to clarify that we are submitting this manuscript as a review article and not as an original research article. Following are itemized responses to the reviewer comments (shown in **bold**, coloured red) and editorial comments (shown in **bold**, coloured blue).

The main changes that we have incorporated are:

1. **Change in training and testing period:** the updated manuscript now sets a training period from March 15 till October 15, 2020 and a testing period from October 16 till December 31, 2020.
2. **Predictions with uncertainty:** the updated manuscript includes information regarding prediction uncertainty by reporting 95% credible intervals for the parameter estimates, predictions and comparing the width of the said intervals for each model considered in our study.
3. **Sensitivity analyses and performance of models in context of data from other nations:** the updated manuscript contains information on parameters which are critical to the fitting and projection generating process of each model. In the interest of brevity, we do not carry out sensitivity analyses ourselves but provide references to other publications which implement sensitivity analyses of the models studied. We further provide information on how the models perform when studying COVID-data from other countries beyond India.
4. **We added a new co-author Dr. Debashree Ray to the team** for her contribution to the revised version and in particular addressing item 3 of the response. New authorship forms were completed with a revised statement of authorship contribution.

Thank you for your consideration of our revised manuscript. We hope you find the revised manuscript suitable for publication in *BMC Infectious Diseases*.

Sincerely,

Bhramar Mukherjee

Bhramar Mukherjee

Chair and Professor, Department of Biostatistics, University of Michigan School of Public Health.

Response to Reviewer Panel: Reviewer 1

Summary of the paper: The paper is overall well written. The authors implement and compare five epidemiological models and assess their predictive accuracy on real COVID-19 data from India. Under reporting of cases which has been a major hurdle is taken into account by three of the models. Data from March 15 to June 18 is used as training set while June 19 to July 18 data as a test set. The models are presented in a clear manner and so are the results stemming from them. While no new extension is proposed to the existing models used, their comparison and performance on real data offer interesting insights. However, some parts of the paper need clarification (see below for more details).

1. The terms "unascertained" and "asymptomatic" seem to be used interchangeably throughout the paper. Do unascertained cases consist of mild symptomatic and asymptomatic cases or do both terms refer to the same thing? If the latter is true, wouldn't it be simpler to use only one of the terms? c.f pg 19, line 116: "In the previous subsection we have seen an extension which includes the 'asymptomatic infectious' compartment (people who are infected and contributing to the spread of the virus, but do not show any symptoms)." However, in the previous subsection, there is only mention of unascertained infectious.

We thank the reviewer for their feedback and agree with this comment. Our identification of cases as COVID-negative or positive is based entirely on reporting of test results (by means of diagnostic RT-PCR or antigen tests) and not their underlying disease status (on which we have no data). It is indeed incorrect to use asymptomatic and unascertained interchangeably. We apologize for the confusion and note that wherever possible, we have replaced 'unascertained' with 'unreported' (and 'ascertained' with 'reported') in the manuscript to improve readability and stay true to the data.

2. **Page 7 line 128: "an" exponential process**

We thank the reviewer for noticing this error and note that we have made the appropriate correction.

3. **Page 2 line 33: 23. ? eSIR. It seems that something is missing here.**

We thank the editor for noticing this error. The correct sentence should have read

23.10 (for eSIR)

in accordance with Table 2. We add that we have re-fit all five models on a training period from March 15 – October 15 and test how well the projections match with observed case and death-counts on testing period from October 16 till December 31.

4. **Page 18 line 307: "using data from Singapore". Can you provide a reference for this?**

We apologise for leaving out an important reference from the text. In order to obtain an initial estimate of ascertainment rate, we followed the approach outlined in Hao et al., 2020 (*Hao, X., Cheng, S., Wu, D., Wu, T., Lin, X., & Wang, C. (2020). Reconstruction of the full transmission*

dynamics of COVID-19 in Wuhan. Nature, 584(7821), 420-424). With growing research in this area we obtained a more up-to-date prior distribution for the ascertainment rate (specifically, we now assume the ascertainment rate follows a Beta(10, 90) prior distribution) as described in a study by Rahmandad et al., 2020 (*Rahmandad, H., Lim, T. Y., & Sterman, J. (2020). Estimating COVID-19 under-reporting across 86 nations: implications for projections and control. Available at SSRN 3635047*) on under-reporting in 86 nations including India. The modified manuscript reflects this change.

5. Why use the term "node" in section 2.1.d when compartment has been used throughout the paper? It would be less confusing to keep to the same convention here.

We agree with the reviewer – interchangeably using ‘node’ and ‘compartment’ is confusing. Further, we thank the reviewer for raising this point and note that the modified manuscript is consistent in using ‘compartment’ instead of ‘node’ for all the compartmental models.

6. page 29 line 485: yields instead of yield

We thank the reviewer for spotting this grammatical error and apologise for our oversight. The modified manuscript reflects the suggested correction.

7. page 30 line 492: "we do not include the same in this specific comparison method". What do you mean by this statement?

We apologise for the lack of clarity in the sentence being discussed. In addition to making changes to the manuscript to improve readability, we note that we were able to model and project reported deaths from the ICM model, thereby widening the scope of our model comparisons. As it stands, the ICM model yields projections of reported deaths and total (sum of reported and unreported) cumulative cases.

8. In Figure 6, SAPHIRE is mentioned in the legend but not shown on the graph.

We thank the reviewer for this comment – the projections from SAPHIRE are indeed included in the figure, but given how closely the projections from SAPHIRE and SEIR-fansy agree with each other, the deeper colour for the SEIR-fansy curve makes it very hard to read the SAPHIRE curve from the figure. We note that the new figures (generated with new projections based on updated training and test periods from each of the models) differentiate across the models more, are more informative and easier to read.

Reviewer 1, Major remark:

It is problematic to properly compare the performances of the methods without confidence intervals on the predictions to quantify uncertainty.

We agree with the reviewer’s feedback and note that all projections are now accompanied by uncertainty estimates (by means of 95% credible intervals). We also provide uncertainty quantification for parameters common to all models, say the basic reproduction number R_0 . We

present model projections on specific dates along with their prediction intervals. Additionally, we include an extra figure to compare uncertainty in estimation by comparing boxplots showing widths of credible intervals associated with projections in the testing period (October 16 to December 31) for each of the models, whenever projections are available.

Reviewer 2

In this paper, the authors consider five mathematical models that aim to describe the population-level transmission of SARS-CoV-2 and provide forward projections of various epidemiological quantities of interest. The authors provide a useful exploration of the main features of each model considered, as well as the methods each model uses to produce forward projections. The study focuses on the context of the SARS-CoV-2 outbreak in India, using data from a test period between March and June 2020 to inform the various models considered. The forward projections resulting from each model are compared with data on what happened during the following period between June and July 2020. The authors use various metrics to assess the accuracy of the five models in making forward projections and also to estimate the extent of underreporting in the Indian context considered.

There is clearly utility in comparing different epidemiological modelling approaches and improving our understanding of which models provide the best predictive ability in which contexts. The work done so far by the authors is able to assess the predictive ability of the models under consideration, but it lacks strong conclusions about which modelling approaches are preferable and why. My view is that this kind of comparative modelling assessment will be significantly strengthened if the authors can make stronger conclusions about the models considered and their use and suitability in different contexts. Further, the work will be significantly strengthened by repeating the model comparisons in a couple of different contexts.

Firstly, it would be useful to repeat the same assessment across the five models during different phases of the epidemic. For example, various countries around the world are now experiencing second and third waves of SARS-CoV-2 outbreaks, with much data available during various epidemic phases such as exponential growth and decay, low but sustained prevalence and high and sustained prevalence. I think this work would be improved by assessing the abilities of the models under consideration during various phases of transmission. Further, the current assessment would be strengthened by providing more context to the reader on the epidemic dynamics that India was experiencing during the test and project periods considered (March - July 2020), earlier on in the text. A second comparison which I believe would strengthen the work is a cross-country comparison. The authors note that the degree of underreporting has been a major concern in India and in many other countries. Therefore, it would also seem sensible to compare these five models in a context where the degree of underreporting is lesser, to see if the same model hierarchy emerges in terms of predictive ability.

We changed the training and testing period of our model comparison to address the reviewer's comments. India started experiencing its second wave in late February of 2021, so we did not have enough data for the second wave. While comparing across countries is beyond the scope of the current paper, we provide ample references regarding the use of these models in other countries.

In addition to my overall comments above, I have some more general comments which I think the authors need to address:

1. The authors only provide point estimates and do not discuss the uncertainty estimates produced by the models. It would certainly make sense to include uncertainty in their assessment of the various models' performance.

We agree with the reviewer's feedback and note that all projections are now accompanied by uncertainty estimates (by means of 95% credible intervals). We present model projections on specific dates along with their prediction intervals. Additionally, we include an extra figure to compare uncertainty in estimation by comparing boxplots showing widths of credible intervals associated with projections in the testing period (October 16 to December 31) for each of the models, whenever projections are available.

2. The authors discuss the lockdown introduced in India and refer to four different lockdown periods considered. More work needs to be done in the text to link the policies introduced in India with the four phases under consideration, as well as to define clearly what you mean by these four periods.

We would like to thank the reviewer for raising this issue and note that the updated manuscript attempts to reconcile the findings from the models (in terms of estimated $R(t)$ for each of the four lockdown phases) with intervention policies implemented by the government. Please see Section 5 and Supplementary Table S4 for more information. Please see reference (1) for more information on this.

References

(1) Salvatore M, Basu D, Ray D, et al; *Comprehensive public health evaluation of lockdown as a non-pharmaceutical intervention on COVID-19 spread in India: national trends masking state-level variations*; *BMJ Open* 2020;10:e041778. doi: 10.1136/bmjopen-2020-041778

3. For one of the models considered (ICM), the authors are not able to compare the model performance using all of the metrics used for the other models. Why is this model included if the authors cannot assess its performance in line with the other models? Are there any other metrics the authors can use that would enable a comparison across all five models? Further, I think that the authors should provide more justification for why they have chosen particular models.

We thank the reviewer for this comment and note that we have chosen a curve fitting model as the baseline model. The eSIR, SAPHIRE and SEIR-fansy are all compartmental models but exhibit varying levels of sophistication in being able to model cases and deaths (both reported and unreported). Finally, we examine the ICM model which makes use of birth and death processes which we believe is yet another compelling way of modeling the spread of the pandemic. There is often more belief and accuracy attributed to reported deaths than reported cases (due to different access to testing). We have been able to extract estimates of cumulative reported deaths from the ICM model and the modified manuscript reflects this change. While the ICM model does not yield projections of reported cases, it does yield projections of total (sum of reported and unreported) cumulative infections which may be leveraged to obtain underreporting factors associated with COVID-cases and deaths, which has been a key point of discussion (please see references (1) and (2) below).

References

- (1) *Behavioral dynamics of COVID-19: estimating under-reporting, multiple waves, and adherence fatigue across 91 nations*, Hazhir Rahmandad, Tse Yang Lim, John Sterman
medRxiv 2020.06.24.20139451; doi: <https://doi.org/10.1101/2020.06.24.20139451>
- (2) Lau, Hien, et al. "Evaluating the massive underreporting and undertesting of COVID-19 cases in multiple global epicenters." *Pulmonology* 27.2 (2021): 110-115.

4. Figure captions should define model parameters and variables.

We thank the reviewer for this comment and note that given the large number of parameters in each model it is not possible to include details on model parameters and variables within the caption in the interest of conciseness. However, we have included information on parameters in each subsection detailing how each model works. Additionally, supplementary table S1 presents a tabular view of the same.

5. Equation (2) - why is there an I subscript on the left hand side?

We thank the reviewer for raising this important question. To clarify, Equation (1) describes the growth rate of infections by means of an exponential function, controlled by tuning parameter λ , i.e., the cumulative number of infections at time t is given by $I(t) = \exp(\lambda t)$. We allow the growth rate λ to vary with time, and is estimated by a difference equation analogue of Equation (1), as given by Equation (2), where we replace $\frac{dI(t)}{dt}$ by $\frac{\Delta I(t)}{\Delta t}$, where $\Delta I(t) = I(t) - I(t-2)$ and $\Delta t = 2$. This leads us to Equation (2), where the time-varying growth rate parameter $\lambda(t)$ is approximated by the relation

$$\hat{\lambda}(t) = \frac{I(t)-I(t-2)}{2I(t)}.$$

Having estimated $\hat{\lambda}(t)$ in the manner described above, we fit an exponential time-varying curve to obtain future projections of $\hat{\lambda}(t)$, which are then used to generate projections of cumulative reported infections.

The original manuscript made use of subscripts in order to distinguish between time-points, hence the use of subscripts. We believe this notation may be confusing and have made modifications to improve readability.

6. Page 13, line 224 - define the adaptation number

We thank the reviewer for this comment. As noted in the manuscript, the eSIR algorithm is implemented by means of the rjags package in R, which is an interface from R to the JAGS library for Bayesian data analysis. JAGS uses Markov Chain Monte Carlo (MCMC) to generate a sequence of dependent samples from the posterior distribution of the parameters. The MCMC samplers that JAGS uses to sample the posterior are governed by tunable parameters that affect their precise behavior. Proper tuning of these parameters can produce gains in the speed or de-correlation of the sampling. JAGS contains machinery to tune these parameters automatically and does so as it draws posterior samples. This process is called *adaptation*, but it is non-Markovian; the resulting samples do not constitute a Markov chain. The sequence of samples generated during this adaptive phase is not a Markov chain, and

therefore may not be used for posterior inference on the model. The adaptation number is thus, the number of samples which are to be discarded as part of the adaptation phase. In the interest of brevity, we had not included a discussion on adaptation numbers in the original submission. The modified manuscript has a brief description of adaptation numbers.

7. Page 14, line 226 - start with 4 chains but end with what?

We thank the reviewer for noting the poor clarity of this sentence and note that the updated manuscript now reads as follows

To ensure the quality of the MCMC procedure, we fix the adaptation number (which denotes the number of MCMC samples discarded by JAGS in order to tune parameters which improves speed or de-correlation of sampling) at 10^4 , thin the chain by keeping one draw from every 10 random draws to further reduce autocorrelation, set a burn-in period of 10^5 draws under 2×10^5 iterations for four parallel chains.

8. Page 14, line 234 - define what is meant by COVID-19 counts. Same comment on page 18, line 305

We apologise for the lack of clarity and note that the updated manuscript now defines COVID-counts as follows

COVID-counts (i.e., case and death counts associated with COVID-19)

9. Ensure that justification and/or references are provided for parameterizations. In fact, I think this element would be strengthened if parameter values were justified/motivated across all models in the text, before introducing each model.

We thank the reviewer for raising this important issue and note that the modified manuscript now contains a section justifying choices of parameter values with relevant references.

10. The authors do not allow for population movement between the Indian states. This seems like a key limitation, especially since there were reports during the early stages of the outbreak in India of migration of workers from urban to rural locations. Can the authors discuss the implications of not considering population movement on the results? Or incorporate population movement into the results as a sensitivity analysis?

We thank the author for raising this crucial point and note that with the lockdown in India being severe (several states closed their respective borders) and data on population movement not being available, it was not possible to incorporate population movement within the country. We further note that sensitivity analysis for each model has been carried out in several papers and do not compare them numerically in the current paper for brevity. Instead, we include information on which parameters are critical to each of the respective models and comment on what makes the predictions change in each model (see section 4). Additionally, we provide references which support our comments.

11. It is not clear what is meant by active case counts -> please define

We thank the reviewer for this comment and note that the updated manuscript has the following definition of active case counts

For active reported cases (cases that are active on a given day which is the difference of cumulative reported cases and cumulative reported counts of recoveries and deaths)..

12. Page 16, lines 263-267 - please define n and N here

We apologise for the omission and thank the reviewer for bringing this to our notice. The modified manuscript now has information on what these variables are. For completeness we include a brief description here: *N is the total population size of India, while n denotes the total number of inbound and outbound travelers (assumed to be equal).*

13. The authors assume that unascertained cases have lower transmissibility than ascertained cases (lines 275-6). Intuitively, I would assume the opposite (i.e. ascertained cases would have lower transmissibility relative to unascertained cases, due to increased awareness). I would suggest that the authors consider doing sensitivity analysis on this aspect

We thank the reviewer for raising this important question. Our thoughts on this matter are as follows.

Evidence suggests that about one in five infected people will experience no symptoms, and they will transmit the virus to significantly fewer people than someone with symptoms (see reference (1)). Researchers were initially not certain about whether asymptomatic individuals (i.e., people whose infection went unreported) act as ‘silent drivers’ of the pandemic. A recent meta-analysis shows the rate of asymptomatic infections to be 17% (see reference (2)). The analysis defined asymptomatic people as those who showed none of the key COVID-19 symptoms during the entire follow-up period, and the authors included only studies that followed participants for at least seven days. Another recent publication conducted a systematic review and meta-analysis of 79 studies on the viral dynamics and transmissibility of SARS-CoV-2 (see reference (3)). The authors note that asymptomatic people seem to ‘clear’ the virus faster and are infectious for a shorter period. They further note that immune systems of asymptomatic individuals might be able to neutralize the virus more rapidly, thereby leading us to assume that unascertained cases have lower viral load (and therefore lower transmissibility) than ascertained cases.

References

- (1) Nogrady, Bianca. "What the data say about asymptomatic COVID infections." *Nature* (2020). DOI <https://doi.org/10.1038/d41586-020-03141-3>
- (2) Byambasuren, Oyungerel, et al. "Estimating the extent of asymptomatic COVID-19 and its potential for community transmission: systematic review and meta-analysis." *Official Journal of the Association of Medical Microbiology and Infectious Disease Canada* 5.4 (2020): 223-234.

(3) Cevik, Muge, et al. "SARS-CoV-2, SARS-CoV-1 and MERS-CoV viral load dynamics, duration of viral shedding and infectiousness: a living systematic review and meta-analysis." *SARS-CoV-1 and MERS-CoV Viral Load Dynamics, Duration of Viral Shedding and Infectiousness: A Living Systematic Review and Meta-Analysis* (2020).

14. Page 17, lines 284-285 - the authors assume an isolation period of 30 days, but don't provide justification for this assumption (this seems a long period to assume). Further, the authors say that this choice has no effect on model fitting or estimates. Can the authors explain why?

We thank the reviewer for this question and note that we assume the same isolation period of 30 days as what was successfully applied in the SAPHIRE modeling for Wuhan, China (see reference (1) below) since we assumed that the hospital stay would be similar in India and in Wuhan at the early stage of pandemic. This choice has no effect on model fitting procedure and estimates. Based on a more relevant publication investigating the hospital stay in Karnataka, India (see reference (2) below), we changed the assumed isolation period in hospital to 17 days and updated the results in the manuscript.

To explain why we stated this choice has no effect on model fitting or estimates, we fitted the daily new cases and estimated means of daily new cases for each day and assuming the observed daily cases follow a Poisson distribution with the estimated mean as its parameter. According to the schematic diagram (see Figure 3 in manuscript) for the SAPHIRE model, the cases in hospital and deaths have no contribution to the new cases onset, therefore the estimated mean of daily new cases only depends on the 5 compartments: susceptible (S), exposed (E), pre-symptomatic infectious (P), ascertained infectious (I) and unascertained infectious (A), and all parameters except for the isolation period in hospital. Thus, we state that

"this parameter has no effect on the model fitting procedure, or the final parameter estimate".

References

- (1) Hao, X., Cheng, S., Wu, D., Wu, T., Lin, X., & Wang, C. (2020). Reconstruction of the full transmission dynamics of COVID-19 in Wuhan. *Nature*, 584(7821), 420-424.
- (2) Mishra, V., Burma, A. D., Das, S. K., Parivallal, M. B., Amudhan, S., & Rao, G. N. (2020). COVID-19-hospitalized patients in Karnataka: survival and stay characteristics. *Indian journal of public health*, 64(6), 221.

15. Page 17, line 290 - strange phrasing where the authors talk about the assumed value for r₀

We apologise for the lack of clarity and thank the reviewer for noticing this. The modified manuscript provides an updated value of r_0 with a reference to justify our choice as follows:

The initial ascertainment rate is assumed to be $r_0 = 0.10$,

Where the reference is

Rahmandad, Hazhir and Lim, Tse Yang and Sterman, John, Behavioral Dynamics of COVID-19: Estimating Under-Reporting, Multiple Waves, and Adherence Fatigue Across 92 Nations (February 17, 2021). Rahmandad, H., Lim, TY., Sterman, J.,

Behavioral Dynamics of COVID-19: Estimating Under-Reporting, Multiple Waves, and Adherence Fatigue Across 92 Nations, System Dynamics Review, Forthcoming, Available at SSRN: <http://dx.doi.org/10.2139/ssrn.3635047>

- 16. Page 18, line 307 - the authors parametrize the ascertainment rate using data from Singapore. I assume that the ascertainment rate in Singapore is going to differ from India. Can the authors instead use an estimate more relevant to the Indian context considered? This links back to my earlier point about doing this analysis for a different country context -- perhaps Singapore would be a good country to choose for this comparison.**

We agree with the reviewer about using an ascertainment rate that is more appropriate in context of the pandemic in India. As such, we use an informative prior for initial ascertainment rate, in accordance with the findings presented in

Rahmandad, Hazhir and Lim, Tse Yang and Sterman, John, Behavioral Dynamics of COVID-19: Estimating Under-Reporting, Multiple Waves, and Adherence Fatigue Across 92 Nations (February 17, 2021). Rahmandad, H., Lim, TY., Sterman, J., Behavioral Dynamics of COVID-19: Estimating Under-Reporting, Multiple Waves, and Adherence Fatigue Across 92 Nations, System Dynamics Review, Forthcoming, Available at SSRN: <http://dx.doi.org/10.2139/ssrn.3635047>.

We have presented information of how well the models studied in this manuscript perform in the context of other countries based on a literature search, since we feel running and comparing performance of these models for other countries is beyond the scope of this paper.

- 17. Section 2.1.d. SEIR-fansy model - the authors use the 'node' terminology multiple times but I think 'compartment' would be a more appropriate term.**

We agree with the reviewer – interchangeably using ‘node’ and ‘compartment’ is confusing. Further, we thank the reviewer for raising this point and note that the modified manuscript is consistent in using ‘compartment’ instead of ‘node’ for all the compartmental models.

- 18. Page 19, lines 324-329 - the authors discuss modelling of false negatives but don't mention consideration of false positives. Please outline what assumptions/considerations are made here**

We thank the reviewer for raising this issue. In the context of testing for COVID-19 in India, studies note that the RT-PCR tests used have high false negatives (as high as 30% with corresponding sensitivity falling to almost 70%) and low false positives (as low as 5% with corresponding specificity nearly 95%). Since the specificity is appreciably high, we model only false negatives. For reference, please see the following reference.

Reconciling epidemiological models with misclassified case-counts for SARS-CoV-2 with seroprevalence surveys: A case study in Delhi, India; Rupam Bhattacharyya, Ritwik Bhaduri, Ritoban Kundu, Maxwell Salvatore, Bhramar Mukherjee; medRxiv 2020.07.31.20166249; doi: <https://doi.org/10.1101/2020.07.31.20166249>

19. Page 20, line 333 - do the authors mean exponentially distributed times?

We apologise for the lack of clarity and note that we assume a stochastic process model where the duration any individual spends in a particular compartment follows an exponential distribution. For example, the time any individual who has contacted COVID-19 spends in the E compartment is assumed to follow exponential distribution with mean D_E .

20. Page 20, lines 336-337 - alpha_p is a ratio and then alpha_u is a scaling factor - why the difference in terminology?

We thank the reviewer for raising this question. To clarify, α_p is a factor that quantifies the rate of spread of infection by patients who test positive for COVID-19 relative to the rate of spread of infection by patients who are infected but do not test positive for COVID-19 (i.e., false negatives).

21. Page 20, line 340 - "disease times" -> "disease multiplied by"

We apologise for this error and thank the reviewer for spotting this mistake – the modified manuscript reflects the change suggested by the reviewer.

22. Page 20, lines 349-350 - the authors talk about their assumption of testing being instantaneous as being reasonable. I feel this statement is a bit strong.

We thank the reviewer for raising this issue and note that the typical duration between collection of samples and declaration of test results for RT-PCR tests ranges between 1-3 days. With the progression of the pandemic, the number of available tests has increased considerably, further reducing the delay in obtaining test results. Hence, we have assumed testing to be instantaneous to simplify the model. For the model with non-instantaneous testing please refer to supplementary materials of the following reference

*Extending Susceptible-Exposed-Infected-Removed (SEIR) model to handle the high false negative rate and symptom-based administration of COVID-19 diagnostic tests: SEIRfansy, Ritwik Bhaduri, Ritoban Kundu, Soumik Purkayastha, Michael Kleinsasser, Lauren J. Beesley, Bhramar Mukherjee
medRxiv 2020.09.24.20200238; doi: <https://doi.org/10.1101/2020.09.24.20200238>*

23. Figure 4 - labelling of transitions needs improving, it's not clear which quantities related to which transition e.g. alpha_u*beta. In fact, it seems that a slightly different Figure has been uploaded separately to the one included in the text? Perhaps the in text Figure is missing arrows

We agree with the reviewer – it seems the original submission did not render the images properly. We are taking care to ensure this does not happen in the future.

24. Page 22 - line 373 - what does daily differences mean? Are you using a time step of one day?

We thank the reviewer for raising this question and note that the phrase *daily differences* does indeed imply taking time steps of one day. Specifically, we use the difference $X(t) - X(t - 1)$ to approximate the differential $\frac{dx(t)}{dt}$ using a time-difference of one day.

25. Page 23 - lines 380-382 - can the authors explain this working?

We thank the reviewer for raising this question. The original submission interchangeably used RR and R, and DR and R. We have made modifications to the manuscript to avoid any further confusion. We expand on the working a little - we assumed a Bayesian hierarchical model in which the conditional distribution of count of new individuals in the Positive (P) compartment (given by P_{new}) is independent of the number of new individuals in Recovered and Reported (RR) compartment and Deceased and Reported (DR) compartments (denoted by DR_{new} and RR_{new} respectively). The first line of the equation follows from this observation. Next, we assume that P_{new} depends only on E_{t-1} whereas RR_{new} and DR_{new} are dependent only on P_{t-1} , thus yielding the third line of the equation.

26. Page 27 - line 436 - define the star superscript notation

We apologise for the lack of clarity and note that the updated manuscript describes the notation in greater detail.

27. Page 27 - lines 446-447 - make the notation for $R_{t,m}$ consistent across these lines

We apologise for the lack of clarity and note that the updated manuscript describes the model using consistent notation and terminology.

28. Page 28 - lines 450-451 - make the notation here consistent with what you have used in equation (16)

We apologise for the lack of clarity and note that the updated manuscript describes the model using consistent notation and terminology.

29. Page 28 - section 2.2.a Choice of parameters - seems like this section should come before introducing and discussing the parameterization of each model

We thank the reviewer for this comment and note that each subsection discussing the models individually now have information on the parameters that are critical to the estimation/projection generation process.

30. Page 29 - equation (18) - define the norm notation used

We are grateful for the reviewer's feedback and note that the norm defined is the L_1 norm – the modified manuscript reflects this change.

31. Page 29 - equations (18) and (19) - the right hand side of both measures seems to be calculated from t=1 to t=T but the left hand side are defined as being relevant to time t only

We sincerely apologise for this error and thank the reviewer for bringing this to our notice. We would like to add that the modified manuscript now reflects the following changes to Equations (18) and (19).

$$SMAPE(T) = \frac{100}{T} \cdot \sum_{t=1}^{t=T} \frac{|P_t - O_t|}{(|P_t| + |O_t|)/2}, \quad (18)$$

$$MSRPE(T) = \left[T^{-1} \sum_{t=1}^T \left(1 - \frac{P_t}{O_t} \right)^2 \right]^{1/2}. \quad (19)$$

We note that the metrics defined depend on the set of observed values $\{O_t\}$ and projected values $\{P_t\}$ and are calculated over a time $1 \leq t \leq T$. To avoid further confusion, we refrain from mentioning (O_t, P_t) on the left side of the Equations.

32. Page 30 - lines 501-502 - can the authors provide some context as to what values of the Rel-MSPE mean? E.g. are smaller / larger values better?

We thank the reviewer for raising this question. We compare the projections at time point t from models A and B by comparing their ratios: if the projection from model B performs better than the projection from model A, it is expected that $(O_t - P_t^A)^2$ would be larger than $(O_t - P_t^B)^2$. As a result, the ratio $(O_t - P_t^A)^2/(O_t - P_t^B)^2$ would be larger than one. The more number of times projections from model B outperform projections from model A, the resultant sum (over all time points $1 \leq t \leq T$) would keep increasing, implying that higher values of Rel-MSPE(B:A) indicate better performance of model B over model A.

33. Page 30 - lines 504-505 and equation (20) - it seems that the left hand side of the equation doesn't match the right hand side. As far as I can tell, the right hand side would calculate the Rel-MSPE of model A with respect to model B

We thank the reviewer for this comment. In light of comment #32 and our response, we feel the notation is correct as we wish to examine the performance of model B relative to model A's performance and the current formulation indicates that larger values of Rel-MSPE(B:A) imply better performance of model B projections relative to model A.

34. Page 31 - lines 523-524 - over what time period is the data taken?

We apologise for not including this information in the section highlighted and note that the modified manuscript now has the relevant information, as follows.

While the models are trained using data from March 15 till October 15, 2020, their performances are compared by examining their respective projections from October 16 till December 31, 2020.

35. Page 31 - lines 525-526 - how is the interactive dashboard relevant to this work?

We value the reviewer's comments and note that the dashboard helps understand the progression of the pandemic in India. Since the projections and parameters explaining transmission dynamics in the dashboard are generated by the eSIR model, we included this information in the manuscript.

36. Page 32 - lines 540-542 - how do these results compare with data on population movement/behaviour? It would be useful to compare these results with contextual information on what was happening during the various lockdown stages considered.

We would like to thank the reviewer for raising this issue and note that the updated manuscript attempts to reconcile the findings from the models (in terms of estimated $R(t)$ for each of the four lockdown phases) with intervention policies implemented by the government. Please see Section 5 and Supplementary Table S4 for more information.

37. Page 35 - lines 600-603 - how do these results compare to another country with a different degree of underreporting?

We thank the reviewer for raising this question. While it would be very useful to compare these results with those obtained from another country, we feel it is beyond the scope of this paper, since we have focused on comparing the models in terms of their projections and estimated parameters for the trajectory of the pandemic in India.

38. Page 35 - lines 608-609 - if the authors assume that there are no changes in either interventions or behaviour of people during the four lockdown periods considered, then why is there a need to divide the lockdown into these four periods at all?

We thank the reviewer for this comment. We would like to note that lines 608-609 indicate that we have assumed no intervention or behavioral changes of people in the *forecast phase* only. Whenever possible (in eSIR, SAPHIRE and SEIR-fansy) we made adjustments to (A) initially allow for four different stages corresponding to each lockdown stage and (B) the current manuscript makes further modifications to allow for intervention or behavioral changes in the different unlock stages as well.

39. Page 35/36 - lines 612-614 - I think the authors need to be more explicit about the limiting assumptions of the modelling approach, e.g. that there is no age structuring so individuals of all ages mix homogeneously, and also that you do not allow for movement between Indian states considered.

We agree with the reviewer's comments on the limitations of the models discussed – while most standard compartmental models do not allow for age-structuring, we also did not have access to population movement data across states and hence could not incorporate the same into our comparative analyses. We have mentioned a paragraph on limitations in the Discussion section.

40. Page 36 - lines 615-617 - it is not clear what the authors mean by this sentence: if the uncertainty estimates play a key role in model choice, then why don't you report them?

We agree with the reviewer's feedback and note that all projections on specific dates are now accompanied by uncertainty estimates (by means of 95% credible intervals). We also include an extra figure to compare uncertainty in estimation by comparing boxplots showing widths of credible intervals associated with projections in the testing period (October 16 to December 31) for each of the models, whenever projections are available.

41. Figure 6 - use numbers for vertical axis, consider providing a zoomed in segment of the lines for observed, baseline and SAPHIRE and SEIR-fansy - as you can't see the difference between these lines easily

We thank the reviewer for helping us greatly improve the quality of the figures. Given the new training and testing periods, the projections are more easily distinguished, and we hope the reviewer is able to make sense of the differences.

42. Figure 7 - it is hard to see the red line for observed, would be helpful to provide a zoomed in segment, similar to comment above

We thank the reviewer for helping us greatly improve the quality of the figures. Given the new training and testing periods, the projections are more easily distinguished, and we hope the reviewer is able to make sense of the differences.

43. Figure 9 - use numbers for axes.

We thank the reviewer for helping us greatly improve the quality of the figures and note that the modified manuscript now reflects the change suggested by the reviewer.

44. Figures 9, 10, 11 - difficult to interpret the densities plotted horizontally and vertically - these may look better if the authors provide their own separate axes. It is also difficult to see the various model's density plots when they are plotted on top of each other

We thank the reviewer for helping us greatly improve the quality of the figures and note that the modified manuscript now reflects the change suggested by the reviewer.

Editor's Comments

Assessing and comparing different models of SARS-CoV-2 transmission is certainly useful in the current context. However, this comparison needs to be performed in the most robust way possible. This requires major revisions to the current version of the paper. In particular, I strongly support the suggestion made by the two reviewers to add uncertainty estimates to model predictions in order to be able to determine whether differences are significant.

We agree with the editor's feedback and note that all projections on specific dates are now accompanied by uncertainty estimates (by means of 95% credible intervals). We also include an extra figure to compare uncertainty in estimation by comparing boxplots showing widths of credible intervals associated with projections in the testing period (October 16 to December 31) for each of the models, whenever projections are available.

I also agree with Reviewer 2's suggestion to try and assess whether the conclusions reached in terms of model comparison still hold under conditions other than those of the first epidemic wave in India. In other words, some kind of sensitivity analysis is missing from the paper.

We agree with the editor's feedback and note that since sensitivity analysis for each model has been carried out in several other papers, we do not compare them numerically in the current paper for brevity. Instead, we include information on which parameters are critical to each of the respective models and comment on what makes the predictions change in each model (see section 4). Additionally, we provide references which support our comments. We have also changed the training and testing period to account for more updated data. Though predicted numbers changed, the conclusions in terms of relative merits of the methods remain largely unchanged.

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We appreciate this convention.

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Debashree Ray, Assistant Professor from the Department of Epidemiology, Johns Hopkins University was added as a co-author to this manuscript for her help with the revision. Debashree had some thoughtful suggestions that helped address reviewer comments. She read, edited and crafted the section on sensitivity analysis of the different models, integrating input from other co-authors.

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Soumik Purkayastha drafted the main paper and prepared all numerical items (Tables and Figures). Rupam Bhattacharyya and Maxwell Salvatore (eSIR), Xuelin Gu (SAPHIRE), Ritoban Kundu and Ritwik Bhaduri (SEIR-fansy) and Swapnil Mishra (ICM) ran the different models. Debasree Ray helped with devising analysis and writing strategies to address reviewer concerns in the revised version. Bhramar Mukherjee designed the study, revised the draft, provided strategic guidance and oversaw the analysis and the writing.

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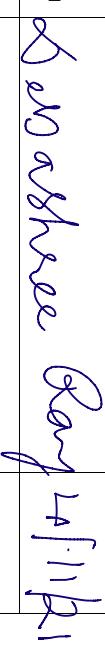
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1 *A comparison of five epidemiological models for transmission of SARS-CoV-2 in India*

2

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17

18

19 ***ABSTRACT***

20 *Background*

21 Many popular disease transmission models have helped nations respond to the COVID-19 pandemic by
22 informing decisions about pandemic planning, resource allocation, implementation of social distancing
23 measures, lockdowns, and other non-pharmaceutical interventions. We study how five epidemiological
24 models forecast and assess the course of the pandemic in India: a baseline curve-fitting model, an
25 extended SIR (eSIR) model, two extended SEIR (SAPHIRE and SEIR-fansy) models, and a semi-
26 mechanistic Bayesian hierarchical model (ICM).

27 *Methods*

28 Using COVID-19 case-recovery-death count data reported in India from March 15 to October 15 to train
29 the models, we generate predictions from each of the five models from October 16 to December 31. To
30 compare prediction accuracy with respect to reported cumulative and active case counts and reported
31 cumulative death counts, we compute the symmetric mean absolute prediction error (SMAPE) for each
32 of the five models. For reported cumulative cases and deaths, we compute Pearson's and Lin's correlation
33 coefficients to investigate how well the projected and observed reported counts agree. We also present
34 underreporting factors when available, and comment on uncertainty of projections from each model.

35 *Results*

36 For active case counts, SMAPE values are 35.14% (SEIR-fansy) and 37.96% (eSIR). For cumulative
37 case counts, SMAPE values are 6.89% (baseline), 6.59% (eSIR), 2.25% (SAPHIRE) and 2.29% (SEIR-
38 fansy). For cumulative death counts, the SMAPE values are 4.74% (SEIR-fansy), 8.94% (eSIR) and
39 0.77% (ICM). Three models (SAPHIRE, SEIR-fansy and ICM) return total (sum of reported and

40 unreported) cumulative case counts as well. We compute underreporting factors as of October 31 and
41 note that for cumulative cases, the SEIR-fansy model yields an underreporting factor of 7.25 and ICM
42 model yields 4.54 for the same quantity. For total (sum of reported and unreported) cumulative deaths
43 the SEIR-fansy model reports an underreporting factor of 2.97. On October 31, we observe 8.18 million
44 cumulative reported cases, while the projections (in millions) from the baseline model are 8.71 (95%
45 credible interval: 8.63 – 8.80), while eSIR yields 8.35 (7.19 – 9.60), SAPHIRE returns 8.17 (7.90 – 8.52)
46 and SEIR-fansy projects 8.51 (8.18 – 8.85) million cases. Cumulative case projections from the eSIR
47 model have the highest uncertainty in terms of width of 95% credible intervals, followed by those from
48 SAPHIRE, the baseline model and finally SEIR-fansy.

49 *Conclusions*

50 In this comparative paper, we describe five different models used to study the transmission dynamics of
51 the SARS-CoV-2 virus in India. While simulation studies are the only gold standard way to compare the
52 accuracy of the models, here we were uniquely poised to compare the projected case-counts against
53 observed data on a test period. The largest variability across models is observed in predicting the “total”
54 number of infections including reported and unreported cases (on which we have no validation data).
55 The degree of under-reporting has been a major concern in India and is characterized in this report.
56 Overall, the SEIR-fansy model appeared to be a good choice with publicly available R-package and
57 desired flexibility plus accuracy.

58 **KEYWORDS**

59 Compartmental Models; Low and Middle Income Countries; Prediction Uncertainty, Statistical Models;

60

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62

63 ***DECLARATIONS***

64 *Ethics approval and consent to participate:* Not applicable (uses publicly available data).

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72 *Authors' contributions:* SP drafted the main paper and prepared all numerical items (Tables and Figures).

73 RB1 and MS (eSIR), XG (SAPHIRE), RK and RB2 (SEIR-fansy) and SM (ICM) implemented the
74 different models. DR helped with planning analysis and writing strategies to address reviewer concerns
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83 **1. BACKGROUND**

84 Coronavirus disease 2019 (COVID-19) is an infectious disease caused by severe acute respiratory
85 syndrome coronavirus 2 (SARS-CoV-2) (1). At the time of revising this paper (March 24, 2020), roughly
86 124 million cases have been reported worldwide. The disease was first identified in Wuhan, Hubei
87 Province, China in December 2019 (2). Since then, more than 2.74 million lives have been lost as a direct
88 consequence of the disease. Notable outbreaks were recorded in the United States of America, Brazil and
89 India -- which remains a crucial battleground against the outbreak. The Indian government imposed very
90 strict lockdown measures early in the course of the pandemic in order to reduce the spread of the virus.
91 Said measures have not been as effective as was intended (3), with India now reporting the largest number
92 of confirmed cases in Asia, and the third highest number of confirmed cases in the world after the United
93 States and Brazil (4), with the number of confirmed cases crossing the 10 million mark on December 18,
94 2020. On March 24, 2020, the Government of India ordered a 21-day nationwide lockdown, later
95 extending it until May 3. This was followed by two-week extensions starting May 3 and 17 with
96 substantial relaxations. From June 1, the government started ‘unlocking’ most regions of the country in
97 five unlock phases. In order to formulate and implement policy geared toward containment and
98 mitigation, it is important to recognize the presence of highly variable contagion patterns across different
99 Indian states (5). India saw a decay in the virus curve in September, 2020 with daily number of cases
100 going below 10000. At the time of revising the paper, the daily incidence curve is sharply rising again,
101 as India faces its second wave. There is a rising interest in studying potential trajectories that the infection
102 can take in India to improve policy decisions.

103 A spectrum of models for projecting infectious disease spread have become widely popular in wake of
104 the pandemic. Some popular models include the ones developed at the Institute of Health Metrics (IHME)
105 (6) (University of Washington, Seattle) and at the Imperial College London (7). The IHME COVID-19
106 project initially relied on an extendable nonlinear mixed effects model for fitting parametrized curves to
107 COVID-19 data, before moving to a compartmental model to analyze the pandemic and generate
108 projections. The Imperial College model (henceforth referred to as ICM) works backwards from
109 observed death counts to estimate transmission that occurred several weeks ago, allowing for the time
110 lag between infection and death. A Bayesian mechanistic model is introduced - linking the infection
111 cycle to observed deaths, inferring the total population infected (attack rates) as well as the time-varying
112 reproduction number $R(t)$. With the onset of the pandemic, there has been renewed interest in multi-
113 compartment models, which have played a central role in modeling infectious disease dynamics since
114 the 20th century (8). The simplest of compartmental models include the standard SIR (9) model, which
115 has been extended (10) to incorporate various types of time-varying quarantine protocols, including
116 government-level macro isolation policies and community-level micro inspection measures. Further
117 extensions include one which adds a spatial component to this temporal model by making use of a cellular
118 automata structure (11). Larger compartmental models include those which incorporate different states
119 of transition between susceptible, exposed, infected and removed (SEIR) compartments, which have been
120 used in the early days of the pandemic in the Wuhan province of China (12). The SEIR compartmental
121 model has been further extended to the SAPHIRE model (13), which accounts for the infectiousness of
122 asymptomatic (14) and pre-symptomatic (15) individuals in the population (both of which are crucial
123 transmission features of COVID-19), time varying ascertainment rates, transmission rates and population
124 movement.

125 Researchers and policymakers are relying on these models to plan and implement public health policies
126 at the national and local levels. New models are emerging rapidly. Models often have conflicting
127 messages, and it is hard to distinguish a good model from an unreliable one. Different models operate
128 under different assumptions and provide different deliverables. In light of this, it is important to
129 investigate and compare the findings of various models on a given test dataset. While some work has
130 been done in terms of trying to reconcile results from different models of disease transmission that can
131 be fit to emerging data (16), more comparisons need to be done to investigate how differences between
132 competing models might lead to differing projections on the same dataset. In the context of India, such
133 head-to-head comparison across models are largely unavailable.

134 We consider five different models of different genre, starting from the simplest baseline model. The
135 baseline model we investigate relies on curve-fitting methods, with cumulative number of infected cases
136 modeled as an exponential process (17). Next, we consider the extended SIR (eSIR) model (10), which
137 uses a Bayesian hierarchical model to generate projections of proportions of infected and removed people
138 at future time points. The SAPHIRE (13) model has been demonstrated to reconstruct the full-spectrum
139 dynamics of COVID-19 in Wuhan between January and March 2020 across five periods defined by
140 events and interventions. Using this, we study the evolution of the pandemic in India over nine well-
141 defined lockdown and unlock periods, each with distinct transmission and ascertainment features.
142 Another model, SEIR-fansy (18) modifies the SEIR model to account for high false negative rate and
143 symptom-based administration of COVID-19 tests. Finally, we study the ICM model, which utilizes a
144 semi-mechanistic Bayesian hierarchical model based on renewal equations that model infections as a
145 latent process and links deaths to infections with the help of survival analysis. Each of the models

146 mentioned above have had appreciable success in being able to satisfactorily analyze and project the
147 trajectory of the pandemic in different countries (19)-(20)-(21).

148 In order to fairly compare and contrast the models mentioned above, we study their respective treatment
149 of the different lockdown and unlock periods declared by the Government of India. Additionally, we
150 compare their projections based on reported data, with special emphasis on how the models deal with (if
151 they do, at all) under-reporting and under-detection of COVID-cases, which has been a major point of
152 discussion in the scientific community, particularly for India (22). We also compare the uncertainty
153 associated with the projections across the models which is often overlooked in the literature.

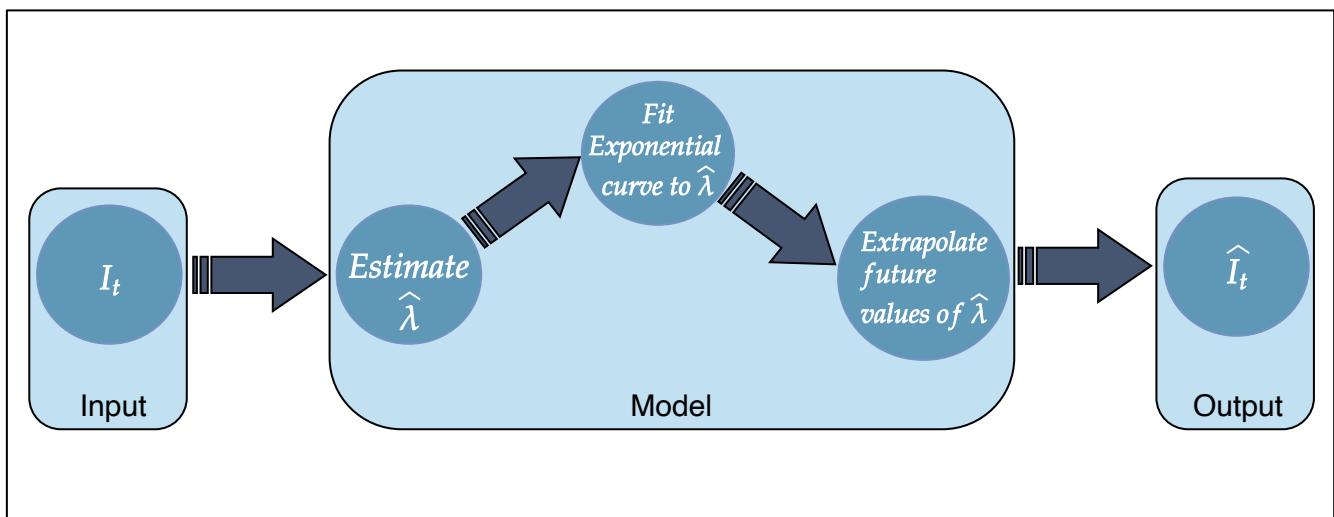
154 The rest of the paper is organized as follows. In *Section 2* we provide an overview of the various models
155 considered in our analysis. The supplement has detailed discussion on the formulation, assumptions and
156 estimation methods utilized by each of the models. We present the numerical findings of our comparative
157 investigation of the models in *Section 3* by comparing projected COVID-counts (i.e., case and death
158 counts associated with COVID-19) and (wherever possible) parameter estimates which help understand
159 transmission dynamics of the pandemic. Next, in *Section 4* we discuss sensitivity analyses and note
160 applications of the models studied in the context of data from countries other than India. Finally, we
161 discuss the implications of our findings in *Section 5*.

162 **2. METHODS**163 **2.1. Overview of models**

164 In this section, we discuss the assumptions and formulation of each of the five classes of models described
 165 above.

166 **2.1.a. Baseline model**

167 *Overview:* The baseline model we investigate aims to predict the evolution of the COVID-19 pandemic
 168 by means of a regression-based predictive model (17). More specifically, the model relies on a
 169 regression analysis of the daily cumulative count of infected cases based on the least-squares fitting.
 170 In particular, the growth rate of the infection is modeled as an exponentially decaying process. *Figure*
 171 *1* provides a schematic overview of this model.



172 *Figure 1: Schematic overview of the baseline model.*

173 *Formulation:* The baseline model assumes that the following simple differential equation governs
 174 the evolution of a disease in a fixed population:

175

$$\frac{dI(t)}{dt} = \lambda I(t), \quad (1)$$

176 where $I(t)$ is defined as the number of infected people at time t and λ is the growth rate of infection.
 177 Unlike the other models described in subsequent sections, the baseline model analyses and projects only
 178 the cumulative number of infections, and not counts/proportions associated with other compartments like
 179 deaths and recoveries. The model uses reported field data of the infections in India over a specific time
 180 period. The growth rate can be numerically approximated from Equation (1) above as

181

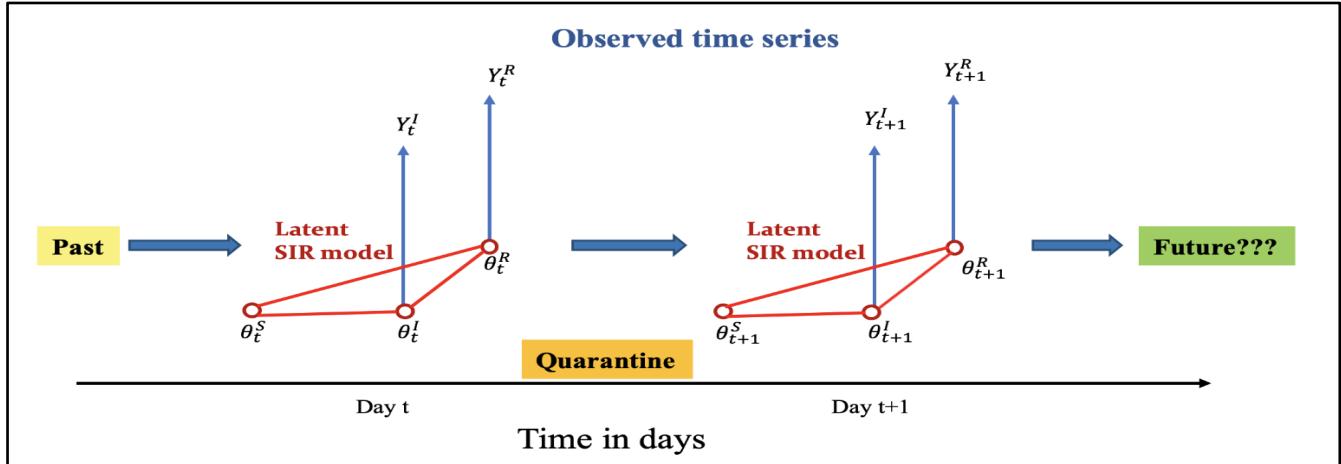
$$\hat{\lambda}_t = \frac{I_t - I_{t-2}}{2 \cdot I_t} \quad (2)$$

182 Having estimated the growth rate, the model uses a least-squares method to fit an exponential time-
 183 varying curve to $\hat{\lambda}_t$, obtained from Equation (2) above. Since all the other methods involve Bayesian
 184 estimation methods and use posterior distributions to obtain estimates and associated credible intervals,
 185 we place a non-informative prior on the random error in the above curve fitting method (23) to ensure
 186 comparable results. Specifically, we consider a uniform prior for the log of error variance. Using
 187 projected values of $\hat{\lambda}_t$, we extrapolate the number of infections which will occur in future. The baseline
 188 model described above has been implemented in R (24) using standard packages for exponential curve
 189 fitting.

190 **2.1.b. Extended SIR (eSIR) model**

191 *Overview:* We use an extension of the standard susceptible-infected-removed (SIR) compartmental
 192 model known as the extended SIR (eSIR) model (10). To implement the eSIR model, a Bayesian
 193 hierarchical framework is used to model time series data on the proportion of individuals in the infected
 194 and removed compartments. Markov chain Monte Carlo (MCMC) methods are used to implement this

195 model, which provides not only posterior estimation of parameters and prevalence values associated with
 196 all three compartments of the SIR model, but also predicted proportions of the infected and the removed
 197 people at future time points. *Figure 2* is a diagrammatic representation of the eSIR model.



198

Figure 2: The eSIR model with a latent SIR model on the unobserved proportions. Reproduced from Wang et al., 2020 (10).

199 *Formulation:* The eSIR model assumes the true underlying probabilities of the three compartments
 200 follow a latent Markov transition process and require observed daily proportions of infected and removed
 201 cases as input.

202 The observed proportions of infected and removed cases on day t are denoted by Y_t^I and Y_t^R , respectively.
 203 Further, we denote the true underlying probabilities of the S, I, and R compartments on day t by θ_t^S , θ_t^I ,
 204 and θ_t^R , respectively, and assume that for any t , $\theta_t^S + \theta_t^I + \theta_t^R = 1$. Assuming a usual SIR model on the
 205 true proportions we have the following set of differential equations

206

$$\frac{d\theta_t^S}{dt} = -\beta\theta_t^S\theta_t^I, \quad (3a)$$

207

$$\frac{d\theta_t^I}{dt} = \beta\theta_t^S\theta_t^I - \gamma\theta_t^I, \quad (3b)$$

208

$$\frac{d\theta_t^R}{dt} = \gamma\theta_t^I, \quad (3c)$$

209 where $\beta > 0$ denotes the disease transmission rate, and $\gamma > 0$ denotes the removal rate. The basic
 210 reproduction number $R_0 := \beta/\gamma$ indicates the expected number of cases generated by one infected case
 211 in the absence of any intervention and assuming that the whole population is susceptible. We assume a
 212 Beta-Dirichlet state space model for the observed infected and removed proportions, which are
 213 conditionally independently distributed as

$$214 \quad Y_t^I | \boldsymbol{\theta}_t, \boldsymbol{\tau} \sim Beta(\lambda^I\theta_t^I, \lambda^I(1 - \theta_t^I)) \quad (4a)$$

$$215 \quad Y_t^R | \boldsymbol{\theta}_t, \boldsymbol{\tau} \sim Beta(\lambda^R\theta_t^R, \lambda^R(1 - \theta_t^R)). \quad (4b)$$

216 Further, the Markov process associated with the latent proportions is built as:

$$217 \quad \boldsymbol{\theta}_t | \boldsymbol{\theta}_{t-1}, \boldsymbol{\tau} \sim Dirichlet(\kappa f(\boldsymbol{\theta}_{t-1}, \beta, \gamma)) \quad (5)$$

218 where $\boldsymbol{\theta}_t$ denotes the vector of the underlying population probabilities of the three compartments, whose
 219 mean is modeled as an unknown function of the probability vector from the previous time point, along
 220 with the transition parameters. $\boldsymbol{\tau} = (\beta, \gamma, \boldsymbol{\theta}_0^T, \boldsymbol{\lambda}, \kappa)$ denotes the whole set of parameters where λ^I, λ^R and
 221 κ are parameters controlling variability of the observation and latent process, respectively. The function
 222 $f(\cdot)$ is then solved as the mean transition probability determined by the SIR dynamic system, using a
 223 fourth order Runge-Kutta approximation (25).

224 *Priors and MCMC algorithm:* The prior on the initial vector of latent probabilities is set as
 225 $\boldsymbol{\theta}_0 \sim \text{Dirichlet}(1 - Y_1^I - Y_1^R, Y_1^I, Y_1^R)$, $\theta_0^S = 1 - \theta_0^I - \theta_0^R$. The prior distribution of the basic reproduction
 226 number is lognormal such that $E(R_0) = 3.28$ (26) (this value was also confirmed by calculating the
 227 average time-varying $R(t)$ by from January 30 till March 24, 2020, using the package developed by (27)).
 228 The prior distribution of the removal rate is also lognormal such that $E(\gamma) = 0.5436$. We use the
 229 proportion of death within the removed compartment as 0.0184 so that the initial infection fatality ratio
 230 is 0.01 (28). For the variability parameters, the default choice is to set large variances in both observed
 231 and latent processes, which may be adjusted over the course of epidemic with more data becoming
 232 available: $\kappa, \lambda^I, \lambda^R \stackrel{iid}{\sim} \text{Gamma}(2, 10^{-4})$.

233 Denoting t_0 as the last date of data availability, and assuming that the forecast spans over the period
 234 $[t_0 + 1, T]$, the eSIR algorithm is as follows.

235 Step 0. Take M draws from the posterior $[\boldsymbol{\theta}_{1:t_0}, \boldsymbol{\tau} | \mathbf{Y}_{1:t_0}]$.

236 Step 1. For each solution path $m \in \{1, \dots, M\}$, iterate between the following two steps via MCMC.

237 i. Draw $\boldsymbol{\theta}_t^{(m)}$ from $[\boldsymbol{\theta}_t | \boldsymbol{\theta}_{t-1}^{(m-1)}, \boldsymbol{\tau}^{(m)}], t \in \{t_0 + 1, \dots, T\}$.

238 ii. Draw $\mathbf{Y}_t^{(m)}$ from $[\mathbf{Y}_t | \boldsymbol{\theta}_t^{(m)}, \boldsymbol{\tau}^{(m)}], t \in \{t_0 + 1, \dots, T\}$.

239 *Implementation:* We implement the proposed algorithm in R package *rjags* (29) and the differential
 240 equations were solved via the fourth-order Runge–Kutta approximation. To ensure the quality of the
 241 MCMC procedure, we fix the adaptation number (which denotes the number of MCMC samples
 242 discarded by JAGS in order to tune parameters which in turn improves speed or de-correlation of
 243 sampling) at 10^4 , thin the chain by keeping one draw from every 10 random draws to further reduce

244 autocorrelation, set a burn-in period of 10^5 draws under 2×10^5 iterations for four parallel chains. This
245 implementation provides not only posterior estimation of parameters and prevalence of all the three
246 compartments in the SIR model, but also predicts proportions of the infected and the removed people at
247 future time point(s). The R package for implementing this general model for understanding disease
248 dynamics is publicly available at <https://github.com/lilywang1988/eSIR>.

249 **2.1.c. SAPHIRE model**

250 *Overview:* This model (13) extends the classic SEIR model to estimate COVID-related transmission
251 parameters, in addition to projecting COVID-19 case counts, while accounting for pre-symptomatic
252 infectiousness, time-varying ascertainment rates (i.e. reporting rates), transmission rates and population
253 movements. *Figure 3* provides a schematic diagram of the compartments and transitions conceptualized
254 in this model. The model includes seven compartments: susceptible (S), exposed (E), pre-symptomatic
255 infectious (P), reported infectious (I), unreported infectious (A), isolation in hospital (H) and removed
256 (R). Compared with the classic SEIR model, SAPHIRE explicitly models population movement and
257 introduce two additional compartments (A and H) to account for the fact that only reported cases would
258 seek medical care and thus be quarantined by hospitalization. The model described and implemented
259 here relies on the same methodology and arguments as presented by (13). The only difference is that
260 while the original model analyzed data from China over a time period of December 2019 to March 2020
261 (which constituted the initial days of the pandemic in China), we analyze data from India. Additionally,
262 the original manuscript adjusted the model to account for population movement. Data on population
263 movement not being available consistently over time and regions in India, we make no such
264 modifications. We further note that the SAPHIRE model returns reported and unreported cumulative
265 COVID-case counts, in addition to cumulative counts of the removed compartment. As such, for the

266 purpose of comparisons, the SAPHIRE model is used only to study cumulative COVID-case counts
 267 (reported and unreported). The R package for implementing this general model for understanding disease
 268 dynamics is publicly available at <https://github.com/chaolongwang/SAPHIRE>.

269 *Formulation:* The dynamics of the 7 compartments described above at time t are described by the set of
 270 ordinary differential equations

$$271 \quad \frac{dS}{dt} = n - \frac{bS(\alpha P + \alpha A + I)}{N} - \frac{nS}{N}, \quad (6a)$$

$$272 \quad \frac{dE}{dt} = \frac{bS(\alpha P + \alpha A + I)}{N} - \frac{E}{D_e} - \frac{nE}{N}, \quad (6b)$$

$$273 \quad \frac{dP}{dt} = \frac{E}{D_e} - \frac{P}{D_p} - \frac{nP}{N}, \quad (6c)$$

$$274 \quad \frac{dA}{dt} = \frac{(1-r)P}{D_p} - \frac{A}{D_i} - \frac{nA}{N}, \quad (6d)$$

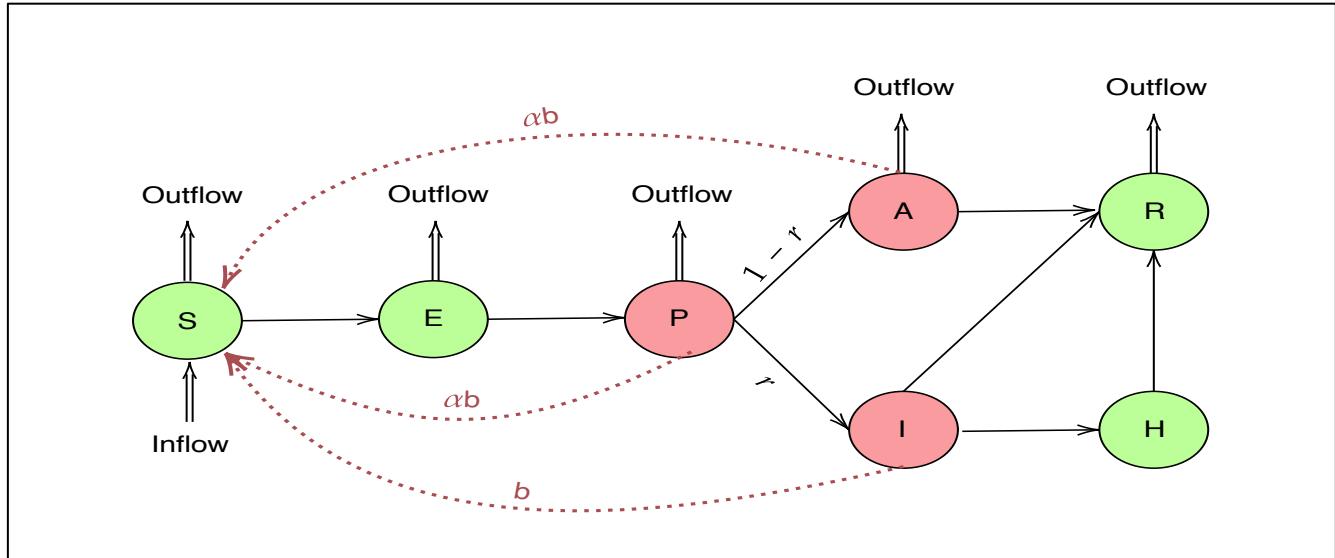
$$275 \quad \frac{dI}{dt} = \frac{rP}{D_p} - \frac{I}{D_i} - \frac{I}{D_q}, \quad (6e)$$

$$276 \quad \frac{dH}{dt} = \frac{I}{D_q} - \frac{H}{D_h}, \quad (6f)$$

$$277 \quad \frac{dR}{dt} = \frac{A + I}{D_i} + \frac{H}{D_h} - \frac{nR}{N}, \quad (6g)$$

278 in which b is the transmission rate for reported cases (defined as the number of individuals that an
 279 reported case can infect per day), α is the ratio of the transmission rate of unreported cases to that of
 280 reported cases, r is the ascertainment rate, D_e is the latent period, D_p is the pre-symptomatic infectious

281 period, D_i is the symptomatic infectiousness period, D_q is the duration from illness onset to isolation and
 282 D_h is the isolation period in the hospital. Further, we set $N = 1.34 \times 10^9$ as the population size for India
 283 and set $n = 0$ to indicate no incoming or outgoing travelers.



284

Figure 3: The SAPHIRE model includes seven compartments: susceptible (S), exposed (E), pre-symptomatic infectious (P), reported infectious (I), unreported infectious (A), isolation in hospital (H) and removed (R).

285 Under this setup, the reproductive number R (as presented in the original manuscript) may be expressed
 286 as

$$287 \quad R = ab \left(D_p^{-1} + \frac{n}{N} \right)^{-1} + (1 - r)ab \left(D_i^{-1} + \frac{n}{N} \right)^{-1} + rb(D_i^{-1} + D_q^{-1})^{-1}, \quad (7)$$

288 in which the three terms represent infections contributed by pre-symptomatic individuals, unreported
 289 cases and reported cases, respectively. The model adjusts the infectious periods of each type of case by
 290 taking isolation of patients who test positive (by means of D_q^{-1}) into account.

291 *Initial states and parameter settings:* We set $\alpha = 0.55$, assuming lower transmissibility for unreported
292 cases (30). Compartment P contains both reported and unreported cases in the pre-symptomatic phase.
293 We set the transmissibility of P to be the same as unreported cases, because it has previously been
294 reported that the majority of cases are unreported (30). We assume an incubation period of 5.2 days and
295 a pre-symptomatic infectious period $D_p = 2.3$ days (31,32). The latent period was $D_e = 2.9$ days. Since
296 pre-symptomatic infectiousness was estimated to account for 44% of the total infections from reported
297 cases (31), we set the mean of total infectious period as $(D_p + D_i) = D_p/0.44 = 5.2$ days, assuming
298 constant infectiousness across the pre-symptomatic and symptomatic phases of reported cases (33) – thus
299 the mean symptomatic infectious period was $D_i = 2.9$ days. We set a long isolation period of $D_h = 17$
300 days, based on a study investigating hospitalisation of COVID-19 patients in the state of Karnataka (34).
301 The duration from the onset of symptoms to isolation was estimated to be $D_q = 7$ (35,36) as the median
302 time length from onset to confirmed diagnosis. On the basis of the parameter settings above, the initial
303 state of the model is specified on March 15. The initial number of reported symptomatic cases $I(0)$ is
304 specified as the number of reported cases who experienced symptom onset during 12-14 March. The
305 initial ascertainment rate is assumed to be $r_0 = 0.10$ (37), and thus the initial number of unreported
306 cases is $A(0) = r_0^{-1}(1 - r_0)I(0)$. $P_1(0)$ and $E_1(0)$ denote the numbers of reported cases in which
307 individuals experienced symptom onset during 15–16 March and 17–19 March, respectively. Then, the
308 initial numbers of exposed and pre-symptomatic individuals are set as $E(0) = r_0^{-1}E_1(0)$ and $P(0) =$
309 $r_0^{-1}P_1(0)$, respectively. The initial number of the hospitalized cases $H(0)$ is set as half of the cumulative
310 reported cases on 8 March since $D_q = 7$ and there would be more severe cases among the reported cases
311 in the early phase of the epidemic.

312 *Likelihood and MCMC algorithm:* Considering the time-varying strength of control measures
 313 implemented in India over the trajectory of the pandemic, we chose to break the training period into ten
 314 sequential blocks: pre-lockdown (March 15 – 24), lockdown phases 1, 2, 3, and 4 (March 25 – April 14,
 315 April 15 – May 3, May 4 – 17, and May 18 – 31 respectively) followed by unlock phases 1, 2, 3, 4 and
 316 5 (June 1 – 30, July 1 – 31, August 1 – 31, September 1 – 30 and October 1 – 15 respectively). In other
 317 words, the model assumes that the value of b (and r) corresponding to the i^{th} lockdown period to vary
 318 as b_i (and r_i) for $i = 1, 2, 3, \dots, 10$. The observed number of reported cases in which individuals
 319 experience symptom onset on day t – denoted by x_t – is assumed to follow a Poisson distribution with
 320 rate $\lambda_t = rP_{t-1}D_p^{-1}$, with P_t denoting the expected number of pre-symptomatic individuals on day t . The
 321 following likelihood equation is used to fit the model using observed data from March 15 (T_0) to October
 322 15 (T_1).

$$L(b_1, b_2, \dots, b_{10}, r_1, r_2, \dots, r_{10}) = \prod_{t=T_0}^{T_1} \frac{e^{-\lambda_t} \lambda_t^{x_t}}{x_t!},$$

323 and the model is used to predict COVID-counts from October 16 to December 31. A non-informative
 324 prior of $U(0,2)$ is used for b_1, b_2, \dots, b_{10} . For r_1 , an informative prior of Beta(10, 90) is used based on
 325 the findings of (37). We reparameterise r_2, \dots, r_{10} as
 326

$$\text{logit}(r_i) = \text{logit}(r_{i-1}) + \delta_i \text{ for } i = 2, 3, \dots, 10$$

327 where $\text{logit}(t) = \log(t/(1-t))$ is the standard logit function. In the MCMC, $\delta_i \sim N(0,1)$ for $i =$
 328 2, 3, ..., 10. A burn-in period of 100,000 iterations is fixed, with a total of 200,000 iterations being run.
 329

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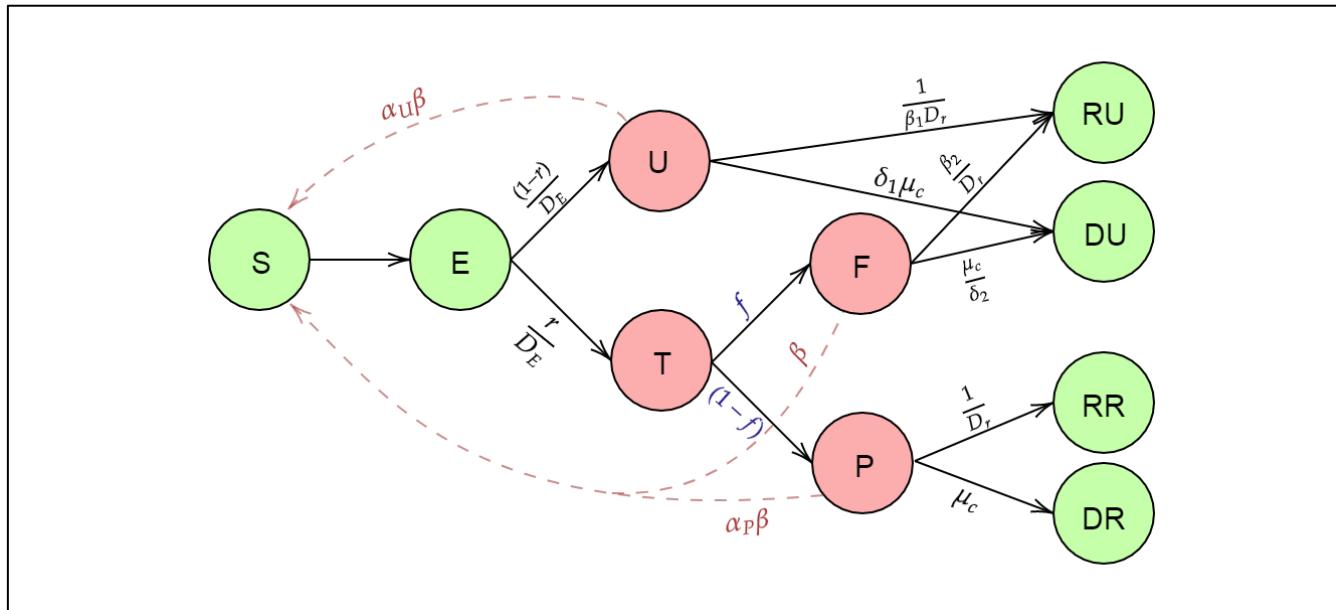
331 **2.1.d. SEIR-fansy model**

332 *Overview:* One of the problems with applying a standard SIR model in the context of the COVID-19
333 pandemic is the presence of a long incubation period. As a result, extensions of SIR model like the SEIR
334 model are more applicable. In the previous subsection, we have seen an extension which includes the
335 ‘pre-symptomatic infectious’ compartment (people who are infected at time t and contributing to the
336 spread of the virus, but do not show any symptom yet). In the SEIR-fansy model, we use an alternate
337 formulation by defining an ‘untested infectious’ compartment for infected people who are spreading
338 infection but are not tested after the incubation period. This compartment is necessary because there is a
339 large proportion of infected people who are not being tested (a part of them are asymptomatic or mildly
340 symptomatic but for a country like India there are other reasons like access to care and stigma that can
341 prevent someone from getting tested/diagnosed). We have assumed that after the ‘exposed’ compartment,
342 a person enters either the ‘untested infectious’ compartment or the ‘tested infectious’ compartment. To
343 incorporate the possible effect of misclassifications due to imperfect testing, we include a compartment
344 for false negatives (infected people who are tested but reported as negative). As a result, after being
345 tested, an infected person enters either into the ‘false negative’ compartment or the ‘tested positive’
346 compartment (infected people who are tested and reported to be positive). We keep separate
347 compartments for the recovered and deceased persons coming from the untested and false negatives
348 compartments which are ‘recovered unreported’ and ‘deceased unreported’ respectively. For the ‘tested
349 positive’ compartment, the recovered and the death compartments are denoted by ‘recovered reported’
350 and ‘deceased reported’ respectively. Thus, we divide the entire population into ten main compartments:
351 S (Susceptible), E (Exposed), T (Tested), U (Untested), P (Tested positive), F (Tested False Negative),

352 RR (Reported Recovered), RU (Unreported Recovered), DR (Reported Deaths) and DU (Unreported
353 Deaths). This model is implemented using the R package SEIRfansy (38).

354 *Formulation:* Like most compartmental models, this model assumes exponential times for the duration
355 of an individual staying in a compartment. For simplicity, we approximate this continuous-time process
356 by a discrete-time modeling process. The main parameters of this model are β (rate of transmission of
357 infection by false negative individuals), α_p (scaling factor that measures the rate of spread of infection
358 by patients who test positive for COVID-19 relative to infected patients who return false negative test
359 results), α_u (scaling factor for the rate of spread of infection by untested individuals), D_e (incubation
360 period in days), D_r (mean days till recovery for positive individuals), D_t (mean number of days for the
361 test result to come after a person is being tested), μ_c (death rate due to COVID-19 which is the inverse
362 of the average number of days for death due to COVID-19 starting from the onset of disease multiplied
363 by the probability death of an infected individual due to COVID), λ and μ (natural birth and death rates
364 respectively, assumed to be equal for the sake of simplicity), r (probability of being tested for infectious
365 individuals), f (false negative probability of RT-PCR test), β_1 and β_2^{-1} (scaling factors for rate of
366 recovery for undetected and false negative individuals respectively), δ_1 and δ_2^{-1} (scaling factors for
367 death rate for undetected and false negative individuals respectively). The number of individuals at the
368 time point t in each compartment is governed by the system of differential equations given by Equations
369 (8a) – (8i). To simplify this model, we assume that testing is instantaneous. In other words, we assume
370 there is no time difference from the onset of the disease after the incubation period to getting test results.
371 This is a reasonable assumption to make as the time for testing is about 1-2 days which is much less than
372 the mean duration of stay for the other compartments. Further, once a person shows symptoms for

373 COVID-19 like diseases, they are sent to get tested almost immediately. *Figure 4* provides a schematic
 374 overview of the model.



375

Figure 4: Schematic diagram for the SEIR-fansy model with imperfect testing and misclassification. The model has ten compartments: S (Susceptible), E (Exposed), T (Tested), U (Untested), P (Tested positive), F (Tested False Negative), RR (Reported Recovered), RU (Unreported Recovered), DR (Reported Deaths) and DU (Unreported Deaths). Reproduced from Bhaduri, Kundu et al., 2020 (18).

376 The following differential equations summarize the transmission dynamics being modeled.

377

$$\frac{\partial S}{\partial t} = -\beta \frac{S(t)}{N} (\alpha_P P(t) + \alpha_U U(t) + F(t)) + \lambda N - \mu S(t), \quad (8a)$$

378

$$\frac{\partial E}{\partial t} = \beta \frac{S(t)}{N} (\alpha_P P(t) + \alpha_U U(t) + F(t)) - \frac{E(t)}{D_e} - \mu E(t), \quad (8b)$$

379

$$\frac{\partial U}{\partial t} = (1 - r) \frac{E(t)}{D_e} - \frac{U(t)}{\beta_1 D_r} - \delta_1 \mu_c U(t) - \mu U(t), \quad (8c)$$

380
$$\frac{\partial P}{\partial t} = (1-f)r \frac{E(t)}{D_e} - \frac{P(t)}{D_r} - \mu_c P(t) - \mu P(t), \quad (8d)$$

381
$$\frac{\partial F}{\partial t} = fr \frac{E(t)}{D_e} - \frac{\beta_2 F(t)}{D_r} - \frac{\mu_c F(t)}{\delta_2} - \mu F(t), \quad (8e)$$

382
$$\frac{\partial RU}{\partial t} = \frac{U(t)}{\beta_1 D_r} + \frac{\beta_2 F(t)}{D_r} - \mu RU(t), \quad (8f)$$

383
$$\frac{\partial RR}{\partial t} = \frac{P(t)}{D_r} - \mu RR(t), \quad (8g)$$

384
$$\frac{\partial DU}{\partial t} = \delta_1 \mu_c U(t) + \frac{\mu_c F(t)}{\delta_2}, \quad (8h)$$

385
$$\frac{\partial DR}{\partial t} = \mu_c P(t). \quad (8i)$$

386 Using the Next Generation Matrix Method (39), we calculate the basic reproduction number

387
$$R_0 = \frac{\beta S_0}{\mu D_e + 1} \left(\frac{\alpha_U (1-r)}{\frac{1}{\beta_1 D_r} + \delta_1 \mu_c + \mu} + \frac{\alpha_P r (1-f)}{\frac{1}{D_r} + \mu_c + \mu} + \frac{rf}{\frac{\beta_2}{D_r} + \frac{\mu_c}{\delta_2} + \mu} \right), \quad (9)$$

388 where $S_0 = \lambda/\mu = 1$ since we assume that natural birth and death rates are equal within this short period

389 of time. *Supplementary Table S1* describes the parameters in greater detail.

390 *Likelihood assumptions and estimation:* Parameters are estimated using Bayesian estimation techniques

391 and MCMC methods (namely, Metropolis-Hastings method (40) with Gaussian proposal distribution).

392 First, we approximated the above set of differential equations by a discrete time approximation using

393 daily differences. After we start with an initial value for each of the compartments on the day 1, using

394 the discrete time recurrence relations we obtain the counts for each of the compartments at the next days.
 395 To proceed with the MCMC-based estimation, we specify the likelihood explicitly. We assume
 396 (conditional on the parameters) the number of new confirmed cases on day t depend only on the number
 397 of exposed individuals on the previous day. Specifically, we use multinomial modeling to incorporate
 398 the data on recovered and deceased cases as well. The joint conditional distribution is

$$\begin{aligned}
 399 \quad & P[P_{new}(t), RR_{new}(t), DR_{new}(t)|E(t-1), P(t-1)] \\
 400 \quad & = P[P_{new}(t)|E(t-1), P(t-1)].P[RR_{new}(t), DR_{new}(t)|E(t-1), P(t-1)] \\
 401 \quad & = P[P_{new}(t)|E(t-1)].P[RR_{new}(t), DR_{new}(t)|P(t-1)].
 \end{aligned}$$

402 A multinomial distribution-like structure is then defined

$$403 \quad P_{new}(t)|E(t-1) \sim Bin(E(t-1), r(1-f)/D_e) \quad (10a)$$

$$404 \quad RR_{new}(t), DR_{new}(t)|P(t-1) \sim Mult(P(t-1), (D_r^{-1}, \mu_c, 1 - D_r^{-1} - \mu_c)) \quad (10b)$$

405 Note: the expected values of $E(t-1)$ and $P(t-1)$ are obtained by solving the discrete time differential
 406 equations specified by Equations (8a) – (8i).

407 *Prior assumptions and MCMC:* For the parameter r , we assume a $U(0,1)$ prior, while for β , we assume
 408 an improper non-informative flat prior with the set of positive real numbers as support. After specifying
 409 the likelihood and the prior distributions of the parameters, we draw samples from the posterior
 410 distribution of the parameters using the Metropolis-Hastings algorithm with a Gaussian proposal
 411 distribution. We run the algorithm for 200,000 iterations with a burn-in period of 100,000. Finally, the
 412 mean of the parameters in each of the iterations are obtained as the final estimates of β and r for the
 413 different time periods. As in the case of the SAPHIRE model, we again break the training period into ten

414 sequential blocks: pre-lockdown (March 15 – 24), lockdown phases 1, 2, 3, and 4 (March 25 – April 14,
415 April 15 – May 3, May 4 – 17, and May 18 – 31 respectively) followed by unlock phases 1, 2, 3, 4 and
416 5 (June 1 – 30, July 1 – 31, August 1 – 31, September 1 – 30 and October 1 – 15 respectively).

417 **2.1.e. Imperial College London model (ICM)**

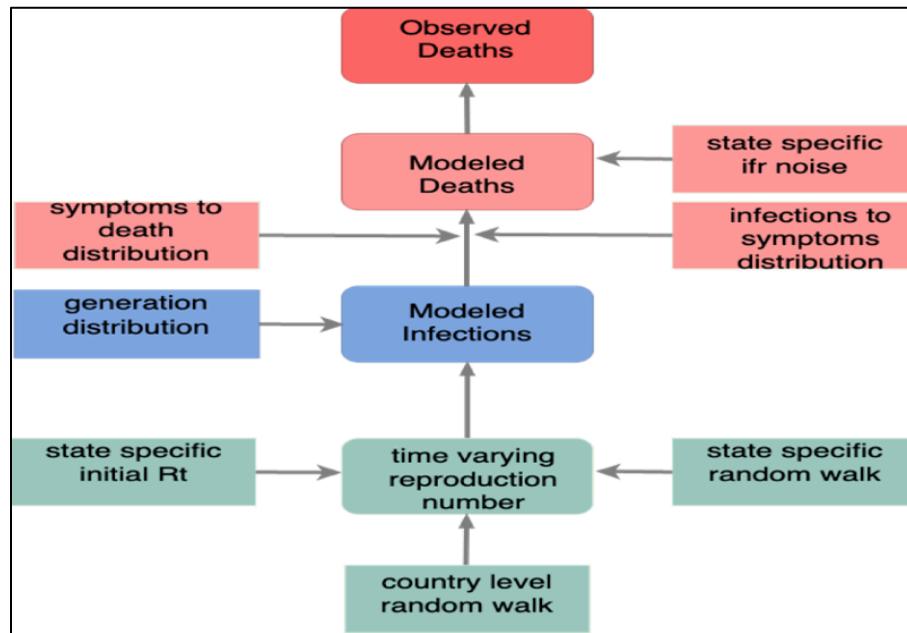
418 *Overview:* We examine a Bayesian semi-mechanistic model for estimating the transmission intensity of
419 SARS-CoV-2 (7). The model defines a renewal equation using the time-varying reproduction number R_t
420 to generate new infections. As a lot of cases in SARS-CoV-2 are asymptomatic and reported case data is
421 unreliable especially in early part of the epidemic in India, the model relies on observed deaths data and
422 calculates backwards to infer the true number of infections. The latent daily infections are modeled as
423 the product of R_t with a discrete convolution of the previous infections, weighted using an infection-to-
424 transmission distribution specific to SARS-CoV-2. We implement this Bayesian semi-mechanistic model
425 in the context of COVID-19 data arising from India in order to estimate the reproduction number over
426 time, along with plausible upper and lower bounds (95% Bayesian credible intervals (CrI)) of the daily
427 infections and the daily number of infectious people. We parametrize R_t with a fixed effect and a random
428 effect for each week over the course of the epidemic for each state. The fixed effect accounts for the
429 variations in R_t across India as a whole whereas the random effect allows for variations among different
430 states. The weekly effects are encoded as a random walk, where at each successive step the random effect
431 has an equal chance of moving upwards or downwards from its current value. The model is implemented
432 using epidemia (41), a general purpose R package for semi-mechanistic Bayesian modelling of
433 epidemics. *Figure 5* represents a schematic overview of the model.

434 *Formulation:* The true number of infected individuals, i , is modelled using a discrete renewal process.
 435 We specify a generation distribution (42) g with density $g(\tau)$ as $g \sim \text{Gamma}(6.5, 0.62)$. Given the
 436 generation distribution, the number of infections $i_{t,m}$ on a given day t , and state m is given by the
 437 discrete convolution function:

$$438 \quad i_{t,m} = S_{t,m} R_{t,m} \sum_{\tau=0}^{t-1} i_{\tau,m} g_{t-\tau}, \quad (11a)$$

$$439 \quad S_{t,m} = 1 - \frac{\sum_{j=0}^{t-1} i_{j,m}}{N_m}, \quad (11b)$$

440 where the generation distribution is discretized by $g_s = \int_{s-0.5}^{s+0.5} g(\tau) d\tau$ for $s = 2, 3, \dots$, and $g_1 =$
 441 $\int_0^{1.5} g(\tau) d\tau$. The population of state m is denoted by N_m . We include the adjustment factor $S_{t,m}$ to
 442 account for the number of susceptible individuals left in the population.



443 *Figure 5: Schematic overview of ICM.*

444 We define daily deaths, $D_{t,m}$, for days $t \in \{1, \dots, n\}$ and states $m \in \{1, \dots, M\}$. These daily deaths are
 445 modelled using a positive real-valued function $d_{t,m} = E[D_{t,m}]$ that represents the expected number of
 446 deaths attributed to COVID-19. The daily deaths $D_{t,m}$ are assumed to follow a negative binomial
 447 distribution with mean $d_{t,m}$ and variance $d_{t,m} + d_{t,m}^2/\psi_1$, where ψ_1 follows a positive half normal
 448 distribution, i.e.,

$$449 \quad D_{t,m} \sim NB(d_{t,m}, d_{t,m} + d_{t,m}^2/\psi_1), \quad t = 1, \dots, n, \quad (12a)$$

$$450 \quad \psi_1 \sim N^+(0,5). \quad (12b)$$

451 We link our observed deaths mechanistically to transmission (7). We use a previously estimated COVID-
 452 19 infection fatality ratio (IFR, probability of death given infection) of 0.1% (43,44) together with a
 453 distribution of times from infection to death π . To incorporate the uncertainty inherent in this estimate
 454 we modify the ifr for every state to have additional noise around the mean, denoted by ifr_m^* . Specifically,
 455 we assume

$$456 \quad \text{ifr}_m^* \sim \text{ifr} \cdot N(1, 0.1), \quad (13)$$

457 where ifr_m^* represents the noise-added analog of ifr . Using estimated epidemiological information from
 458 previous studies, we assume the distribution of times from infection to death π (infection-to-death) to
 459 be the convolution of an infection-to-onset distribution (π') (45) and an onset-to-death distribution (28)

$$460 \quad \pi \sim \text{Gamma}(5.1, 0.86) + \text{Gamma}(17.8, 0.45). \quad (14)$$

461 The expected number of deaths $d_{t,m}$, on a given day t , for state m is given by the following discrete sum

$$462 \quad d_{t,m} = \text{ifr}_m^* \sum_{\tau=0}^{t-1} i_{\tau,m} \pi_{t-\tau}, \quad (15)$$

463 where $i_{\tau,m}$ is the number of new infections on day τ in state m and where, similar to the generation
464 distribution, π is discretized via $\pi_s = \int_{s-0.5}^{s+0.5} \pi(\tau) d\tau$ for $s = 2, 3, \dots$, and $\pi_1 = \int_0^{1.5} \pi(\tau) d\tau$, where $\pi(\tau)$
465 is the density of π .

466 We parametrize $R_{t,m}$ with a random effect for each week of the epidemic as follows

467
$$R_{t,m} = R_0 \cdot f(-\epsilon_{w(t,m)} - \epsilon_{m,w(t,m)}^{state}), \quad (16)$$

468 where $f(x) = 2 \exp(x) / (1 + \exp(x))$ is twice the inverse logit function, and $\epsilon_{w(t)}$ and
469 $\epsilon_{m,w(t,m)}^{state}$ follow a weekly random walk process, that captures variation between $R_{t,m}$ in each subsequent
470 week. $\epsilon_{w(t)}$ is a fixed effect estimated across all the states and $\epsilon_{m,w(t,m)}^{state}$ is the random effect specific to
471 each state in India. The prior distribution for R_0 (26) was chosen to be

472
$$R_0 \sim N(3.28, 0.5). \quad (17)$$

473 We assume that seeding of new infections begins 30 days before the day after a state has cumulatively
474 observed 10 deaths. From this date, we seed our model with 6 sequential days of an equal number of
475 infections: $i_1 = \dots = i_6 \sim \text{Exponential}(\tau^{-1})$, where $\tau \sim \text{Exponential}(0.03)$. These seed infections are
476 inferred in our Bayesian posterior distribution. Fitting was done with the R package *epidemia* (41) which
477 uses STAN (46), a probabilistic programming language, using an adaptive Hamiltonian Monte Carlo
478 (HMC) sampler.

479

480 **2.2 Comparing models and evaluating performance**

481 Having established differences in the formulation of the different models, we compare their respective
482 projections and inferences. In order to do so, we use the same data sources (47)-(48) for all five models.

483 Well-defined time points are used to denote training (March 15 to October 15) and test (October 16 to
484 December 31) periods.

485 Using the parameter values specified above along with data from the training period as inputs, we
486 compare the projections of the five models with observed data from the test period. In order to do so, we
487 use the symmetric mean absolute prediction error (SMAPE) and mean squared relative prediction error
488 (MSRPE) metrics as measures of accuracy. Given observed time-varying data $\{O_t\}_{t=1}^T$ and an analogous
489 time-series dataset of projections $\{P_t\}_{t=1}^T$, the SMAPE metric is defined as

$$490 \quad SMAPE(T) = \frac{100}{T} \cdot \sum_{t=1}^{t=T} \frac{|P_t - O_t|}{(|P_t| + |O_t|)/2}, \quad (18)$$

491 where $|x|$ denotes the absolute value of x . The metric MSRPE is defined as

$$492 \quad MSRPE(T) = \left[T^{-1} \sum_{t=1}^T \left(1 - \frac{P_t}{O_t} \right)^2 \right]^{1/2}. \quad (19)$$

493 It can be seen that $0 \leq SMAPE \leq 100$, with smaller values of both MSRPE and SMAPE indicating a
494 more accurate fit. For active reported cases (cases that are active on a given day which is the difference
495 of cumulative reported cases and cumulative reported counts of recoveries and deaths), we compute and
496 compare the metrics defined above for projections from eSIR and SEIR-fansy models as no other model
497 returns relevant projections. For cumulative reported cases we obtain projections from all models apart
498 from ICM (which yields total, i.e., sum of reported and unreported, cumulative cases). For cumulative
499 reported deaths we compare projections from eSIR, SEIR-fansy and ICM, since the baseline and
500 SAPHIRE models do not yield relevant projections. *Supplementary Table S2* gives an overview of output
501 from each of the models we consider and *Table 2* reports the values of accuracy metrics described above.

502 Further, we compare (when possible) the estimated time-varying reproduction number $R(t)$ over the
503 different lockdown and unlock stages in India. Specifically, for each lockdown stage, we report the
504 median $R(t)$ value along with the associated 95% credible interval (CrI). The values are presented in
505 *Table 2*.

506 Since we are interested in comparing relative performances of the models (specifically, their projections),
507 we define another metric – the relative mean squared prediction error (Rel-MSPE). Given time series
508 data on observed cumulative cases (or deaths) $\{O_t\}_{t=1}^T$, projections from a model A $\{P_t^A\}_{t=1}^T$, and
509 projections from some other model B, $\{P_t^B\}_{t=1}^T$, the Rel-MSPE of model B with respect to model A is
510 defined as

$$511 \quad Rel-MSPE(B:A) = \left[\sum_{t=1}^T \left(\frac{O_t - P_t^A}{O_t - P_t^B} \right)^2 \right]^{1/2} \quad (20)$$

512 Higher values of Rel-MSPE(B:A) indicate better performance of model B over model A. Since the
513 baseline model yields projections of cumulative reported cases, we compute Rel-MSPE for the other
514 models with respect to the baseline model for reported cumulative cases. Projections from ICM represent
515 total (i.e., sum of reported and unreported) cumulative cases and are left out of this comparison of
516 reported counts. For cumulative reported deaths, we compute Rel-MSPE of the SEIR-fansy and ICM
517 models relative to the eSIR model. In addition to comparing the accuracy of fits that arise from the
518 different models, we also investigate if projections from the different models are correlated with observed
519 data. We use the standard Pearson's correlation coefficient and Lin's concordance correlation coefficient
520 (49) as summary measures to study said correlation. Higher values of these correlation metrics indicate
521 better concordance of model projections and the observed data from the test period. Rel-MSPE and

522 correlation metrics are presented in *Table 3*. Since we have projections for total (sum of reported and
523 unreported cases) for active cases from SEIR-fansy, for cumulative cases from SAPHIRE, SEIR-fansy
524 and ICM, and for cumulative deaths from SEIR-fansy, we present the projected totals along with 95%
525 credible intervals and associated underreporting factors on three specific dates – October 31, November
526 30 and December 31 in *Table 4*. The table also includes projected cumulative reported counts (which are
527 available from all models under investigation apart from ICM) with 95% credible intervals for the three
528 dates mentioned above.

529 **2.3 Data source**

530 The data on confirmed cases, recovered cases and deaths for India and the 20 states of interest are taken
531 from COVID-19 India (47) and the JHU CSSE COVID-19 GitHub repository (48). In addition to this
532 and other similar articles concerning the spread of this disease in India, we have created an interactive
533 dashboard (50) summarizing COVID-19 data and forecasts for India and its states (generated with the
534 eSIR model discussed in this paper). While the models are trained using data from March 15 to October
535 15, 2020, their performances are compared by examining their respective projections from October 16
536 to December 31, 2020.

537

538 **3. RESULTS**

539 **3.1. Estimation of the reproduction number**

540 From *Table 2*, we compare the mean of the time-varying effective reproduction number $R(t)$ over the
541 four phases of lockdown and subsequent unlock phased in India. The eSIR model returns a mean value

542 of 2.08 (95% credible interval: 1.41– 2.12) over the entire training period. Factoring in different levels
543 of government interventions which modified transmission dynamics during lockdown, we get period
544 specific estimates ranging from 2.12 (1.44 – 2.16) in lockdown phase 1, which drops to 1.48 (1.00 – 1.51)
545 in lockdown phase 2 and then reports a steady decline over the subsequent lockdown and unlock phases.
546 The mean values returned by the SAPHIRE model varied from 2.54 (2.41 – 2.74) during phase 1 of the
547 lockdown, 1.60 (1.36 – 2.17) for phase 2, 1.69 (1.46 – 1.97) for phase 3 and 1.54 (1.29 – 2.00) for the
548 fourth and final lockdown phase. The estimated values for subsequent unlock phases are quite close to
549 each other, starting from 1.27 (1.19 – 1.32) in unlock phase 1 and dropping to 1.09 (0.91– 1.69) in the
550 fifth unlock phase. The SEIR-fansy notes that the mean $R(t)$ drops from 5.03 (5.01 – 5.04) during the
551 first phase of lockdown, to 1.90 (1.89 – 1.91) during the second lockdown phase, before rising again to
552 2.33 (2.30 – 2.36) during lockdown phase 4. The estimated mean drops steadily from 1.80 (1.79 – 1.81)
553 during unlock phase 2 to 0.86 (0.85 – 0.87) during unlock phase 5. The ICM-based mean values fluctuate,
554 from 1.77 (1.58 – 1.96) during the first lockdown phase, followed by 1.22 (1.18 – 1.27), then dropping
555 to 1.33 (1.28 – 1.38) and finally rising to 1.41 again (1.35 – 1.47) for the fourth phase of lockdown.
556 Estimates from ICM during unlock phases behave like those from the SEIR-fansy model – in unlock
557 phase 2 the estimated mean is 1.11 (1.08 – 1.14) and in unlock phase 5, the mean is 0.83 (0.82 – 0.84).
558 In terms of agreement of reported values, SAPHIRE, SEIR-fansy and ICM report the highest mean R for
559 phase one of the lockdown. Values reported by SAPHIRE, SEIR-fansy and ICM report a drop in
560 intermediate lockdown phases, followed by a rise. Values during unlock period increase from phase 1 to
561 phase 2, followed by a steady decline. SAPHIRE, SEIR-fansy and ICM report the lowest value of R for
562 unlock phase 5.

563 ***3.2 Estimation of reported case counts***

564 From *Figure 6* and *Figure 9*, we note that the eSIR model overestimates the count of active cases – a
565 behavior which gets worse with time. While the observed counts decrease steadily in the test period, the
566 eSIR model fails to capture this behaviour and returns projections which rise over time. In comparison,
567 the SEIR-fansy model is able to replicate the decreasing behaviour but yields projections which are
568 higher than observed counts. In terms of prediction accuracy, the SEIR-fansy model has an SMAPE
569 value of 35.14% and an MSRPE value of 1.11. For eSIR model, those values are at 37.96% (SMAPE)
570 and 2.28 (MSRPE).

571 From *Figure 7* and *Figure 10* we note that while the SAPHIRE model underestimates the count of
572 cumulative cases, the baseline, eSIR and SEIR-fansy models overestimate the count. *Table 2* reveals that
573 SAPHIRE performs the best in terms of SMAPE metric with a value of 2.25%, followed closely by
574 SEIR-fansy (2.29%). The eSIR and baseline models perform poorly in comparison, yielding 6.59% and
575 6.89% respectively. The SEIR-fansy model performs best in terms of MSRPE with a value of 0.05,
576 followed closely by SAPHIRE (0.06). *Table 3* further reveals a similar relative performance through Rel-
577 MSPE values (all Rel-MSPE figures reported here are relative to the baseline model). The SEIR-fansy
578 model performs the best with Rel-MSPE value of 3.27, followed by SAPHIRE (3.01), and finally, the
579 eSIR model (1.72). All four sets of projections are highly correlated with the observed time series – with
580 all model projections having a Pearson’s correlation coefficient of nearly 1 with the observed data. Lin’s
581 concordance coefficient yields an ordering (from worst to best) of the eSIR model (0.48), followed by
582 the baseline model (0.51), the SAPHIRE model (0.74) and finally, the SEIR-fansy model (0.89).

583 **3.3. Estimation of reported death counts**

584 From *Figure 8* and *Figure 11*, we note that the eSIR and SEIR-fansy models almost always overestimate,
585 whereas the ICM model slightly underestimates the confirmed cumulative death counts. From *Table 2*

586 and Table 3, the SMAPE and MSRPE values, along with comparison of projections with observed data
587 reveal that the ICM model is most accurate (SMAPE: 0.77%, MSRPE: 0.020), followed by SEIR-fansy
588 (SMAPE: 4.74%, MSRPE: 0.12) followed by the eSIR model (SMAPE: 8.94%, MSRPE: 0.25). Relative
589 to the eSIR model, the Rel-MSPE values of the models reveal that the SEIR-fansy model performs better
590 (Rel-MSPE: 6.96), followed by ICM (Rel-MSPE: 3.64). Judging by values of Pearson's correlation
591 coefficient, all three sets of projections are highly correlated with the observed data. Lin's concordance
592 coefficient yields an ordering (from best to worst) of ICM (0.96), followed by SEIR-fansy (0.62) and
593 finally eSIR (0.34).

594 **3.4. Estimation of unreported case and death counts**

595 From Table 4, we note that the SEIR-fansy model yields underreporting factors of about 10 for active
596 cases on October 31, November 30 and December 31. Further, we observe that the SAPHIRE model
597 projects the maximum count of total cumulative cases on the above three dates, followed by the SEIR-
598 fansy and then ICM. SAPHIRE returns under-reporting factors of the order of approximately 65, while
599 SEIR-fansy and ICM return under-reporting factors which are approximately 7 and 4 respectively. For
600 cumulative deaths, SEIR-fansy estimates underreporting factors approximately equal 3.

601 **3.5 Uncertainty quantification of estimates and predictions**

602 From Figure 12 we observe that the width of 95% credible intervals associated with projections from
603 each of the models vary significantly. While the eSIR model consistently returns the widest intervals,
604 SEIR-fansy has the narrowest intervals. In case of cumulative counts, the ordering (best to worst) starts
605 with SEIR-fansy, followed by the baseline, followed by SAPHIRE and finally the eSIR model. For
606 cumulative deaths, the ordering (best to worst) starts with SEIR-fansy, followed by ICM and finally

607 eSIR. From *Table 4*, we compare projections of reported cumulative cases for each model (apart from
608 ICM which returns projections of cumulative total cases and not cumulative reported cases) and their
609 associated prediction intervals on October 31, November 30 and December 31, 2020. On October 31, we
610 observe 8.18 million cumulative reported cases, while the projections (in millions) from the baseline
611 model are 8.71 (95% credible interval: 8.63 – 8.80), while eSIR yields 8.35 (7.19 – 9.60), SAPHIRE
612 returns 8.17 (7.90 – 8.52) and SEIR-fansy projects 8.51 (8.18 – 8.85) million cases. We do not present
613 our projections for November 30 and December 31, 2020 here in the interest of conciseness.

614

615 **4. SENSITIVITY ANALYSES AND PERFORMANCE IN OTHER COUNTRIES**

616 Sensitivity analyses for some of the discussed models have been carried out in several other publications.
617 In the interest of conciseness, we refer to said publications and comment on what parameters are central
618 to estimation and generating projections for the models examined here. We also include information on
619 how these models have performed in the context of data from other countries.

620 **4.1 eSIR**

621 Evaluation of the model results in terms of their sensitivity to initial parameter choices and under-
622 reporting and clustering issues within the data have been discussed in the context of India in prior
623 literature (51). The range of scenarios considered earlier include 10-fold underreporting of cases,
624 clustering of cases in metropolitan areas, and prior mean of R_0 ranging from 2-4 (See Supplementary
625 Table S3). Even though the posterior estimates and predictions changed in scale to some extent across
626 these scenarios, they did not significantly change the broad conclusions. It is undeniable that the exact
627 predicted case counts are sensitive to the choice of priors, but with new data coming in over a longer

628 time frame, as seen in the results from this work, the model is capable of washing out the prior effects in
629 the posterior outcomes.

630 The eSIR model has been successfully implemented and utilized in the context of COVID-19 across
631 different geographical locations, including China (52–54), Poland (55), Italy (52), Bangladesh and
632 Pakistan (56). These countries cover a broad range in terms of socio-economic status, health
633 infrastructure and pandemic management strategies. In each of these cases the eSIR model was seen to
634 be successfully capturing the patterns of growth of the pandemic via estimated parameters, as well as
635 efficiently forecasting future case counts via predictive modeling.

636 **4.2. SAPHIRE**

637 We conducted the sensitivity analysis (results not shown) by changing the initial parameters as 20%
638 lower or higher than the specified values in the SAPHIRE model. The estimated R and ascertainment
639 rates were robust to misspecification of the duration from the onset of symptoms to isolation and of the
640 relative transmissibility of unreported versus reported cases. R estimates were positively correlated with
641 the specified latent and infectious periods, and the estimated ascertainment rates were positively
642 correlated with the specified ascertainment rate in the initial state. This finding is consistent with
643 sensitivity analyses of the SAPHIRE model implemented in Wuhan (13). The estimated ascertainment
644 rates were positively correlated with the specified ascertainment rate in the initial state while the under-
645 reported factors were negatively associated with initial ascertainment. The estimated under-reported
646 factor on October 31 (see Table 4) decreases dramatically from 117 to 0.07 with the initial ascertainment
647 rate increasing from 0.07 to 0.14, with an initial ascertainment rate of 0.10 providing the best fit, which
648 is presented in this article.

649 The SAPHIRE model was originally developed in the context of data from China and was successfully
650 able to delineate the transmission dynamics of COVID-19 in Wuhan (13) and in South Africa (57).

651 **4.3 SEIR-fansy**

652 In the paper, we fix most parameters in our model and examine transmission dynamics only through β
653 and r . It is necessary to design and implement a sensitivity analysis focusing on various combinations of
654 the parameters that were previously fixed. The details of the sensitivity analyses are described in detail
655 in (18). The basic findings from the sensitivity analyses are summarized as follows. We observe that the
656 predictions for the reported active cases (P) remains same for all parameter choices. The estimates for
657 R_0 mainly differ in the first period, although some variation is noted for the second period as well.
658 However, the estimated R are almost the same for the later stages of the pandemic in the different models.
659 For the untested cases, in some of the settings of our analysis, there are substantial deviations from the
660 true numbers. The total number of active cases (which include both the unreported and the reported cases)
661 also varies substantially with different parameter values. Consequently, we note how the estimation of
662 unreported cases is sensitive to different choices for the parameter values. In particular, we see different
663 values of E_0 have the most impact on our sensitivity analysis, while different choices of D_E have the least
664 impact.

665 The SEIR-fansy model has not been run for different countries, but it has been implemented for most
666 Indian states separately (18) which showed that the model was able to capture the transmission dynamics
667 of COVID-19 in most states of India quite efficiently. For instance, this model was able to match the
668 sero-survey results of Delhi quite well (43). For other states, the predicted reported cases came out to be

669 quite close to the observed reported cases (with observed cases lying within the credible interval of
670 projections).

671 **4.4. ICM**

672 The parameters critical to the estimation and projection methods include the infection-to-death
673 distribution (28), infection fatality ratio (43,44), generation distribution (42), prior for R_0 (7,26) and
674 seeding (7). Researchers have performed sensitivity analysis for various choices of infection-to-death
675 distribution and found the resultant projections to be robust under changes (7). We used a range of values
676 for our prior of IFR, with mean 1%, 0.4% and 0.1%. We found that the model fits and estimated R_t are
677 more or less the same for all three choices but certainly our estimates for total infections changes. This
678 implies the ascertainment of cases (positive results) will be affected. Sensitivity analyses towards the
679 choice of the generation distribution was performed by other researchers (7) who found the models to be
680 robust against various choices. It has a very minimal effect on the estimation of time varying reproduction
681 number and total infections by the model. We used the R_0 prior suggested in both (7,26). We did run
682 sensitivity on a few other choices and found that our prior choice affected the inferred R_t values for only
683 the first few days and subsequent dynamics are the same irrespective of the choice. Finally, as discussed
684 in (7) we validated our seeding scheme through an importance sampling leave-one-out cross validation
685 scheme (58,59).

686 Different versions of ICM model has been applied to 11 European countries in (7). On a subregional
687 basis the model is used in the USA (60), Brazil (20,61) and Italy (21). At a local level work the model is
688 used for producing daily estimates for all local and regions in the UK (62,63). It is also used by Scotland
689 government (64) and New York State government (65).

690

691 **4. DISCUSSION**

692 In this comparative paper we have described five different models of various stochastic structures that
693 have been used for modeling SARS-CoV-2 disease transmission in various countries across the world.
694 We applied them to a case-study in modeling the full disease transmission of the coronavirus in India.
695 While simulation studies are the only gold standard way to compare the accuracy of the models, here we
696 were uniquely poised to compare the projected case-counts and death-counts against observed data on a
697 test period. We learned several things from these models. While the estimation of the reproduction
698 number is relatively robust across the models, the prediction of active and cumulative number of cases
699 and cumulative deaths show variation across models. Our findings in terms of estimates of $R(t)$ are
700 reflective of the national and state-level implementations of four lockdown phases (66) which are
701 summarized in Supplementary Table S4. The largest variability across models is observed in predicting
702 the “total” number of infections including reported and unreported cases. The degree of underreporting
703 has been a major concern in India and other countries (67). We note from *Table 4* that the underreporting
704 factor from SAPHIRE is much higher than those reported by SEIR-fansy and ICM. This may be
705 attributed to the fact that SEIR-fansy and ICM both fit daily reported deaths with a pre-specified death
706 rate (which is higher than that for unreported cases), SAPHIRE does not include daily reported death
707 counts in the likelihood function. Additionally, SEIR-fansy also considered the false positive/negative
708 rates of tests and the selection bias in testing, which also contribute to more accurate unreported case
709 projections along with untested infectious case counts. With a comprehensive exposition and a single
710 beta-testing case-study we hope this paper will be useful to understand the mathematical nuance and the
711 differences in terms of deliverables for the models.

712 There are several limitations to this work. First and foremost, all model estimates are based on a scenario
713 where we assumed no change in either interventions or behavior of people in the forecast period. This is
714 not true as there is tremendous variation in policies across Indian states in the post lockdown phase. We
715 did observe regional lockdowns that were enacted in the forecast period. None of our models tried to
716 capture this variability. Second, the five models we compare are a subset of a vast amount of work that
717 has been done in this area, including models that incorporate age-specific contact network and
718 spatiotemporal variation (11,68). Third, we have not tested the models for predicting the oscillatory
719 growth and decay behavior of the virus incidence curve, in particular, predicting the second wave.
720 Finally, an extensive simulation study would be the best way to assess the models under different
721 scenarios, but we have restricted our attention to India.

722

723 ***LIST OF ABBREVIATIONS***

724 ICM: Imperial College Model

725 MCMC: Markov Chain-Monte Carlo

726 MSRPE: Mean squared relative prediction error

727 Rel-MSPE: Relative mean squared prediction error

728 SEIR: Susceptible-Exposed-Infected-Removed

729 SIR: Susceptible-Infected-Removed

730 SMAPE: Symmetric mean absolute prediction error

Table 1: Overview of models studied.

Name of model	Comments	Input(s) and output(s)	Parameter(s) and estimation
Baseline (Bhardwaj, R. 2020)	Curve-fitting model. Cumulative number of infected cases modeled as exponential process, with growth rate λ .	Daily time series of number of infected individuals from T_0 till T_1^1 (as input) and from T_1 to T_2^2 (as output).	Time varying growth rate of infection is estimated from input and modeled using least-squares regression. Estimation involves implementing MCMC ³ methods for a Bayesian framework.
eSIR (Wang, L. et al., 2020)	Extension of the standard SIR ² compartmental model.	Daily time series data on proportion of infected and recovered individuals from T_0 till T_1^1 (as input) and from T_1 to T_2^2 along with posterior distribution of parameters and prevalence values of the three compartments in the model (as output).	β and γ control transmission and removal rates respectively. λ and κ control variability of observed and latent processes respectively. Estimation involves implementing MCMC ³ methods for a hierarchical Bayesian framework.
SAPHIRE (Hao, X. et al., 2020)	Extension of the standard SEIR ² compartmental model.	Daily time series data from T_0 till T_1^1 on count of infected individuals (as input) and count of infected and removed individuals from T_1 to T_2^2 along with posterior distributions of parameters (as output). Unreported cases are also presented.	See Section 2.1.c for details on parameters. Estimation involves implementing MCMC ³ methods for a Bayesian framework.
SEIR-fansy (Bhaduri, R., Kundu, R. et al., 2020)	Another extension of standard SEIR ² , accounting for the possible effect of misclassifications due to imperfect testing.	Daily time series data from T_0 till T_1^1 on proportion of dead, infected and recovered individuals (as input) and from T_1 to T_2^2 along with posterior distributions of parameters and prevalence values of compartments in the model (as output). Unreported cases and deaths are also projected.	See Supplementary Table S1 for details on parameters. Estimation involves implementing MCMC ³ methods for a hierarchical Bayesian framework.
ICM (Flaxman et.al., 2020)	Renewal equation used to model infections as a latent process. Deaths are linked to infections via a survival distribution. Accounts for changes in behavior and various governmental policies enacted.	Daily time series data from T_0 till T_1^1 on count of dead individuals (as input) and from T_1 to T_2^2 (as output). Posterior over infections, deaths and various parameters. Infections include both symptomatic and asymptomatic ones.	See Section 2.1.e for details on parameters. Estimation is done via HMC ⁴ using STAN.

(1) T_0 : time of crossing 50 confirmed cases – March 12, 2020. T_1 : October 15, 2020. T_2 : December 31 2020.

(2) $S(E)IR$: susceptible-(exposed)-infected-removed.

(3) MCMC: Markov chain-Monte Carlo.

(4) Hamiltonian Monte Carlo.

Table 2: Comparison of estimated time-varying R_t and prediction accuracy of the models under consideration.

		Model				
		Baseline ^a	eSIR	SAPHIRE ^b	SEIR-fansy	ICM ^c
Estimated mean reproduction number R [95% CrI]	Lockdown 1.0 (March 25 – April 14)	-	2.12 [1.44, 2.16]	2.54 [2.41, 2.74]	5.03 [5.01, 5.04]	1.77 [1.58, 1.96]
	Lockdown 2.0 (April 15 – May 3)		1.48 [1.00, 1.51]	1.60 [1.36, 2.17]	1.90 [1.89, 1.91]	1.22 [1.18, 1.27]
	Lockdown 3.0 (May 4 – May 17)		0.87 [0.59, 0.89]	1.69 [1.46, 1.97]	2.71 [2.67, 2.73]	1.33 [1.28, 1.38]
	Lockdown 4.0 (May 18 – May 31)		0.89 [0.61, 0.91]	1.54 [1.29, 2.00]	2.33 [2.30, 2.36]	1.41 [1.35, 1.47]
	Unlock 1.0 (June 1 – June 30)		0.85 [0.58, 0.87]	1.27 [1.19, 1.32]	1.74 [1.73, 1.75]	1.05 [0.99, 1.10]
	Unlock 2.0 (July 1 – July 31)		0.77 [0.52, 0.78]	1.31 [1.22, 1.36]	1.80 [1.79, 1.81]	1.11 [1.08, 1.14]
	Unlock 3.0 (August 1 – August 31)		0.79 [0.54, 0.81]	1.16 [1.06, 1.31]	1.25 [1.24, 1.26]	1.05 [1.04, 1.07]
	Unlock 4.0 (September 1 – September 30)		0.69 [0.47, 0.7]	1.12 [0.98, 1.49]	1.06 [1.05, 1.07]	0.89 [0.86, 0.91]
	Unlock 5.0 (October 1 – October 15)		0.67 [0.45, 0.68]	1.09 [0.91, 1.69]	0.86 [0.85, 0.87]	0.83 [0.82, 0.84]
	Active reported cases		-	37.955 (2.283)	-	35.141 (1.114)
Prediction accuracy using %SMAPE (MSRPE) ^d	Cumulative reported cases	6.889 (0.173)	6.593 (0.198)	2.250 (0.056)	2.285 (0.048)	-
	Cumulative reported deaths	-	8.943 (0.253)	-	4.737 (0.115)	
						0.771 (0.020)

^aThe baseline model does not return estimates of time-varying $R(t)$ or projections of active reported cases or cumulative reported deaths.

^bThe SAPHIRE model does not return projections of active reported cases or cumulative reported deaths.

^cThe ICM model does not return projections of active or cumulative reported cases.

^dWe compare model projections with observed reported data from October 16 till December 31, 2020.

Table 3: Comparison of relative performance and correlation with observed data of projections of the models under consideration from October 16 till December 31, 2020.

Observed data (confirmed)	Metric	Model				
		Baseline	eSIR	SAPHIRE	SEIR-fansy	ICM ^e
Cumulative cases	Rel-MSPE ^a	1	1.724	3.013	3.270	-
	Pearson's correlation coefficient ^b	0.996	0.969	0.984	0.999	
	Lin's concordance coefficient ^b	0.507	0.476	0.738	0.891	
Cumulative deaths	Rel-MSPE ^c	-	1	-	6.962	3.64
	Pearson's correlation coefficient ^d		1		1	0.996
	Lin's concordance coefficient ^d		0.339		0.616	0.956

^aFor cumulative reported cases, Rel-MSPE is defined relative to projections from the baseline model.

^bFor cumulative reported cases, the correlation coefficients of the projections are compared with respect to observed data.

^cFor cumulative reported deaths, Rel-MSPE is defined relative to projections from the eSIR model.

^dFor cumulative reported deaths, the correlation coefficients of the projections are compared with respect to observed data.

^eThe ICM model returns total (reported + unreported) cumulative case counts, so we leave it out of our comparisons.

Table 4: Projected counts of reported cumulative cases and total (sum of reported and unreported) counts of cases and deaths (cumulative) from the models under comparison

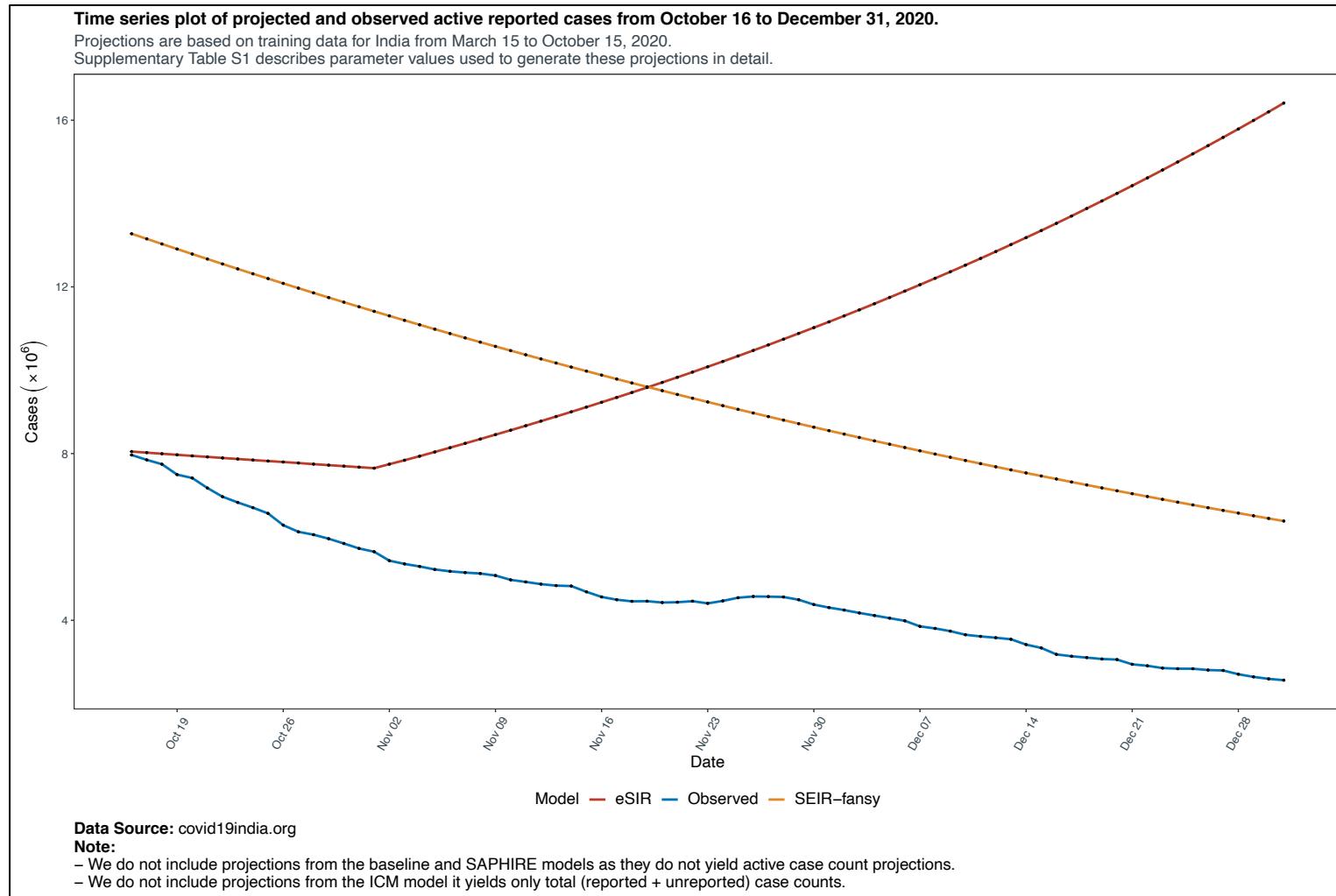
Projected cumulative reported counts (95% CrI) for specific dates in test period ^c				
Counts	Model	October 31, 2020	November 30, 2020	December 31, 2020
Cumulative cases (in millions)	Observed	8.18	9.46	10.29
	Baseline	8.71 (8.63-8.80)	11.12 (10.83-11.43)	13.34 (12.81-13.93)
	eSIR	8.35 (7.19-9.60)	10.91 (8.38-13.93)	14.85 (9.88-21.81)
	SAPHIRE	8.17 (7.90-8.52)	8.93 (8.17-9.67)	9.26 (8.19-10.35)
	SEIR-fansy	8.51 (8.18-8.85)	9.91 (9.54-10.30)	10.97 (10.57-11.4)
Projected total counts ^a (95% CrI) [under-reporting factor ^b] for specific dates in test period ^c				
Counts	Model	October 31, 2020	November 30, 2020	December 31, 2020
Active cases (in millions)	Observed	0.57	0.44	0.26
	SEIR-fansy	5.32 (5.12-5.52) [9.3]	3.99 (3.85-4.14) [9.13]	2.96 (2.85-3.06) [11.53]
Cumulative cases (in millions)	Observed	8.18	9.46	10.29
	SAPHIRE ^d	578.21 (46.41-1134.20) [70.7]	612.79 (52.253-1161.26) [64.8]	622.32 (55.79-1163.17) [60.5]
	SEIR-fansy	59.32 (56.8-61.72) [7.25]	68.71 (65.95-71.47) [7.26]	75.89 (72.89-78.86) [7.38]
	ICM ^d	37.17 (24.78-58.68) [4.54]	39.54 (25.63-63.12) [4.18]	41.38 (26.02-67.88) [4.02]
Cumulative deaths (thousand)	Observed	121.56	137.07	148.43
	SEIR-fansy	361.52 (347.23-375.85) [2.97]	442.25 (425.05-459.64) [3.23]	504.76 (485.50-524.07) [3.4]

^aProjected total count includes both reported as well as unreported values.

^bDefined as projected total/observed reported counts, where total is the sum of reported and unreported cases.

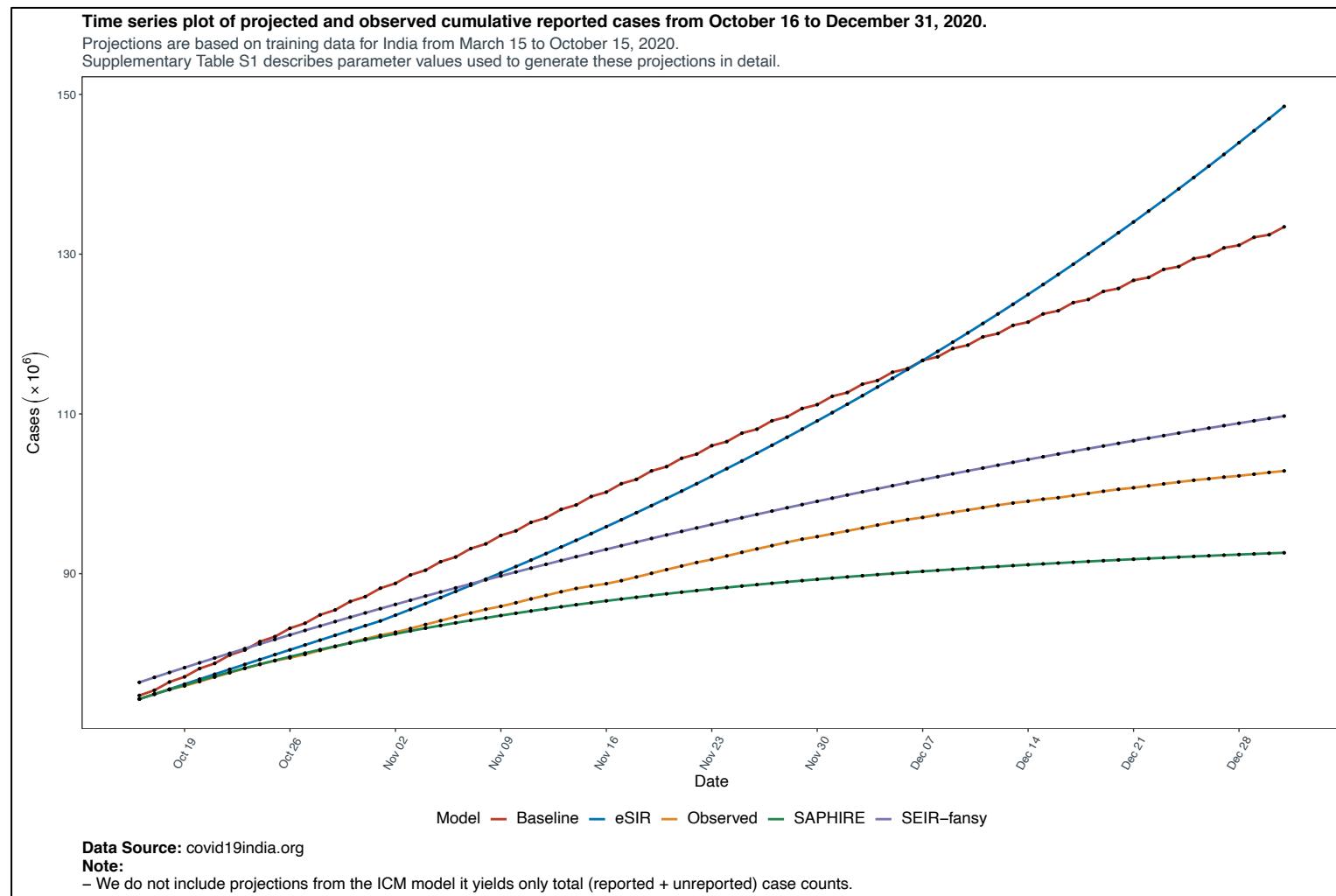
^cThe test period extends from October 16 till December 31, 2020. We examine projections of cumulative cases and counts on three specific dates within that period, namely, October 31, November 30 and December 31, 2020.

^dThe SAPHIRE model does not yield projections of active cases or cumulative deaths while the ICM model does not yield projections of cumulative reported cases, total active cases or total cumulative deaths.

760 **FIGURES**761 *Figure 6: Comparison of projected and observed reported active cases from October 16 to December 31 for India, using training data*
762 *from March 15 to October 15, 2020.*

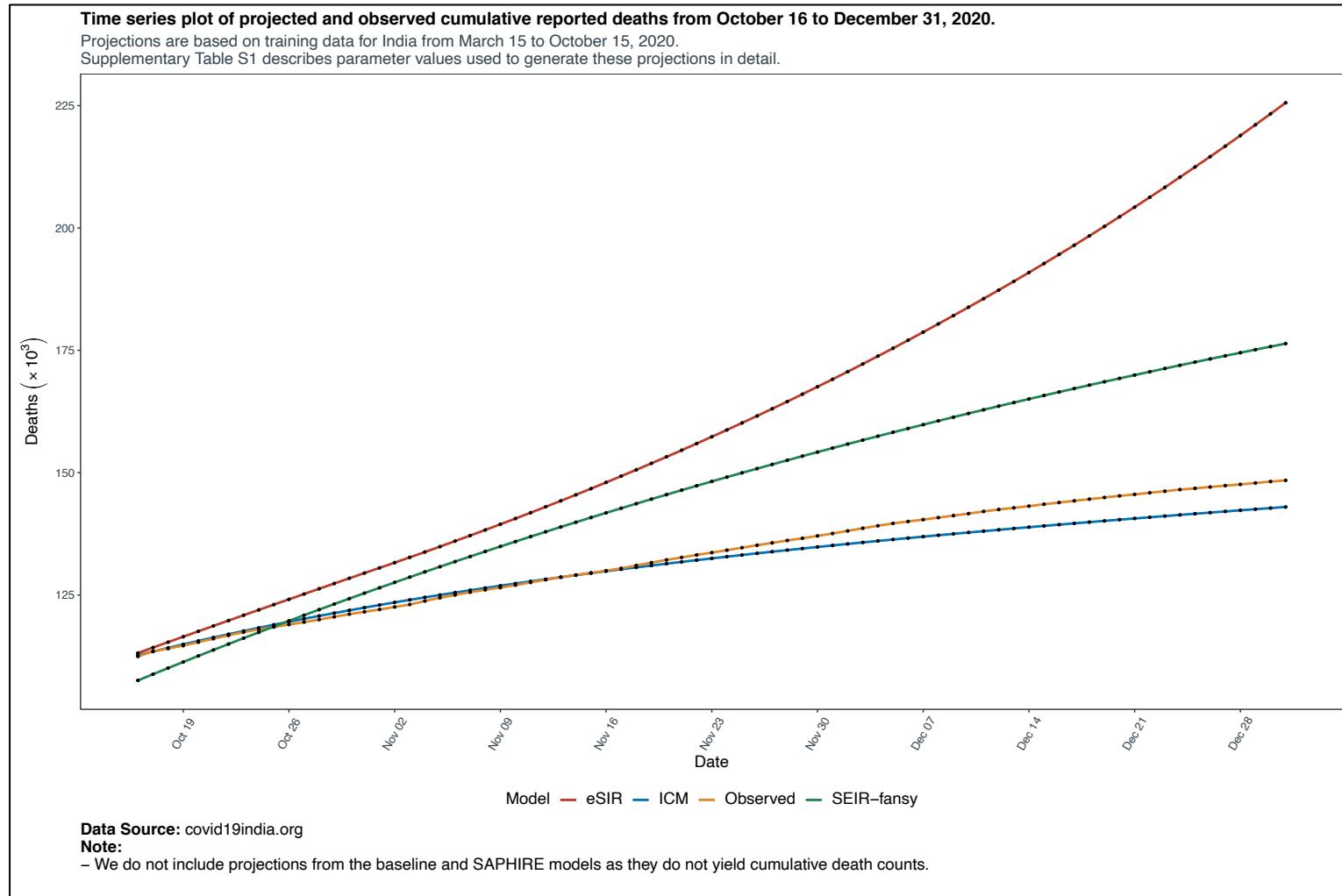
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779 *Figure 7: Comparison of projected and observed reported cumulative cases from October 16 to December 31 for India, using training*
 780 *data from March 15 to October 15, 2020.*



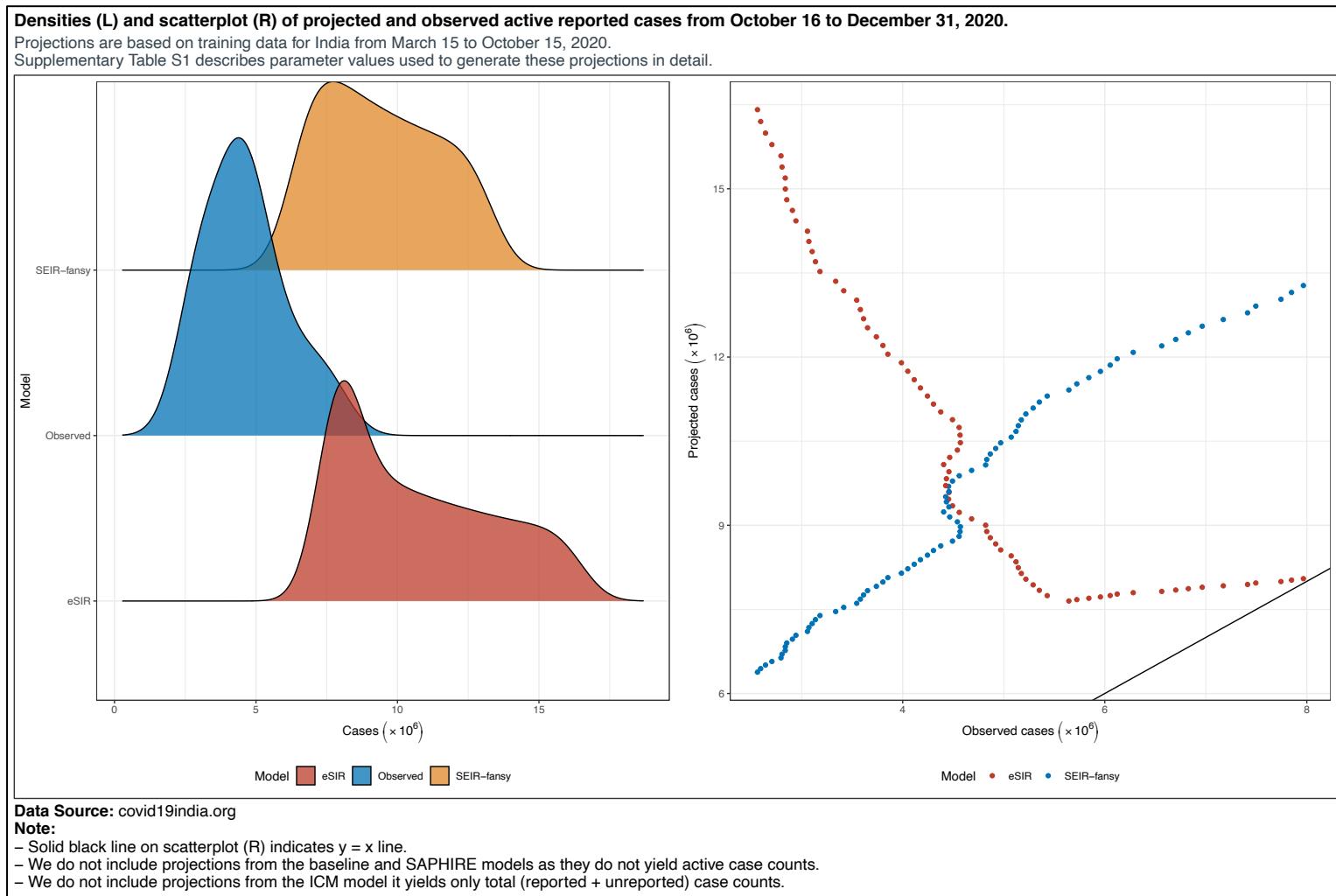
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797 *Figure 8: Comparison of projected and observed reported cumulative deaths from October 16 to December 31 for India, using*
 798 *training data from March 15 to October 15, 2020.*

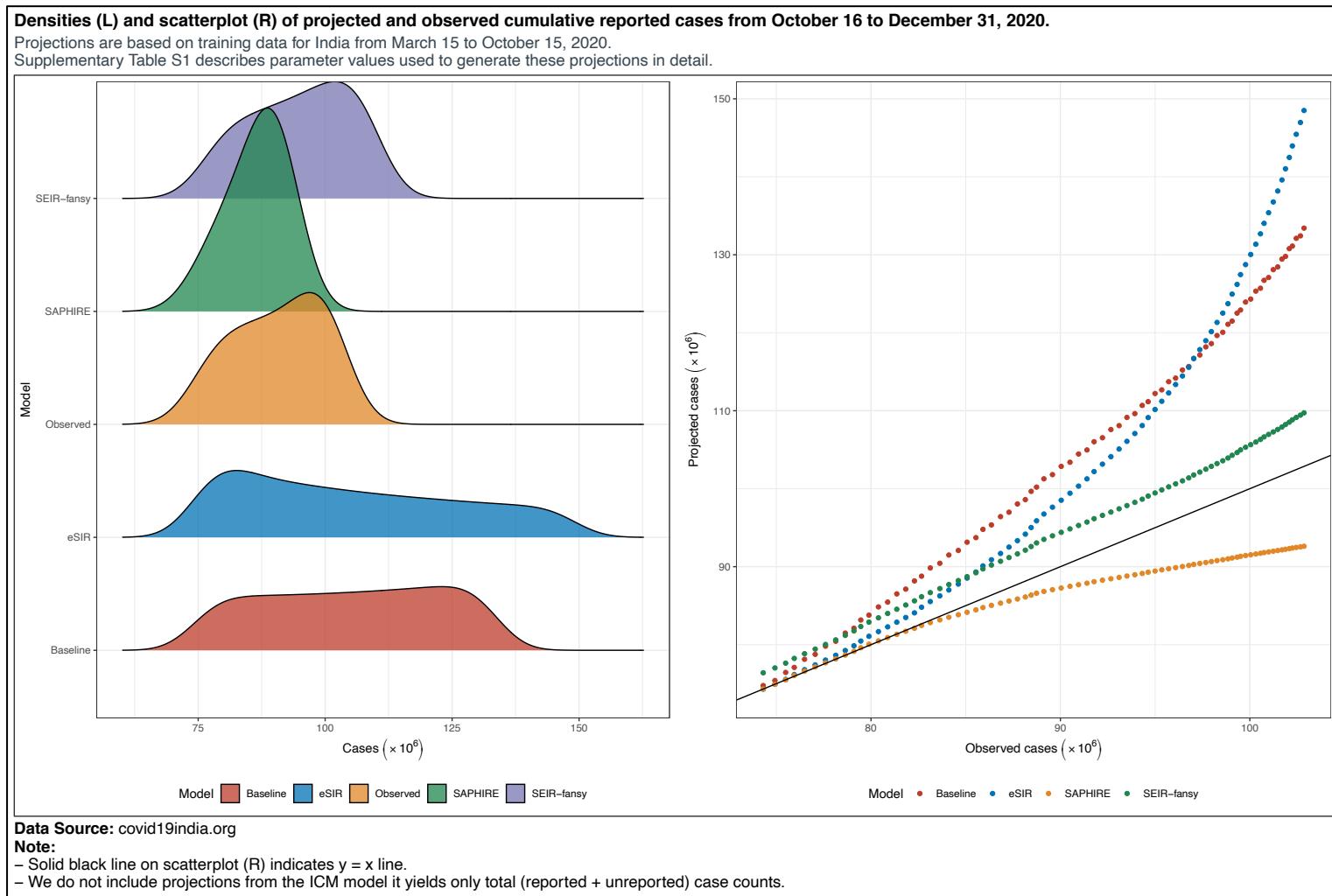


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Figure 9: Scatter plot and marginal densities of projected and observed reported active cases from October 16 to December 31 for India, using training data from March 15 to October 15, 2020.



803 *Figure 10: Scatter plot and marginal densities of projected and observed cumulative cases from October 16 to December 31 for India,*
 804 *using training data from March 15 to October 15, 2020.*



806 *Figure 11: Scatter plot and marginal densities of projected and observed cumulative death from October 16 to December 31 for India,*
 807 *using training data from March 15 to October 15, 2020.*

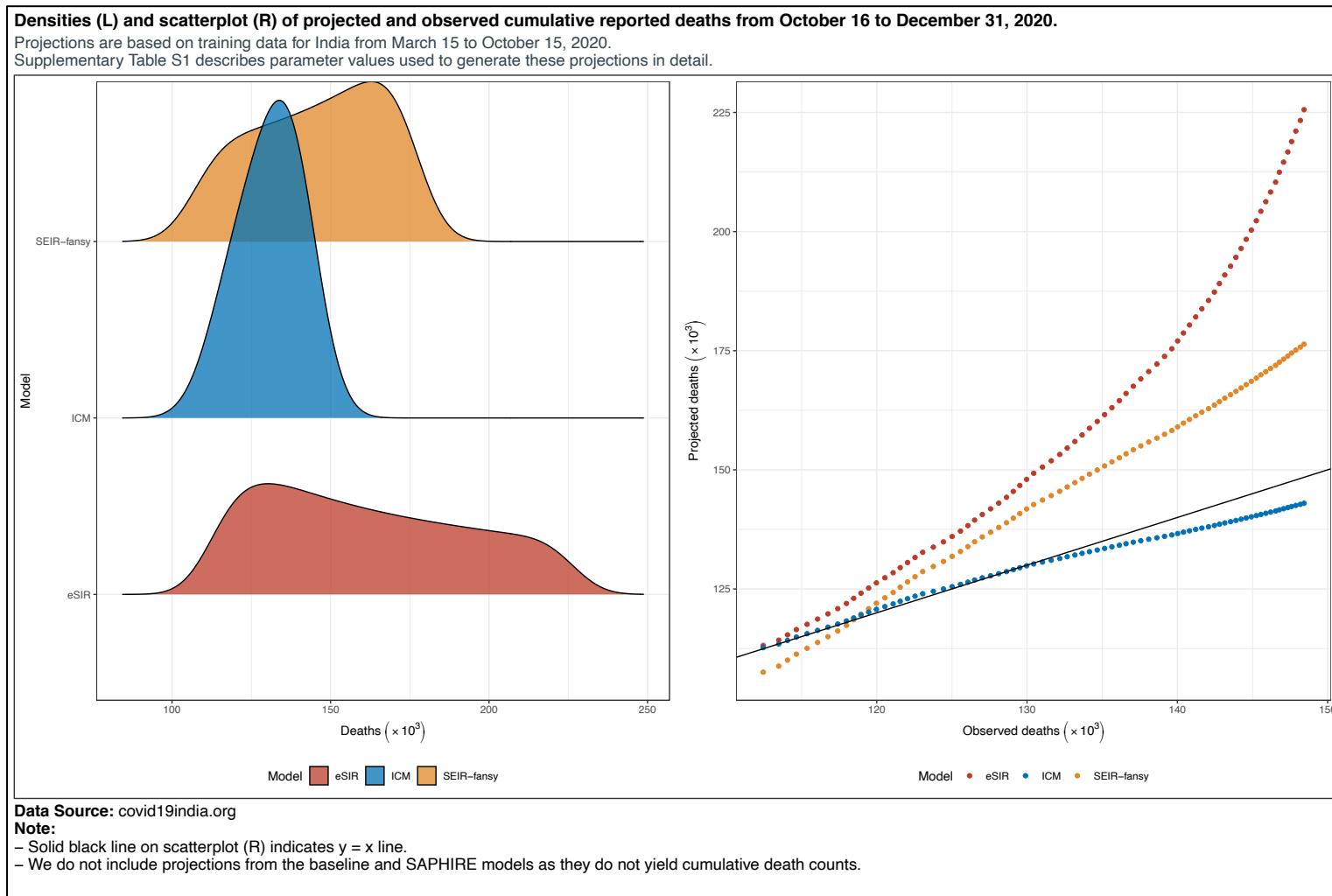
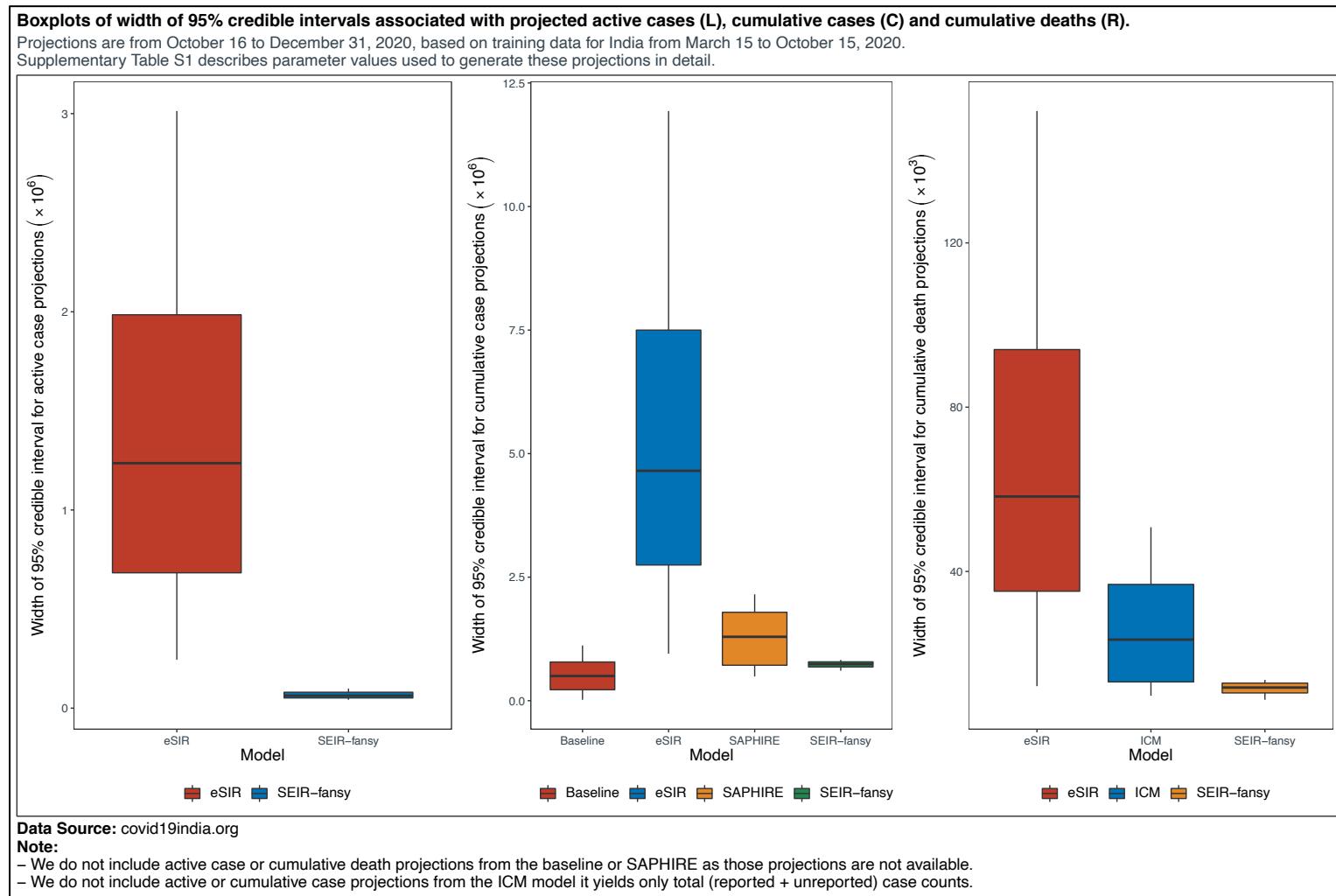


Figure 12: Boxplots showing width of 95% credible interval associated with projected active cases, cumulative cases and cumulative deaths from October 16 to December 31 for India, using training data from March 15 to October 15, 2020.



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Supplementary Table S1: Summary of initial values and parameter settings for application of the SEIR-fansy model in the context of COVID-19 data from India. Unless mentioned otherwise, we use these parameter settings for all other models when applicable.

Parameters	Settings	Description
β	Time-varying	Rate of infectious transmission by infected individuals with false negative test results.
α_p	0.5	Ratio of rate of spread of infection by patients who test positive, to rate of spread of infection by patients who get false negative results ^a .
α_u	0.7	Scaling factor for the rate of spread of infection by untested individuals ^a .
D_e	5.2	Incubation period (in days).
D_r	17	Recovery time (in days) for infected individuals.
D_t	0	Waiting time (in days) for test result for tested individuals.
μ_c	0.0562	Death rate attributable to COVID-19 ^b .
λ, μ	3.95×10^{-5}	Natural birth and death rates, respectively ^b .
r	Time-varying	Probability of being tested for infectious individuals.
f	0.30	Probability of a false negative RT-PCR diagnostic test result.
β_1, β_2	0.6 (β_1) and 0.7 (β_2)	Scaling factors for rate of recovery for undetected and false negative individuals respectively ^c .
δ_1, δ_2	0.3 (δ_1) and 0.7 (δ_2)	Scaling factors for death rate for undetected and false negative individuals respectively ^d .

- a. $\alpha_p < 1$ represents the scenario where individuals who test positive are infecting susceptible individuals at a lower rate than infected individuals with false negative test results. $\alpha_u < 1$ is assumed as U mostly consists of asymptomatic or mildly symptomatic cases who are known to spread the disease at a much lower rate than those with higher levels of symptoms.
- b. Equal to the inverse of the average number of days for death starting from the onset of disease, times the probability of death of an infected individual. Natural birth and death rates are assumed to be equal for simplicity.
- c. $\beta_1 < 1, \beta_2 < 1$ are assumed, since the recovery rate is slower for individuals with false negative test results as compared to those who have been hospitalized. The condition of untested individuals is not as severe as they consist of mostly asymptomatic people. Consequently, they are assumed to recover faster than those with positive test results.
- d. $\delta_1 < 1, \delta_2 < 1$ are assumed. The death rate for those with false negative test results is assumed to be higher than those with positive test results, since the former are not receiving proper treatment. For untested individuals, the death rate is taken to be lesser because they are mostly asymptomatic. As a result, their survival probability is much higher.

Supplementary Table S2: Overview of projected COVID-counts for each model considered.

Type of count projected	COVID-counts		
	Cumulative COVID-cases	Active COVID-cases	Cumulative COVID-deaths
Reported	Baseline, eSIR, SAPHIRE, SEIR-fansy	eSIR, SEIR-fansy	eSIR, SEIR-fansy, ICM
Unreported	SAPHIRE, SEIR-fansy	SEIR-fansy	SEIR-fansy
Total (reported + unreported)	SAPHIRE, SEIR-fansy, ICM	SEIR-fansy	SEIR-fansy

Supplementary Table S3: Comparison of estimated projections and posterior estimates of model parameters across different sensitivity analysis scenarios under 21-day lockdown with moderate return, using observed data till April 14. Prior SD for R_0 is 1.0. Reproduced from Ray et al., 2020 (51).

Sensitivity Analysis		Predictions		Posterior Estimates		
Scenario		May 1	May 15	R_0	β	γ
Under-reporting*	25,248	62,797	2.28	0.20	0.09	
	[104,411]	[343,465]	[1.05, 4.20]	[0.05, 0.39]	[0.03, 0.19]	
Case-clustering**	24,818	57,499	2.81	0.16	0.06	
	[59,525]	[189,010]	[1.47, 4.70]	[0.07, 0.26]	[0.03, 0.10]	
Prior mean for $R_0 = 2$	20,251	42,252	1.80	0.27	0.16	
	[135,034]	[315,348]	[0.87, 3.26]	[0.06, 0.59]	[0.04, 0.35]	
Prior mean for $R_0 = 3$	25,757	86,750	2.43	0.30	0.13	
	[165,287]	[638,770]	[1.41, 4.07]	[0.09, 0.60]	[0.04, 0.30]	
Prior mean for $R_0 = 4$	34,587	253,935	3.38	0.32	0.10	
	[213,556]	[1,854,319]	[2.09, 5.27]	[0.10, 0.63]	[0.03, 0.23]	

* Observed case-counts are multiplied by 10, Prior mean for $R_0 = 2$

** Assume that the cases happen in metro hotspots, use population size $N=32$ million instead of national population 1.34 billion, Prior mean for $R_0 = 2$

Supplementary Table S4: National and state-levels lockdown measures implemented over the course of COVID-19 pandemic in India. Reproduced from Salvatore et al., 2021 (66).

Lockdown phase	Nation-wide measures implemented	State-level variation in measures implemented
Phase one <i>(25 March – 14 April)</i>	All transport services – road, air and rail – were suspended, with exceptions for transportation of essential goods, fire, police and emergency services. Educational institutions, industrial establishments and hospitality services were also suspended. ^a Services such as food shops, banks and ATMs, petrol pumps, other essentials and their manufacturing were exempted. ^b	Gujarat, Himachal Pradesh, Karnataka, Maharashtra, Tamil Nadu, Sikkim and Telengana sealed state borders. Additionally, Maharashtra, Telengana and Tamil Nadu imposed Section 144, outlawing large gatherings of people. ^c
Phase two <i>(15 April – 3 May)</i>	Conditional relaxation promised after 20 April, subject to containment of spread. Lockdown areas classified into red, orange and green zones based on extent of spread of disease. Certain relaxations from 20 April: agricultural businesses, including dairy, aquaculture and plantations allowed to open. Cargo transportation vehicles allowed to operate. Banks and government centers distributing benefits allowed to open as well. ^d	In interest of economic recovery, certain states like Maharashtra chose to allow specific business activities to resume, in addition to national easing of restrictions. Karnataka chose to ease the lockdown in certain areas, while Delhi, Punjab and Telengana chose to enforce strict lockdown measures. ^e
Phase three <i>(4 May – 17 May)</i>	Zonal classification of regions into red, orange and green zones continued, with normal movement allowed in green zones. Movement of private and hired vehicles allowed in orange zones and red zones remained in lockdown. Zonal classifications revised on a weekly basis. ^f	Delhi allowed public- and private-sector offices to reopen, with social distancing measures in place. Maharashtra eased most industrial and commercial activities. Gujarat, and Jharkhand allowed no relaxation, while Bihar, Uttar Pradesh, Rajasthan and Madhya Pradesh chose to mostly adhere to guidelines issued by the Union Home Ministry. ^g
Phase four <i>(18 May – 31 May)</i>	Unlike the previous phases, states were given a larger say in the demarcation of green, orange and red zones and the implementation roadmap. Red zones were further divided into containment and buffer zones. Local administrative bodies were given the authority to demarcate containment and buffer zones. ^h	Restricted individual movement allowed in Delhi, while Maharashtra, Tamil Nadu and Telengana extended the lockdown further. Karnataka allowed public transport with social distancing measures, while West Bengal began easing workplace restrictions. Standalone shops were allowed to open for short durations. ⁱ

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- c. Wikipedia https://en.wikipedia.org/wiki/Indian_state_government_responses_to_the_COVID-19_pandemic
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- i. BBC: India lockdown 4.0: What is allowed in your city? *19 May 2020* (<https://www.bbc.com/news/world-asia-india-52707371>)