
WEEKLY BAYESIAN MODELLING STRATEGY TO PREDICT DEATHS BY COVID-19: A MODEL AND CASE STUDY FOR THE STATE OF SANTA CATARINA, BRAZIL

Pedro Henrique da Costa Avelar^{1,2}, Luis C. Lamb², Sophia Tsoka³, and Jonathan Cardoso-Silva^{*,3}

¹*Data Science Brigade, Porto Alegre, Brazil*

²*Institute of Informatics, Federal University of Rio Grande do Sul, Porto Alegre, Brazil*

³*Department of Informatics, King's College London, London, United Kingdom*

ABSTRACT

Background: The novel coronavirus pandemic has affected Brazil's Santa Catarina State (SC) severely. At the time of writing (24 March 2021), over 764,000 cases and over 9,800 deaths by COVID-19 have been confirmed, hospitals were fully occupied with local news reporting at least 397 people in the waiting list for an ICU bed. Despite initial state-wide measures at the outbreak of the pandemic, the state government passed most responsibilities down to cities local government, leaving them to plan whether and when to apply Non-Pharmaceutical Interventions (NPIs). In an attempt to better inform local policy making, we applied an existing Bayesian algorithm to model the spread of the pandemic in the seven geographic macro-regions of the state. However, as we found that the model was too reactive to change in data trends, here we propose changes to extend the model and improve its forecasting capabilities.

Methods: Our four proposed variations of the original method allow accessing data of daily reported infections and take into account under-reporting of cases more explicitly. Two of the proposed versions also attempt to model the delay in test reporting. We simulated weekly forecasting of deaths from the period from 31/05/2020 until 31/01/2021. First week data were used as a cold-start to the algorithm, after which weekly calibrations of the model were able to converge in fewer iterations. Google Mobility data were used as covariates to the model, as well as to estimate of the susceptible population at each simulated run.

Findings: The changes made the model significantly less reactive and more rapid in adapting to scenarios after a peak in deaths is observed. Assuming that the cases are under-reported greatly benefited the model in its stability, and modelling retroactively-added data (due to the "hot" nature of the data used) had a negligible impact in performance.

Interpretation: Although not as reliable as death statistics, case statistics, when modelled in conjunction with an overestimate parameter, provide a good alternative for improving the forecasting of models, especially in long-range predictions and after the peak of an infection wave.

Keywords Bayesian Model · COVID-19 · Epidemic Forecasting

Introduction

The World Health Organization (WHO) declared COVID-19 a global pandemic in mid-March 2020, prompting countries to take actions to reduce the spread of the virus in view of the serious respiratory problems that require specialized care in Intensive Care Units (ICU) [1, 2]. Little was known about this new strain of coronavirus that threatened to overwhelm health systems, had forced several countries to lockdown, and had already been rapidly spreading across Brazil [3]. With no drug treatments or vaccines in sight at that time and in the face of a lack of national measures to prevent the spread of the disease [4, 5], governors and mayors had to decide independently on the implementation of non-pharmacological measures (NPI) [6]. In the midst of this scenario and despite the harsh inherent challenges of epidemic modeling, mathematical models offered a timely approach to help understand the regional dynamics of contagion of the disease and to predict how this health crisis could unfold in the weeks and months that followed [7–16].

*Corresponding author. E-mails: jon@dsbrigade.com, jonathan.cardoso_silva@kcl.ac.uk

A prominent mathematical model was introduced by the MRC Center for Global Infectious Disease Analysis group at Imperial College London in March 2020 [17], the source code and a technical description of the equations used in this Bayesian inferential model were put online in April 2020 [18], with the study being peer reviewed and published later in June 2020 [19]. This model sought, above all, to estimate the impact and effectiveness of NPI measures that were being taken by European countries. Nonetheless, the model produces other results of interest such as an estimated number of people infected by SARS-CoV-2 and the variations in the reproduction number (R_t) up until the current date.

In this paper, we present four variations of the Flaxman et al model (here called base model) to forecast deaths by COVID-19 and overcome limitations that were observed after replicating the model on a weekly basis to the 7 macro-regions within Santa Catarina, a southern state in Brazil. More specifically, we show that the original model was not able to predict major changes in the trend in mortality data. This was most noticeable in weeks when the number of new reported infections showed a rapid increase or decrease. Since the base model did not have access to this data, it could not anticipate change in the trends of infection. The covariates used in the model have also been identified as inadequate, since it limited the effective reproductive number R_t to change only at predetermined time points where a NPI measure came into effect [20]. Despite these limitations, the model has been used elsewhere to estimate the impact of NPI measures in two Brazilian states [21].

Other obstacles, not related to the algorithm itself but which we also consider, are the under-notification of infected cases [22] and delays in test reporting [23]. The data suggests an average delay of 5 days from RT-PCR test collection until the result is available in the official database of Santa Catarina state. As a consequence, at any given date it is almost guaranteed that the last week of data is incomplete and almost uninformative.

Our proposed alterations to the original method aim at overcoming the limitations mentioned above, allowing this mathematical model to be used more effectively for forecasting. Additional equations and algorithmic strategies allow the model to use reported cases to estimate deaths by COVID-19.

Results

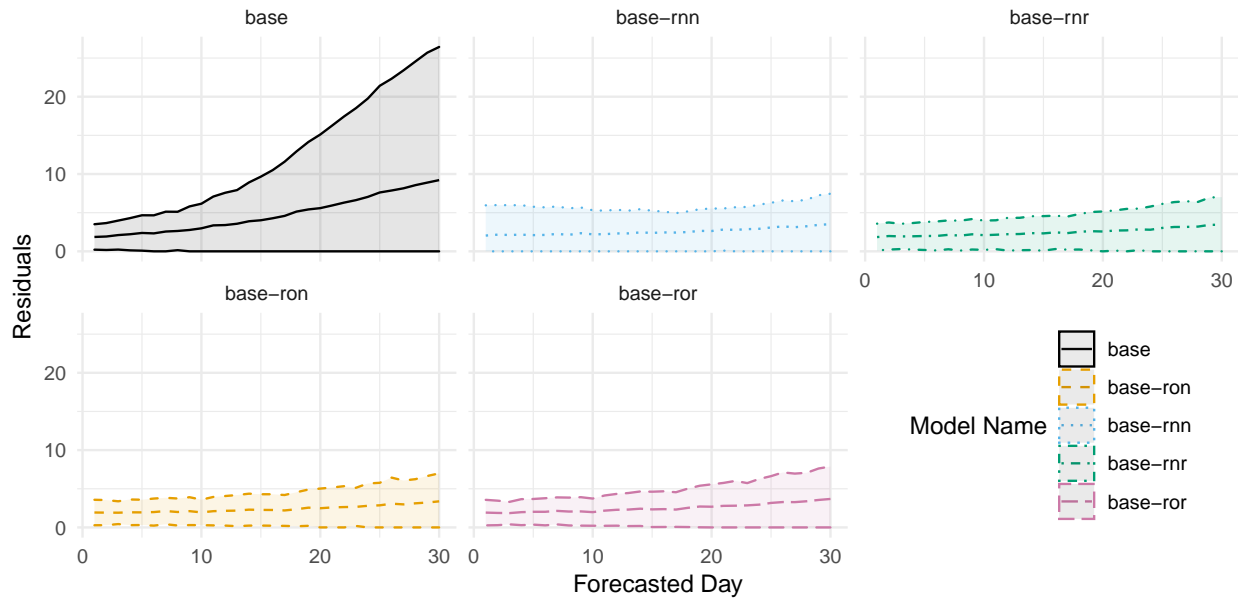


Figure 1: Comparison of the proposed models to the base algorithm for forecasts over a time window of 30 days. The lines and areas show the average and standard deviation of absolute prediction error produced by each model and are here shown aggregated to the entire state of SC over the 35 weeks of modelled simulation.

We simulated the base model and four variations of our proposed model, (base-ron, base-rnn, base-ror, base-rnr) described in Materials and Methods section and summarised in Table 1. All models add the **new reported infections** to the equations but they differ in whether we explicitly **overestimate** infections in the equations and whether an estimated percentage of cases and deaths are added retroactively in the data before running the model to account for **delay in test reporting**.

Each model produced a forecast for the 7 macro-regions of the state of Santa Catarina in weekly snapshots, starting from 31/05/2020 – when daily snapshots of data became available in the official database system of the state – until 31/01/2021. At every simulated week, the models were fed with data exactly as it were available at that current date and produce a forecast to the number of deaths for the following 30 days. The first week is used as a warm-up (to calibrate the method and allow us to run a lighter variant) and from the second week onward, the priors estimated in the previous week are provided to each corresponding model to help speed convergence. More details about the proposed model, its variations, and our test workflow can be seen in the Materials and Methods section.

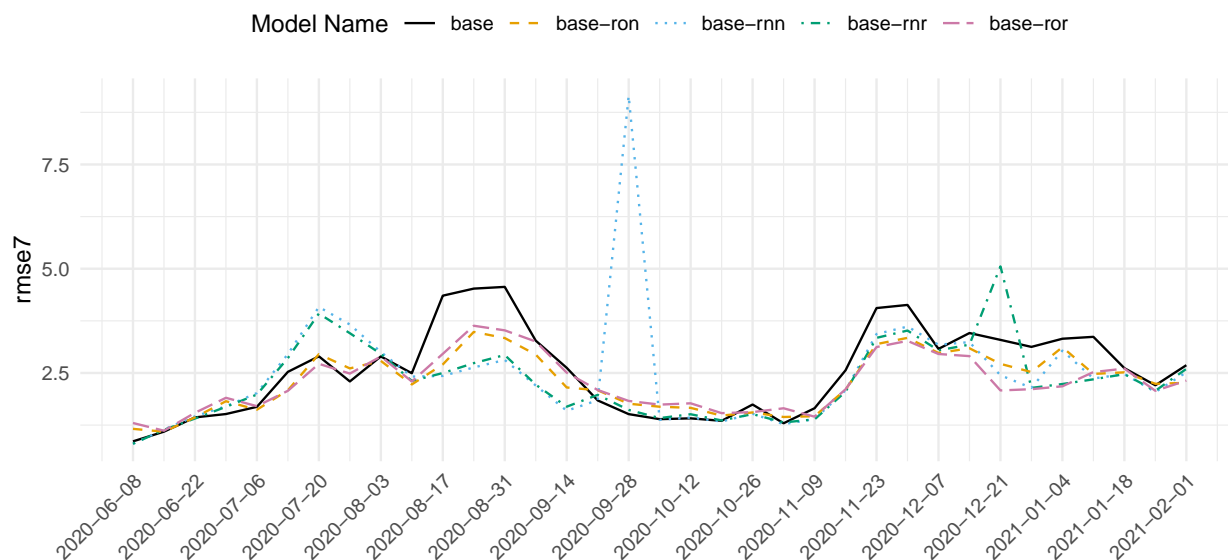


Figure 2: Comparison of the modified models to the base algorithm for forecasts over a time window of 7 days.

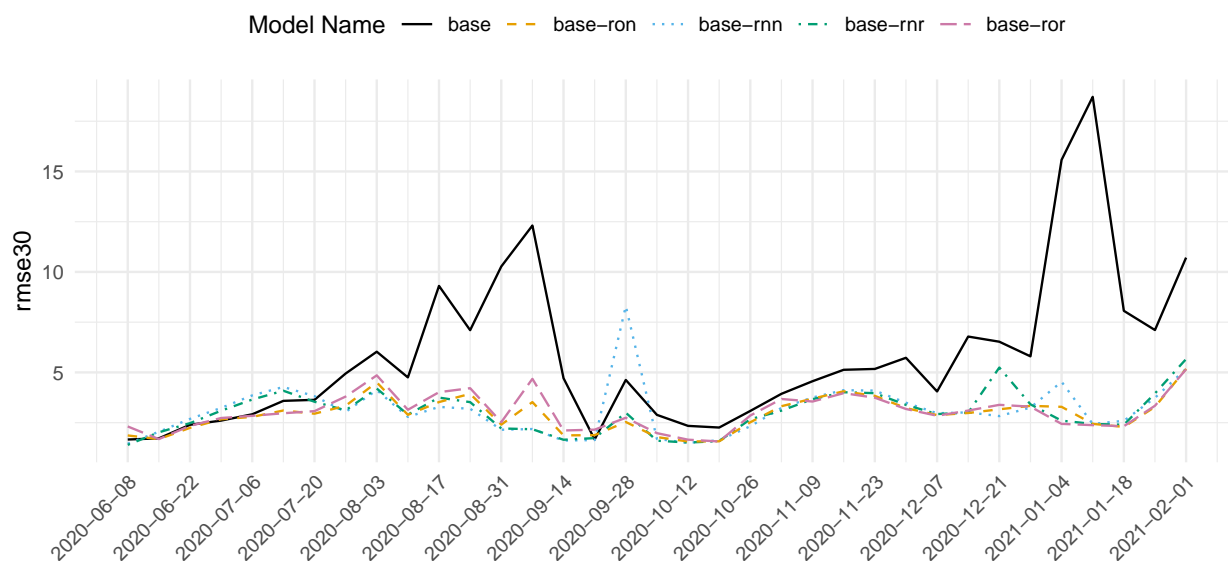


Figure 3: Comparison of the modified models to the base algorithm for forecasts over a time window of 30 days.

On average, both original and alternative models had a similar prediction accuracy on the first 7-10 days of forecast but our proposed models outperformed the base model on the medium term. As shown in Figure 1 which illustrates

residual errors aggregated to the entire state of SC, the margin error of predictions made by base model grew wider over time whereas our models maintained a more stable error throughout the forecasting period. Table S1 also provide a numerical comparison of these errors for a window of 7 and 30 days respectively and on Table S2, one could also inspect the results for each of the seven geographic regions that compose the state of Santa Catarina.

The gap between the baseline model and the proposed method over time are most noticeable in particular points in time, as indicated by RMSE plots for 7-day and 30-day forecasting windows of the models in Figures 2 and 3, respectively. The base model showed the largest short-term error in the middle of August 2020 and at the end of November 2020. On the 30-day window, the baseline algorithm is clearly making the worst predictions particularly during August 2020 and the beginning of 2021 (Figure 3). Compared to the curve of deaths in SC, shown in Figure 4, we observe that these higher errors were made in dates during or immediately after the peaks in daily number of deaths (highlighted dates). Diagnostic graphs produced by the model for these dates confirm that base was unable to reflect major changes in the trend of death data. The model predicted that the number of infections was growing even though data regarding new reported infections already displayed a downward trend (Figures S1a - S1c). One could contrast the diagnostic plots above to the ones obtained by base-rnn model for the same dates in Figures S2a - S2c, where this misdirection in predicting death trend was not present in our proposed models.

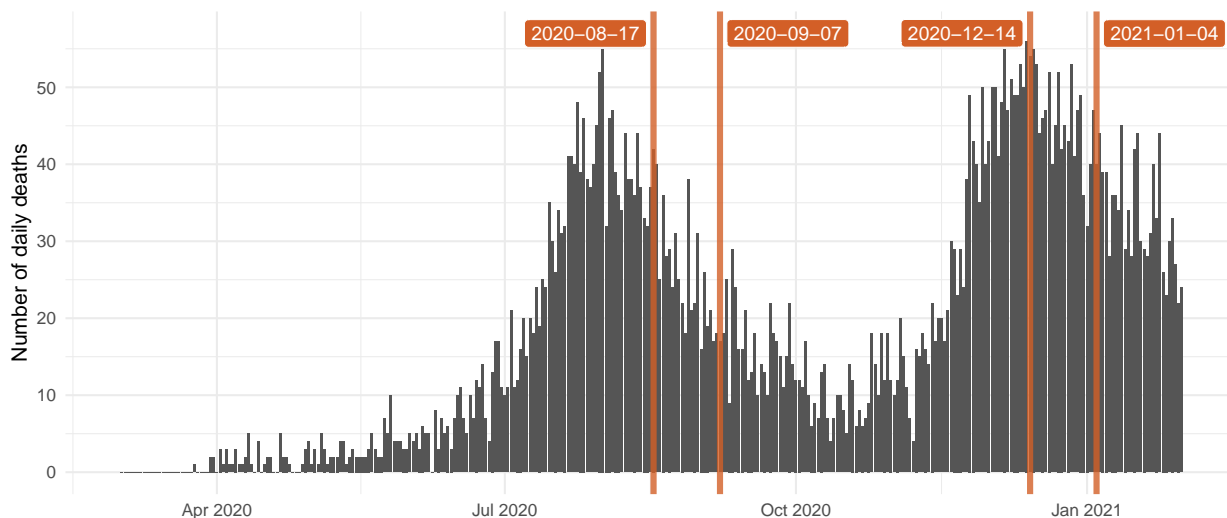


Figure 4: Curve of daily deaths by COVID-19 in the state of Santa Catarina, highlighting the dates in which prediction errors made by base model were higher

Our methods outperform the baseline in almost all runs but the best algorithms were the ones that attempt to overestimate the number of infected individuals from the number of reported cases: base-rnn and base-rnr. Results given by these methods yielded the most stable predictions over both forecasting periods examined. An interesting outcome of these results is that we model overestimate as a Gaussian distribution of the form $\text{overestimate}_m \sim \mathcal{N}(11.5, 2.0)$ but we noticed that in most cases this variable was optimised to a much smaller value, for example $\text{overestimate}_m \leq 5$ for the “Sul” and “Grande Oeste” geographical macro-regions (Figure S6). As it happens, the MCMC inference algorithm automatically converges to a value that makes the most sense to the optimisation problem.

On the other hand, base-rnn and base-rnr exhibited larger errors in predictions for certain periods in time, for example the middle of July 2020, later August 2020 or at the end of December 2020 (Figure 2). Adding an estimate of the retroactive data did not seem to impact the predictive accuracy since this characteristic was present both in one of the best-performing model (base-rnr) and in one of the less predictive ones, base-rnr. Other assumptions embedded in each model variation can be found in the Materials and Methods Section and on Table 1.

Another way to visualize these results is by comparing the graph of cumulative deaths with predictions made by base and one of the best performing models base-rnn (Figure 5). Scenarios 01 and 03 show models’ 95% confidence interval around the average prediction indicated as Scenario 02. It is clear that our model has improved the predictions, providing a narrower confidence interval which was closer to the real value.

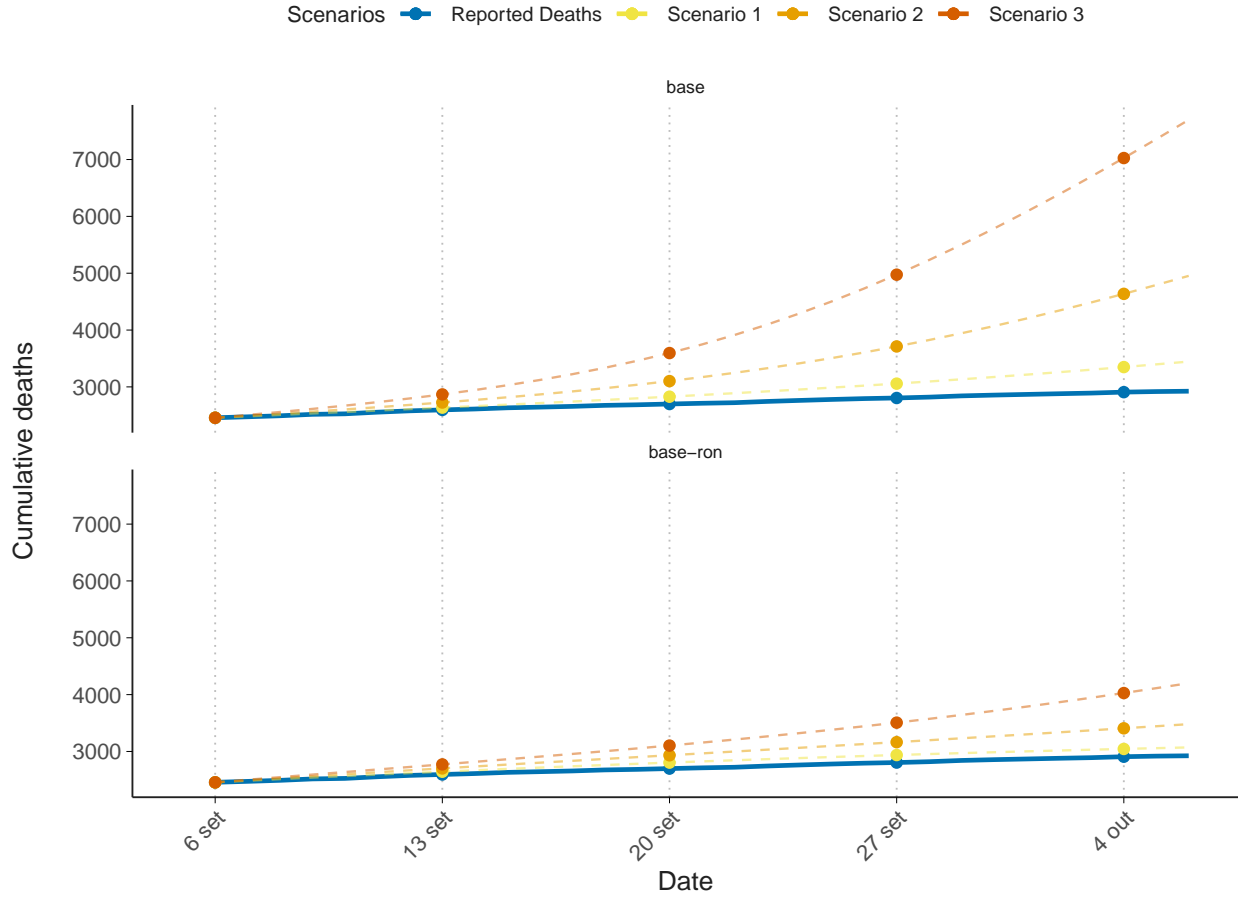


Figure 5: The forecast scenarios produced by base vs base-ron in 07/09 and the four following weeks. Scenarios 01 and 03 are the models’ 95% confidence interval around the average prediction indicated as Scenario 02. It is clear how our model have improved the predictions, providing a narrower confidence interval much closer to the real value.

Discussion

There is evidence in the literature that COVID-19 models are inefficient for long-range forecasting [24]. In this paper we show, however, that one can use “hot” data (i.e., the most recent data, that is constantly being updated and might still not be complete) and update a model on a weekly basis to achieve higher accuracy, and that such “hot” data come with own sets of issues, such as the unreliability, delays in updating, etc. Knowledge of SARS-CoV-2 interactions in the human body, as well as social contagion dynamics of the disease have not been elucidated entirely. A lot is still unknown and epidemic modelling has to address real-time uncertainties and changes as closely as possible. A model which does not take into account the fast pace production of data is bound to underperform when compared to a model based on up-to-date information. Our proposed models overcome some limitations of the original algorithm in Flaxman et al [18] mostly by accessing data regarding daily reported infections and letting it account for under-reporting in a more explicit way. We have also tested some variations in the algorithm to account for the delay within test collection and notification but these did not prove as useful in predicting the death curve in the state of Santa Catarina.

These alternative models, however, are not without their failings. While predictions have improved and some assumptions of the model could be confirmed by inspection of the data – for example, the onset-to-death seems to follow a gamma distribution like the original model assumed – there are just too many assumptions in the original model that have not been thoroughly validated[25] (i.e., is the R_0 really that value of $R_0 = 3.28$?). Another issue is that, from the point of view of the optimisation algorithm, estimated R_t values and estimated number of people daily infected are interchangeable. The algorithm could reach two opposing configurations that are equally valid and optimal: one where the reproduction rate is low but there is a large pool of infected people in the population, and another separate solution in which the number of infected people is small but R_t is larger.

Also, even though adding infection data into the model has given it more adaptability, the same data could make the model more fragile in the future. If the infection dynamic changes (e.g. because of new more transmissible strains of the virus), the model might be biased to readjust its fitting of the historical data to compensate. This could be counteracted by more reliable epidemiological data from other sources (i.e., tracking the prevalence of new virus strains, information about age, or information of entry and exit into ICU) or by including even more granular mobility data, at the expense of the citizens' privacy, all of which are generally more expensive or unfeasible to obtain.

New or data of higher resolution can alleviate some challenges in epidemic modeling, but importantly new observations can help revising assumptions of existing models in search of a more accurate description of real-world cases [24, 26]. Our proposed model is one step in that direction of scientific inquiry. We show that a model can become more accurate by adding one more data source and a new assumption about under-reporting the tests, and therefore more useful for forecasting and decision making. We intend to review the other assumptions built into the original model and continue to investigate how much the changes we have introduced are sustained in the face of new epidemic waves, new variants of the virus and new political measures that affect the dynamics of contagion.

Materials and Methods

Epidemiological Data

Anonymized data on every confirmed case of COVID-19 in SC along with date of onset of first symptoms, date of PCR test collection, date of death and municipality of residence were downloaded from the state government big data platform Plataforma BoaVista [27]. Estimated population in each of the seven regions of Santa Catarina were obtained from the Brazilian Institute of Geography and Statistics IBGE[28] and mobility data for every city was downloaded from Google Mobility [29]. The state of Santa Catarina has over 7 million inhabitants organised in 297 municipalities organised in 6 distinct geographical macro-regions distributed across 95 square kilometers of land area. The state government imposed suspensions of many economic activities after the first deaths were confirmed in SC in March 2020 but ended up relaxing social distancing measures, eventually leading to a decree in June 2020 after which municipal governments would be responsible for most decisions regarding NPI measures. At the time of writing (24 March 2021), over 764,000 cases and over 9,800 deaths by COVID-19 have been confirmed, hospitals were fully occupied with local news reporting at least 397 people in the waiting list for an ICU bed [30].

Bayesian Modelling

The baseline model (base) is almost identical to the Monte-Carlo (MCMC) model made available by Flaxman et al [18], with the exception of the covariates used. Instead of manually curated non-pharmaceutical interventions measures, we used Google Mobility data as covariates to the model. This strategy counteracts an implicit confirmation bias of the model [20] and have been used by the original group in a subsequent work [31]. In terms of practical reasons to amend covariates, we mention that, in contrast to European countries that the original model targets, the State of Santa Catarina did not impose strict state-wide measures consistently during this period, with municipal governments being independently responsible for social distancing measures [6] and rendering changes in legislation hard to track. Our Bayesian models rely on the same distributions as the base model so whenever possible we will use the same symbols to mean the same distributions. We refer the reader to their paper for a full description of the symbols [18, 19].

We now describe the equations and modifications of our proposed models, which are also summarised in Table 1. In mathematical terms, we observe daily deaths $D_{t,m}$ and daily cases $C_{t,m}$ for days $t \in \{1, \dots, n\}$ and regions $m \in \{1, \dots, M\}$. These values might be augmented in some models (e.g. base-ror and base-rnr) to a $D_{t,m}^*$ and $C_{t,m}^*$, which are explained later in this section. The objective function of the original model, and part of the objective of our models is given by:

$$D_{t,m}^* \sim \text{NegativeBinomial} \left(d_{t,m}, d_{t,m} + \frac{d_{t,m}^2}{\Phi} \right), \quad (1)$$

where $d_{t,m}$ represents the number of modelled cases, following:

$$d_{t,m} = \text{xfr}_m^* \sum_{\tau=0}^{t-1} c_{\tau,m} \pi_{t-\tau}, \quad (2)$$

where xfr is either the region-specific case-fatality rate cfr (in models `base-rnn` and `base-rnr`) or the infection-fatality rate $ifr \approx 0.0076$ estimated for Brazil in [31] (in models `base`, `base-ron`, and `base-ror`). All models have an uncertainty factor added in the same way as in the original model.

A key component in all variations of the proposed algorithm is that, instead of relying solely on the death-based data to model the pandemic – largely considered to be the most reliable source – we also use the **reported infections** as a way to make the model less reactive. In some variations, we suppose that the number of reported infections $C_{t,m}$ might be under-reported, so we add a normally distributed **overestimate** variable $overestimate_m \sim \mathcal{N}(11.5, 2.0)$ to model under-reporting explicitly, following estimates that the number of COVID-19 cases in Brazil was about 11 times higher than what is officially reported [22]. So, instead of optimising only the original objective function present in Equation 1, we also rely on Equation 3 below to calibrate our model:

$$C_{t,m}^* \sim \text{NegativeBinomial} \left(p_{t,m}, p_{t,m} + \frac{p_{t,m}^2}{\Phi} \right), \quad p_{t,m} = c_{t,m} / overestimate_m \quad (3)$$

where $p_{t,m}$ estimates the actual number of people infected at time t considering an overestimate. $c_{t,m}$ represents the number of reported cases, and it depends on the same assumptions of susceptible individuals S , reproduction rate R , and generation distribution g as the original model:

$$c_{t,m} = S_{t,m} R_{t,m} \sum_{\tau=0}^{t-1} c_{\tau,m} g_{t-\tau} \quad (4)$$

Our models have $K = 7$ covariates which correspond to the 6 Google Mobility indicators and the percentage of the population of a region which are Susceptible for infection $S_{t,m}$. Since the Google Mobility data is generally unavailable for future dates, when we are simulating the weekly runs, assumed that they remain constant onward from one week before the snapshot date. The reproduction rate $R_{t,m}$ is assumed to vary with the covariates:

$$R_{t,m} = R_{0,m} \exp^{-\sum_{k=1}^K I_{k,t,m} (\alpha_{k,m} + \alpha_k^*) - S_{t,m} (\alpha_{pop,m} + \alpha_{pop}^*)}, \quad (5)$$

the percentage of susceptible population $S_{t,m}$ (the seventh covariate) was modelled with a similar impact measure α_{pop} as the mobility data. On both the `base` and our proposed models we use an extra-region impact measure α_k as well as a per-region impact measure $\alpha_{k,m}$. To consistently simulate the baseline algorithm, our simulations with `base` model did not include $S_{t,m}$ as a covariate, and we also used the same way of weighting these covariates, with both a state-wide α_k and a per-region $\alpha_{k,m}$.

Some of our models (`base-base-ror` and `base-rnr`) also try to take into account the delay between PCR test collection and test result notification. We have looked at how this report delay affects the data in Santa Catarina state and results can be seen on Figure 6 for cases and on Figure 7 for deaths, according to each region of the state. Notice from these plots that infections generally can be between 2.5x to 7.5x higher than their initial reported values, and thus from 60% up to more than 85% of cases are reported with 5 days of delay. Deaths follow a similar, but less volatile, pattern rarely passing values 2x higher than their initial reports, nonetheless possibly having 50% of the data being reported after this period. While this confirms that deaths are the most reliable source of information, this also shows an issue in using such “hot” data for modelling: It can often be incomplete and lead to a false decrease in the number of cases and deaths.

In the aforementioned models, we increase the number of cases and deaths of the past week by a percent delta before running the model to try to compensate for this delay, the distribution of which can be seen in Figures S3 and S4. This gives us:

$$C_{t,m}^* = C_{t,m} (1 + \Delta retroactive_{c,t,m}) \quad (6)$$

and

$$D_{t,m}^* = D_{t,m} (1 + \Delta retroactive_{d,t,m}) \quad (7)$$

Another minor notification was that the original model assumed the onset-to-death distribution to follow the distribution $\text{Gamma}(17.8, 0.45)$. We kept the gamma function but we estimated the average and deviation from the data at each snapshot. For reference, this value was close to $\text{Gamma}(20.67, 0.76)$ on the latest simulated weeks and the distribution of onset-to-death in Santa Catarina can also be seen on Figure S5.

Model Name	Description	Optimisation Objectives	Model Interpretation	Model Inputs
base	Baseline Model	$d_{t,m} \propto k_d * D_{t,m}^*$ $c_{t,m} \propto k_c * C_{t,m}^*$	$d_{t,m} \propto XFR * c_{t,m}$	$C_{t,m}^*, D_{t,m}^*$
base-rnn	Includes reported cases and overestimate infections	$k_d = 1$ $k_c \approx 1^*$	$XFR = IFR$	As reported
base-rnn	Includes reported cases but does not attempt to overestimate infections	$k_d \approx 1^*$ $k_c \sim \mathcal{N}(11.5, 2.0)^{*\dagger}$	$XFR = IFR$	Augmented \ddagger
base-rnr	Includes reported cases, model retroactive data and overestimate infections	$k_d \approx 1^*$ $k_c \approx 1^*$	$XFR = CFR$	Augmented \ddagger
base-rnr	Includes reported cases, model retroactive data but does not attempt to overestimate infections	$k_d \approx 1^*$ $k_c \sim \mathcal{N}(11.5, 2.0)^{*\dagger}$	$XFR = IFR$	As reported
∞		$k_d \approx 1^*$ $k_c \approx 1^*$	$XFR = CFR$	As reported

Table 1: The models differ mainly in which objectives they optimise and how one can interpret the model. For our proposed models, we use infection data (with and without an estimate of under-reporting) to try to make the model less reactive, since data depending on deaths may only reflect the situation from a few weeks back. $d_{t,m}$ represents the number of predicted deaths and $D_{t,m}^*$ the number of deaths used as an input to the model, in the same fashion $c_{t,m}$ and $C_{t,m}^*$ are the number of predicted cases and the number used as an input to the model. $*$ These values may not be exact, since the model has to take into consideration the number of both cases and deaths. $\dagger \mathcal{N}(11.5, 2.0)$ follows from estimates that the number of COVID-19 cases in Brazil was about 11 times higher than officially reported [22]. \ddagger These cases are interpreted as the number of real cases as long as all the assumptions of the model hold true, which most likely they do not. \ddagger Cases $C_{t,m}$ and deaths $D_{t,m}$ from the last week of a data snapshot are augmented according to how historically these values had been retroactively changed, by having $C_{t,m} \approx C_{t,m} k_{c,t,m}$ and $D_{t,m} \approx D_{t,m} k_{d,t,m}$.

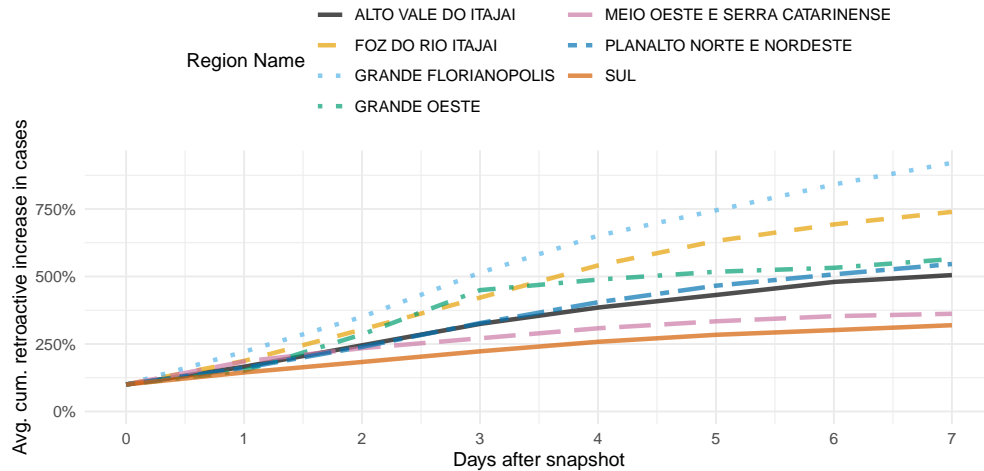


Figure 6: Distribution of cumulative retroactively-added cases on the last date.

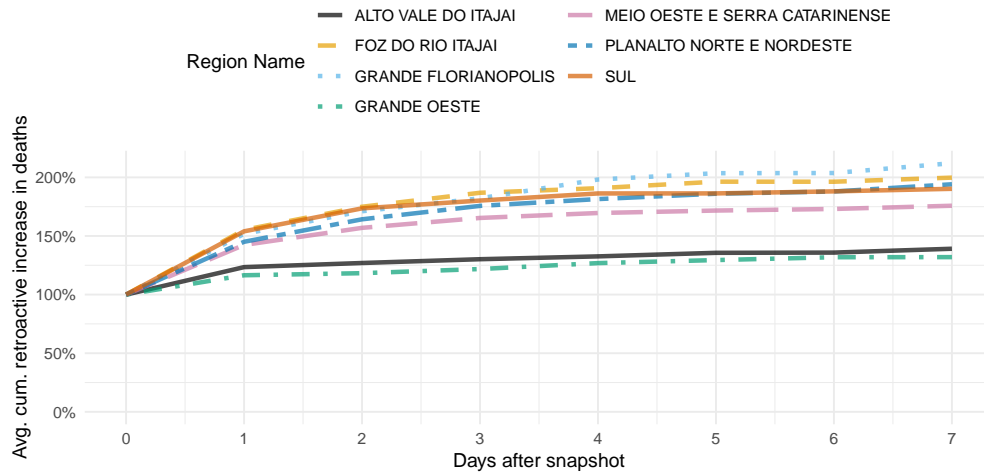


Figure 7: Distribution of cumulative retroactively-added deaths on the last date.

Test Workflow and Validation

Our main goal here is to test which combination of inputs and equations would most accurately forecast the curve of deaths by COVID-19 for the seven demographic macro-regions within Santa Catarina. With this in mind, we planned the test to span the period 31/05/2020 to 31/01/2021, running the model as if it was run weekly using only the data available at that point in time. The results were then aggregated to compose the overall prediction for the entire state.

The models produce an average prediction which we compare to the “ground-truth” number of deaths using Root Mean Squared Error (RMSE) and the Mean Average Error (MAE) metrics (Results in Tables S1-S2 and Figures 2 and 3). Because of test notification delays discussed on the previous section and shown on Figures S3-S4, we selected the data snapshot from 07/03/2021 to represent the “ground-truth” – 1 month after the last run simulation. We also wanted to estimate the error of the model given its confidence intervals and to measure this, we calculated RMSE and MAE of the upper and lower confidence intervals and took their average. These metrics RMSE_conf and MAE_conf provide a measure of how distant the borders of the confidence interval are from the truth values (shown in Tables S1-S2).

Another important part of our testing procedure is that by using the priors estimated on the previous week as starting point to the models, the Bayesian inference optimisation converged much faster and we were able to set much lighter hyper-parameters, with fewer iterations than if we had built the model from the ground up every week. The weekly procedure can also be seen in Algorithm 1. The models were run for many iterations on the first simulated week then we switched to a lighter while loading the priors from the last version (Table 2). These hyper-parameters were chosen

Algorithm 1 Test Workflow

```

1: procedure TEST
2:   last-date  $\leftarrow$  NULL
3:   for current-date in dates do
4:     if last-date is NULL then
5:       run-and-save-model(current-date, initial-hyperparameters)
6:     else
7:       run-and-save-model(current-date, hyperparameters, load-last-model(last-date))
8:       last-date  $\leftarrow$  current-date
9:     end if
10:  end for
11: end procedure

```

in a preliminary phase of testing, analysing the trade-off between reliability and execution time. This testing procedure took more than 56 hours on a personal computer to load, model and save the data, for every model. The sequential nature of the tests, which were designed in a manner that better mirrors the real-world use of the models, was one of the main reasons for why the test takes so long. While this means that we only have a single iteration of the model for each week, we still believe the sample size produced is more than enough to allow us to identify which models are better.

Hyperparameter	First model	Weekly model
Warmup Iterations	2400	600
Sampling Iterations	600	600
Number of Chains	4	4
Google Mobility Moving Average Window Size	7	7
Maximum Tree Depth	8	8
Priors	As per the baseline models[18]	Loaded from previous week

Table 2: List of hyperparameters used in the tests, with the differences shown between the version used in the first week of modelling vs all the other tests.

References

- [1] Domenico Cucinotta and Maurizio Vanelli. WHO declares COVID-19 a pandemic, 2020. ISSN 25316745.
- [2] Tedros Adhanom. Opening remarks at the media briefing on COVID-19. Technical Report March, World Health Organization (WHO), 2020. <https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---16-march-2020>.
- [3] Talha Burki. COVID-19 in Latin America. *The Lancet Infectious Diseases*, 20(5):547–548, may 2020. ISSN 14733099. doi: 10.1016/S1473-3099(20)30303-0. URL <https://linkinghub.elsevier.com/retrieve/pii/S1473309920303030>.
- [4] The Lancet. COVID-19 in Brazil: “So what?”. *The Lancet*, 395(10235):1461, 2020. ISSN 1474547X. doi: 10.1016/S0140-6736(20)31095-3. URL [http://dx.doi.org/10.1016/S0140-6736\(20\)31095-3](http://dx.doi.org/10.1016/S0140-6736(20)31095-3).
- [5] Pedro Baqui, Ioana Bica, Valerio Marra, Ari Ercole, and Mihaela van der Schaar. Ethnic and regional variations in hospital mortality from COVID-19 in Brazil: a cross-sectional observational study. *The Lancet Global Health*, 8(8):e1018–e1026, aug 2020. ISSN 2214109X. doi: 10.1016/S2214-109X(20)30285-0. URL [http://dx.doi.org/10.1016/S2214-109X\(20\)30285-0](http://dx.doi.org/10.1016/S2214-109X(20)30285-0).
- [6] Leandro Pereira Garcia, Jefferson Traebert, Alexandra Crispim Boing, Grazielli Faria Zimmer Santos, Lucas Alexandre Pedebôs, Eleonora D’orsi, Paulo Inacio Prado, Maria Amelia de Sousa Mascena Veras, Giuliano Boava, and Antonio Fernando Boing. The potential spread of covid-19 and government decision-making: A retrospective analysis in Florianópolis, Brazil. *Revista Brasileira de Epidemiologia*, 23:1–12, 2020. ISSN 1415790X. doi: 10.1590/1980-549720200091.
- [7] Nicholas P. Jewell, Joseph A. Lewnard, and Britta L. Jewell. Predictive Mathematical Models of the COVID-19 Pandemic: Underlying Principles and Value of Projections. *Journal of the American Medical Association*, 323(19):1893–1894, may 2020. ISSN 15383598. doi: 10.1001/jama.2020.6585. URL <https://jamanetwork.com/journals/jama/fullarticle/2764824>.

- [8] Ernesto Estrada. COVID-19 and SARS-CoV-2. Modeling the present, looking at the future. *Physics Reports*, 869:1–51, 2020. ISSN 03701573. doi: 10.1016/j.physrep.2020.07.005. URL <https://doi.org/10.1016/j.physrep.2020.07.005>.
- [9] Weston C. Roda, Marie B. Varughese, Donglin Han, and Michael Y. Li. Why is it difficult to accurately predict the COVID-19 epidemic? *Infectious Disease Modelling*, 5:271–281, 2020. ISSN 24680427. doi: 10.1016/j.idm.2020.03.001.
- [10] Andrea L. Bertozzi, Elisa Franco, George Mohler, Martin B. Short, and Daniel Sledge. The challenges of modeling and forecasting the spread of COVID-19. *Proceedings of the National Academy of Sciences of the United States of America*, 117(29):16732–16738, 2020. ISSN 10916490. doi: 10.1073/pnas.2006520117.
- [11] Steven Sanche, Yen Ting Lin, Chonggang Xu, Ethan Romero-Severson, Nick Hengartner, and Ruian Ke. High Contagiousness and Rapid Spread of Severe Acute Respiratory Syndrome Coronavirus 2. *Emerging Infectious Diseases*, 26(7):1470–1477, jul 2020. ISSN 1080-6040. doi: 10.3201/eid2607.200282. URL http://wwwnc.cdc.gov/eid/article/26/7/20-0282_article.htm.
- [12] Adam J. Kucharski, Timothy W. Russell, Charlie Diamond, Yang Liu, John Edmunds, Sebastian Funk, Rosalind M. Eggo, Fiona Sun, Mark Jit, James D. Munday, Nicholas Davies, Amy Gimma, Kevin van Zandvoort, Hamish Gibbs, Joel Hellewell, Christopher I. Jarvis, Sam Clifford, Billy J. Quilty, Nikos I. Bosse, Sam Abbott, Petra Klepac, and Stefan Flasche. Early dynamics of transmission and control of COVID-19: a mathematical modelling study. *The Lancet Infectious Diseases*, 20(5):553–558, may 2020. ISSN 14733099. doi: 10.1016/S1473-3099(20)30144-4. URL <https://linkinghub.elsevier.com/retrieve/pii/S1473309920301444>.
- [13] Timothy W. Russell, Joseph T. Wu, Sam Clifford, W. John Edmunds, Adam J. Kucharski, and Mark Jit. Effect of internationally imported cases on internal spread of COVID-19: a mathematical modelling study. *The Lancet Public Health*, 6(1):e12–e20, 2021. ISSN 24682667. doi: 10.1016/S2468-2667(20)30263-2. URL [http://dx.doi.org/10.1016/S2468-2667\(20\)30263-2](http://dx.doi.org/10.1016/S2468-2667(20)30263-2).
- [14] Uri Goldsztejn, David Schwartzman, and Arye Nehorai. Public policy and economic dynamics of COVID-19 spread: A mathematical modeling study. *PLoS ONE*, 15(12 December):1–16, 2020. ISSN 19326203. doi: 10.1371/journal.pone.0244174. URL <http://dx.doi.org/10.1371/journal.pone.0244174>.
- [15] You Li, Harry Campbell, Durga Kulkarni, Alice Harpur, Madhurima Nundy, Xin Wang, and Harish Nair. The temporal association of introducing and lifting non-pharmaceutical interventions with the time-varying reproduction number (R) of SARS-CoV-2: a modelling study across 131 countries. *The Lancet Infectious Diseases*, 21(2):193–202, 2021. ISSN 14744457. doi: 10.1016/S1473-3099(20)30785-4. URL [http://dx.doi.org/10.1016/S1473-3099\(20\)30785-4](http://dx.doi.org/10.1016/S1473-3099(20)30785-4).
- [16] Jan M. Brauner, Sören Mindermann, Mrinank Sharma, David Johnston, John Salvatier, Tomáš Gavenčiak, Anna B. Stephenson, Gavin Leech, George Altman, Vladimir Mikulik, Alexander John Norman, Joshua Teperowski Monrad, Tamay Besiroglu, Hong Ge, Meghan A. Hartwick, Yee Whye Teh, Leonid Chindelevitch, Yarin Gal, and Jan Kulveit. Inferring the effectiveness of government interventions against COVID-19. *Science*, 9338:eabd9338, 2020. ISSN 0036-8075. doi: 10.1126/science.abd9338.
- [17] Neil M Ferguson, Daniel Laydon, Gemma Nedjati-Gilani, Natsuko Imai, Kylie Ainslie, Marc Baguelin, Sangeeta Bhatia, Adhiratha Boonyasiri, Zulma Cucunubá, Gina Cuomo-Dannenburg, Amy Dighe, Iaria Dorigatti, Han Fu, Katy Gaythorpe, Will Green, Arran Hamlet, Wes Hinsley, Lucy C Okell, Sabine Van Elsland, Hayley Thompson, Robert Verity, Erik Volz, Haowei Wang, Yuanrong Wang, Patrick Gt Walker, Caroline Walters, Peter Winskill, Charles Whittaker, Christl A Donnelly, Steven Riley, and Azra C Ghani. Report 13: Estimating the number of infections and the impact of non-pharmaceutical interventions on COVID-19 in 11 European countries. *Imperial College COVID-19 Response Team*, 2020.
- [18] Seth Flaxman, Swapnil Mishra, Axel Gandy, H Juliette T Unwin, Helen Coupland, Thomas A Mellan, Harrison Zhu, Tresnia Berah, Jeffrey W Eaton, Pablo N P Guzman, Nora Schmit, Lucia Callizo, Imperial College COVID-19 Response Team, Charles Whittaker, Peter Winskill, Xiaoyue Xi, Azra Ghani, Christl A. Donnelly, Steven Riley, Lucy C Okell, Michaela A C Vollmer, Neil M. Ferguson, and Samir Bhatt. Estimating the number of infections and the impact of non-pharmaceutical interventions on COVID-19 in European countries: technical description update. *arXiv*, pages 1–6, apr 2020. URL <http://arxiv.org/abs/2004.11342>.
- [19] Seth Flaxman, Swapnil Mishra, Axel Gandy, H. Juliette T. Unwin, Thomas A. Mellan, Helen Coupland, Charles Whittaker, Harrison Zhu, Tresnia Berah, Jeffrey W. Eaton, Mélodie Monod, Pablo N. Perez-Guzman, Nora Schmit, Lucia Cilloni, Kylie E.C. Ainslie, Marc Baguelin, Adhiratha Boonyasiri, Olivia Boyd, Lorenzo Cattarino, Laura V. Cooper, Zulma Cucunubá, Gina Cuomo-Dannenburg, Amy Dighe, Bimandra Djaafara, Iaria Dorigatti, Sabine L. van Elsland, Richard G. FitzJohn, Katy A.M. Gaythorpe, Lily Geidelberg, Nicholas C. Grassly, William D. Green, Timothy Hallett, Arran Hamlet, Wes Hinsley, Ben Jeffrey, Edward Knock, Daniel J. Laydon, Gemma

- Nedjati-Gilani, Pierre Nouvellet, Kris V. Parag, Igor Siveroni, Hayley A. Thompson, Robert Verity, Erik Volz, Caroline E. Walters, Haowei Wang, Yuanrong Wang, Oliver J. Watson, Peter Winskill, Xiaoyue Xi, Patrick G.T. Walker, Azra C. Ghani, Christl A. Donnelly, Steven Riley, Michaela A.C. Vollmer, Neil M. Ferguson, Lucy C. Okell, and Samir Bhatt. Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe. *Nature*, 584(7820):257–261, 2020. ISSN 14764687. doi: 10.1038/s41586-020-2405-7.
- [20] Christof Kuhbandner and Stefan Homburg. Commentary: Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe. *Frontiers in Medicine*, 7(November):10–12, 2020. ISSN 2296858X. doi: 10.3389/fmed.2020.580361.
- [21] Darlan S. Candido, Ingra M. Claro, Jaqueline G. de Jesus, William M. Souza, Filipe R. R. Moreira, Simon Dellicour, Thomas A. Mellan, Louis du Plessis, Rafael Henrique Moraes Pereira, Flavia C. S. Sales, Erika Regina Manuli, Julien Thézé, Luiz Almeida, Mariane T. Menezes, Carolina Moreira Voloch, Marcilio Jorge Fumagalli, Thaís M. Coletti, Camila A. M. da Silva, Mariana Severo Ramundo, Mariene Ribeiro Amorim, Henrique H. Hoeltgebaum, Swapnil Mishra, Mandev S. Gill, Luiz Max Carvalho, Lewis Fletcher Buss, Carlos Augusto Prete, Jordan Ashworth, Helder I. Nakaya, Pedro S. Peixoto, Oliver J. Brady, Samuel M. Nicholls, Amílcar Tanuri, Átila Duque Rossi, Carlos Kaue Vieira Braga, Alexandra Lehmkuhl Gerber, Ana Paula de C. Guimarães, Nelson Gaburo, Cecila Salete Alencar, Alessandro C. S. Ferreira, Cristiano Xavier Lima, José Eduardo Levi, Celso Granato, Giulia Magalhaes Ferreira, Ronaldo S. Francisco, Fabiana Granja, Marcia Teixeira Garcia, Maria Luiza Moretti, Mauricio Wesley Perroud, Terezinha M. P. P. Castiñeiras, Carolina S. Lazari, Sarah C. Hill, Andreza Aruska de Souza Santos, Camila Lopes Simeoni, Julia Forato, Andrei Carvalho Sposito, Angelica Zaninelli Schreiber, Magnun Nueldo Nunes Santos, Camila Zolini de Sá, Renan Pedra Souza, Luciana Cunha Resende-Moreira, Mauro Martins Teixeira, Josy Hubner, Patricia Asfora Falabella Leme, Rennan Garcias Moreira, Maurício Lacerda Nogueira, Neil M. Ferguson, Silvia Figueiredo Costa, José Luiz Proenca-Modena, Ana Tereza R. Vasconcelos, Samir Bhatt, Philippe Lemey, Chieh-Hsi Wu, Andrew Rambaut, Nick J. Loman, Renato Santana Aguiar, Oliver G. Pybus, Ester C. Sabino, and Nuno Rodrigues Faria. Evolution and epidemic spread of SARS-CoV-2 in Brazil. *Science*, 369(6508):1255–1260, sep 2020. ISSN 0036-8075. doi: 10.1126/science.abd2161. URL <https://www.sciencemag.org/lookup/doi/10.1126/science.abd2161>.
- [22] Marcelo Freitas Do Prado, Bianca Brandão De Paula Antunes, Leonardo Dos Santos Lourenço Bastos, Igor Tona Peres, Amanda De Araújo Batista Da Silva, Leila Figueiredo Dantas, Fernanda Araújo Baião, Paula Maçaira, Silvio Hamacher, and Fernando Augusto Bozza. Analysis of COVID-19 under-reporting in Brazil. *Revista Brasileira de Terapia Intensiva*, 32(2):224–228, 2020. ISSN 19824335. doi: 10.5935/0103-507X.20200030.
- [23] Katelyn M. Gostic, Lauren McGough, Edward B. Baskerville, Sam Abbott, Keya Joshi, Christine Tedijanto, Rebecca Kahn, Rene Niehus, James A. Hay, Pablo M. De Salazar, Joel Hellewell, Sophie Meakin, James D. Munday, Nikos I. Bosse, Katharine Sherrat, Robin N. Thompson, Laura F. White, Jana S. Huisman, Jérémie Scire, Sebastian Bonhoeffer, Tanja Stadler, Jacco Wallinga, Sebastian Funk, Marc Lipsitch, and Sarah Cobey. Practical considerations for measuring the effective reproductive number, Rt. *PLoS Computational Biology*, 16(12):1–21, 2020. ISSN 15537358. doi: 10.1371/journal.pcbi.1008409.
- [24] Shiva Moein, Niloofar Nickaeen, Amir Roointan, Niloofar Borhani, Zarifeh Heidary, Shaghayegh Haghjooy Javanmard, Jafar Ghaisari, and Yousof Gheisari. Inefficiency of SIR models in forecasting COVID-19 epidemic: a case study of Isfahan. *Scientific Reports*, 11(1):4725, dec 2021. ISSN 2045-2322. doi: 10.1038/s41598-021-84055-6. URL <https://doi.org/10.1038/s41598-021-84055-6> <http://www.nature.com/articles/s41598-021-84055-6>.
- [25] Kristian Soltesz, Fredrik Gustafsson, Toomas Timpka, Joakim Jaldén, Carl Jidling, Albin Heimerson, Thomas B. Schön, Armin Spreco, Joakim Ekberg, Örjan Dahlström, Fredrik Bagge Carlson, Anna Jöud, and Bo Bernhardsson. The effect of interventions on COVID-19. *Nature*, 588(7839):E26–E28, 2020. ISSN 14764687. doi: 10.1038/s41586-020-3025-y. URL <http://dx.doi.org/10.1038/s41586-020-3025-y>.
- [26] Jordana Cepelewicz. The Hard Lessons of Modeling the Coronavirus Pandemic. *Quanta Magazine*, pages 1–28, 2021. URL <https://www.quantamagazine.org/the-hard-lessons-of-modeling-the-coronavirus-pandemic-20210128/>.
- [27] CIASC-SC. Plataforma BoaVista, 2021. URL <https://www.sc.gov.br/boavista/>.
- [28] IBGE. Estimativas populacionais dos municípios em 2019. https://ftp.ibge.gov.br/Estimativas_de_Populacao/Estimativas_2019/estimativa_dou_2019.pdf, 2019. Last Accessed: 2021-03-22.
- [29] Ahmet Aktay, Shailesh Bavadekar, Gwen Cossoul, John Davis, Damien Desfontaines, Alex Fabrikant, Evgeniy Gabrilovich, Krishna Gadepalli, Bryant Gipson, Miguel Guevara, Chaitanya Kamath, Mansi Kansal, Ali Lange, Chinmoy Mandayam, Andrew Oplinger, Christopher Pluntke, Thomas Roessler, Arran Schlosberg, Tomer Shekel, Swapnil Vispute, Mia Vu, Gregory Wellenius, Brian Williams, and Royce J. Wilson. Google COVID-19

- Community Mobility Reports: Anonymization Process Description (version 1.1). *arXiv*, pages 1–6, apr 2020. ISSN 23318422. URL <http://arxiv.org/abs/2004.04145>.
- [30] G1-Santa-Catarina. SC tem 9,5 mil mortes por Covid-19 e 397 pacientes na fila por UTI (PT-BR). <https://g1.globo.com/sc/santa-catarina/noticia/2021/03/21/sc-tem-95-mil-mortes-por-covid-19-e-397-pessoas-na-fila-por-uti.ghtml>, mar 2021.
- [31] Thomas A Mellan, Henrique H Hoeltgebaum, Swapnil Mishra, Charlie Whittaker, Ricardo P Schnekenberg, Axel Gandy, H Juliette T Unwin, Michaela A C Vollmer, Helen Coupland, Iwona Hawryluk, Nuno Rodrigues Faria, Juan Vesga, Harrison Zhu, Michael Hutchinson, Oliver Ratmann, Melodie Monod, Kylie Ainslie, Marc Baguelin, Sangeeta Bhatia, Adhiratha Boonyasiri, Nicholas Brazeau, Giovanni Charles, Laura V Cooper, Zulma Cucunuba, Gina Cuomo-Dannenburg, Amy Dighe, Bimandra Djaafara, Jeff Eaton, Sabine L van Elsland, Richard FitzJohn, Keith Fraser, Katy Gaythorpe, Will Green, Sarah Hayes, Natsuko Imai, Ben Jeffrey, Edward Knock, Daniel Laydon, John Lees, Tara Mangal, Andria Mousa, Gemma Nedjati-Gilani, Pierre Nouvellet, Daniela Olivera, Kris V Parag, Michael Pickles, Hayley A Thompson, Robert Verity, Caroline Walters, Haowei Wang, Yuanrong Wang, Oliver J Watson, Lilith Whittles, Xiaoyue Xi, Lucy Okell, Iliaria Dorigatti, Patrick Walker, Azra Ghani, Steven M Riley, Neil M Ferguson, Christl A Donnelly, Seth Flaxman, and Samir Bhatt. Report 21: Estimating COVID-19 cases and reproduction number in Brazil. *medRxiv*, page 2020.05.09.20096701, May 2020.
- [32] Municípios recebem Sala de Situação Digital (SSD) para apoiar o combate à covid-19. <https://www.mpsc.mp.br/noticias/municipios-recebem-sala-de-situacao-digital-ssd-para-apoiar-o-combate-a-covid-1>, jul 2020. Press Release from Coordenadoria de Comunicação - MPSC.
- [33] Ferramenta de apoio no combate à Covid-19 é lançada com a contribuição do Judiciário. <https://www.tjsc.jus.br/web/imprensa/-/ferramenta-de-apoio-no-combate-a-covid-19-e-lancada-com-a-contribuicao-do-judiciario>, jul 2020. Press Release from NCI - TJSC.
- [34] Bang Wong. Points of view: Color blindness. *Nature Methods*, 8(6):441–441, jun 2011. ISSN 1548-7091. doi: 10.1038/nmeth.1618. URL <http://www.nature.com/articles/nmeth.1618>.

Acknowledgements

The research presented in this paper was conceived in the context of the Intersectorial Data Intelligence Center for COVID-19 (NIIDC), a group of volunteers that ran from March until June 2020 from academia, private companies and public local state departments dedicated to discuss data analytic strategies with potential to inform decision-makers in the southern Brazilian state of Santa Catarina (SC) [32, 33]. Special thanks to Dr. Ana Luiza Curi Hallal for the valuable exchanges and discussions about epidemic modelling in the early days of this group. We thank CIASC (SC) for providing us with credentials to download data from Platform BoaVista. Thanks, Bang Wong, for providing with a colour scheme inclusive for colour-blind people [34]. Data Science Brigade acknowledges funding from ICASA (SC). P.H.C.A and L.C.L. acknowledge that this study was financed in part by CNPq (Brazilian Research Council) and Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Finance Code 001.

Author contributions statement

P.H.C.A and J.C.S. conceived the experiment(s), P.H.C.A programmed and conducted the experiment(s), P.H.C.A and J.C.S. analysed the results. All authors reviewed the manuscript.

Code availability

The code for these models can be found on the Github repository: <https://github.com/Data-Science-Brigade/paper-covid19-modelling-2021-03>.

Supplementary Information

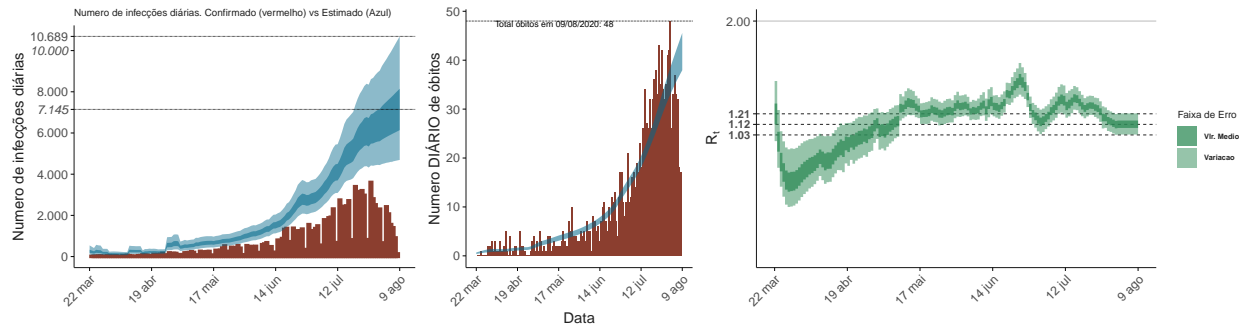
Model	RMSE7		RMSE30	
	pred	conf	pred	conf
base	2.55	2.46	5.79	3.57
base-ron	2.29	2.55	2.92	3.06
base-rnn	2.48	2.55	3.14	3.10
base-ror	2.28	2.20	3.05	2.82
base-rnr	2.31	2.43	3.02	3.01

Model	MAE7		MAE30	
	pred	conf	pred	conf
base	2.19 (± 1.05)	2.09 (± 1.05)	4.77 (± 2.71)	2.96 (± 1.60)
base-ron	1.96 (± 0.95)	2.21 (± 1.01)	2.40 (± 1.32)	2.51 (± 1.38)
base-rnn	2.13 (± 0.98)	2.18 (± 1.06)	2.56 (± 1.45)	2.54 (± 1.41)
base-ror	1.97 (± 0.92)	1.86 (± 0.96)	2.52 (± 1.36)	2.27 (± 1.32)
base-rnr	1.97 (± 0.96)	2.07 (± 1.01)	2.48 (± 1.37)	2.45 (± 1.38)

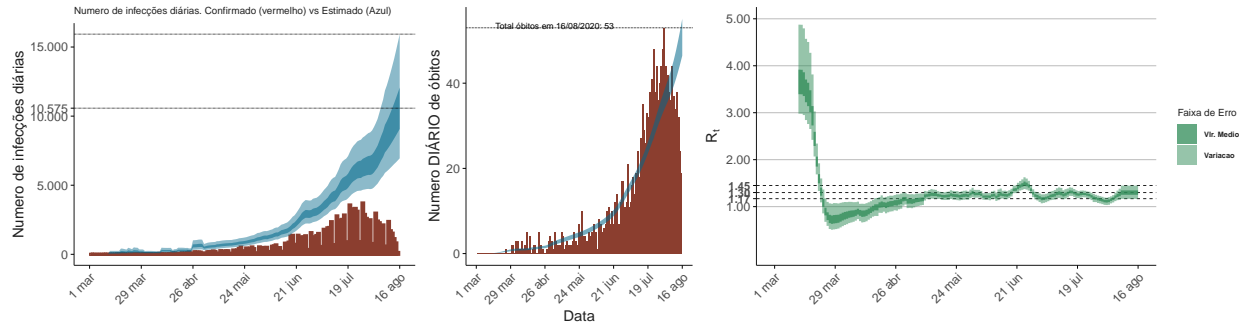
Table S1: This table shows the error values (RMSE and $avg(\pm std)$ MAE) for the predicted value and their confidence interval counterparts in a 7 and 30-day forecasting window.

Region	Model	RMSE7		RMSE30	
		pred	conf	pred	conf
Alto Vale do Itajaí	base	2.44	2.09	7.17	3.06
	base-ron	1.94	2.32	2.39	2.81
	base-rnn	2.11	2.39	2.69	2.87
	base-ror	1.91	1.99	2.32	2.50
	base-rnr	2.13	2.28	2.72	2.79
Foz do Rio Itajaí	base	2.40	2.44	4.61	3.47
	base-ron	2.14	2.36	2.65	2.79
	base-rnn	2.21	2.43	3.03	2.96
	base-ror	2.17	2.12	2.74	2.59
	base-rnr	2.17	2.32	2.81	2.87
Grande Florianopolis	base	2.91	2.75	8.94	4.31
	base-ron	2.65	2.77	3.43	3.30
	base-rnn	2.50	2.65	3.34	3.10
	base-ror	2.67	2.41	3.72	3.10
	base-rnr	2.49	2.62	3.44	3.06
Grande Oeste	base	1.52	1.60	2.96	2.35
	base-ron	1.64	1.62	2.22	2.26
	base-rnn	2.93	1.60	3.00	2.29
	base-ror	1.52	1.46	2.23	2.09
	base-rnr	1.60	1.52	2.19	2.15
Meio Oeste e Serra Catarinense	base	2.10	2.02	3.60	2.75
	base-ron	1.90	2.23	2.22	2.56
	base-rnn	1.93	2.32	2.29	2.71
	base-ror	1.83	1.86	2.27	2.22
	base-rnr	2.01	2.15	2.35	2.54
Planalto Norte e Nordeste	base	2.80	3.14	4.59	4.17
	base-ron	2.59	2.98	3.37	3.77
	base-rnn	2.67	3.10	3.69	3.95
	base-ror	2.58	2.51	3.42	3.34
	base-rnr	2.63	2.90	3.52	3.77
Sul	base	3.66	3.21	8.66	4.86
	base-ron	3.17	3.58	4.13	3.91
	base-rnn	3.01	3.37	3.96	3.85
	base-ror	3.28	3.08	4.62	3.91
	base-rnr	3.11	3.19	4.10	3.86

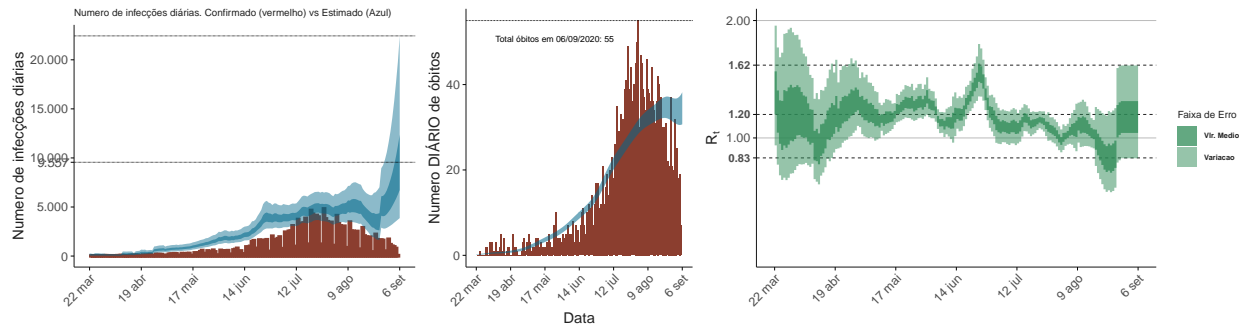
Table S2: This table shows the error values (RMSE) for the predicted value and their confidence interval counterparts in a 7 and 30-day forecasting window, aggregated over each region the model was ran for.



(a) Diagnostic plots for base model for 10/08/2020

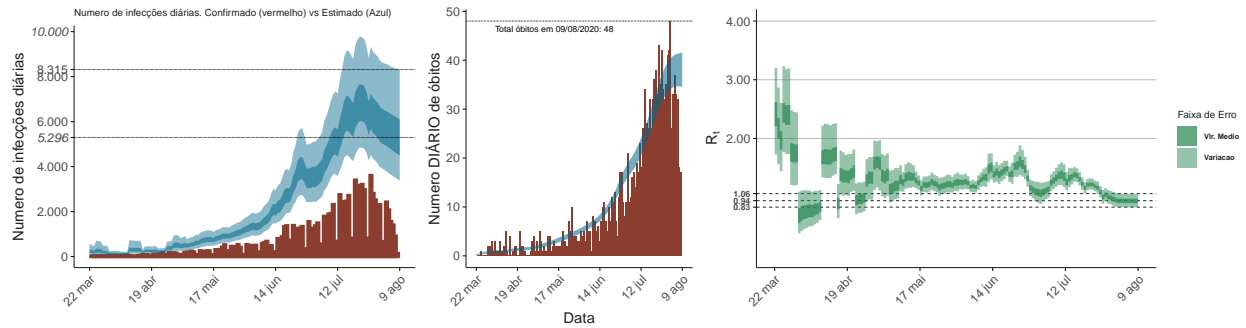


(b) Diagnostic plots for base model for 17/08/2020

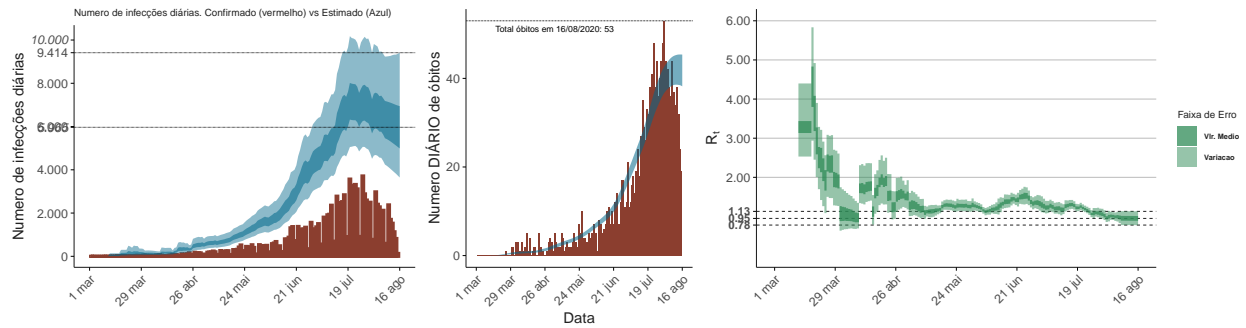


(c) Diagnostic plots for base model for 07/09/2020

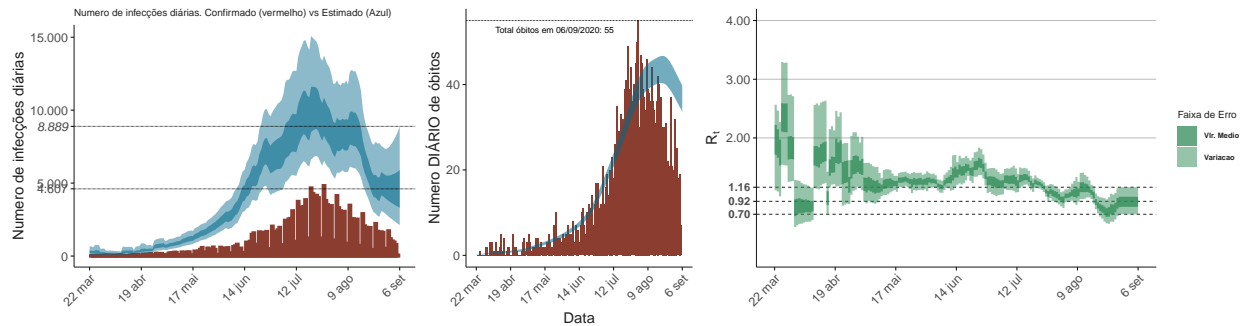
Figure S1: Diagnostics plots for simulations with base model for three selected dates for the state of Santa Catarina. From left to right, the plots indicate: i) number of new reported infections per day (red) and the probable actual number of infections as estimated by the algorithm (blue) ii) number of confirmed deaths per day (red) and the probable actual number of deaths as fitted by the algorithm (blue) iii) the effective reproduction number R_t for the state over the period up until the snapshot date.



(a) Diagnostic plots for base-run model for 10/08/2020



(b) Diagnostic plots for base-run model for 17/08/2020



(c) Diagnostic plots for base-run model for 07/09/2020

Figure S2: Diagnostics plots for simulations with base-run model for three selected dates for the state of Santa Catarina. From left to right, the plots indicate: i) number of new reported infections per day (red) and the probable actual number of infections as estimated by the algorithm (blue) ii) number of confirmed deaths per day (red) and the probable actual number of deaths as fitted by the algorithm (blue) iii) the effective reproduction number R_t for the state over the period up until the snapshot date.

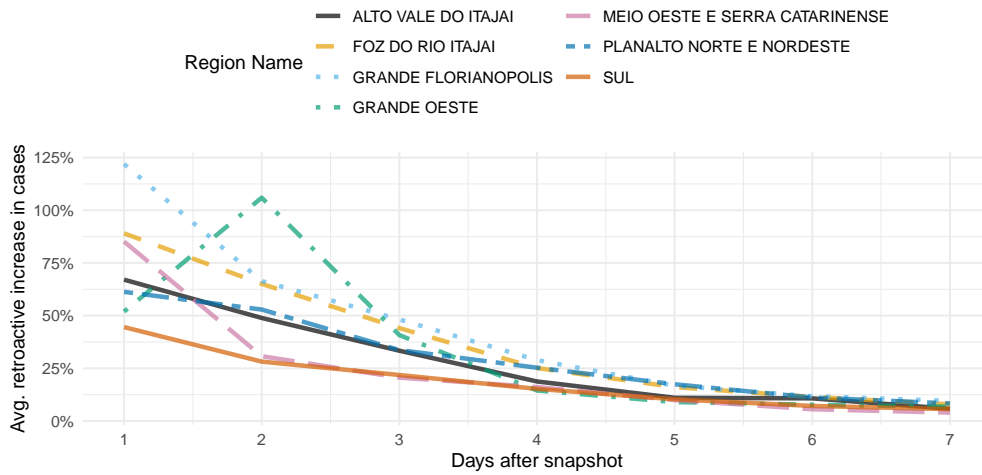


Figure S3: Distribution of retroactively-added cases on the last date. For example, if for a region there are 100% average retroactive increase in cases 2 days after the snapshot, it means that, on the date two days earlier than the snapshot's date, the number of cases should be doubled to represent the true value.

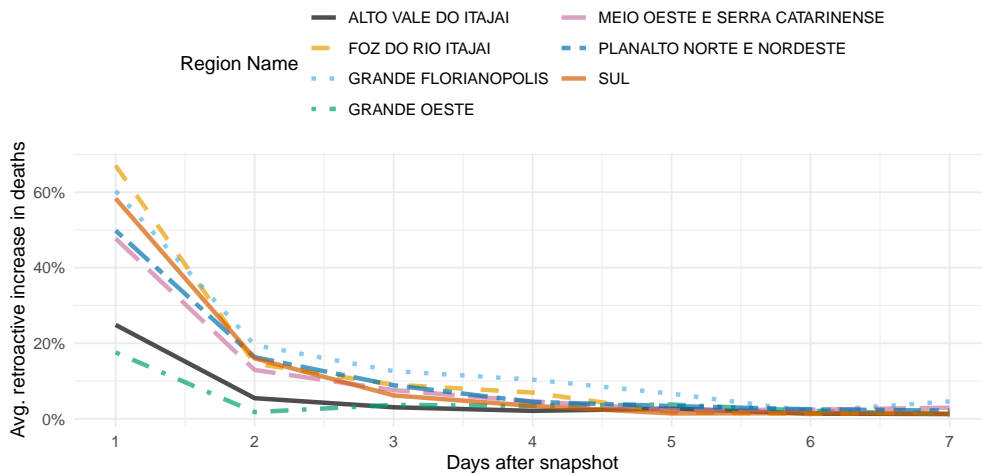


Figure S4: Distribution of retroactively-added deaths on the last date. For example, if for a region there are 100% average retroactive increase in deaths 2 days after the snapshot, it means that, on the date two days earlier than the snapshot's date, the number of deaths should be doubled to represent the true value.

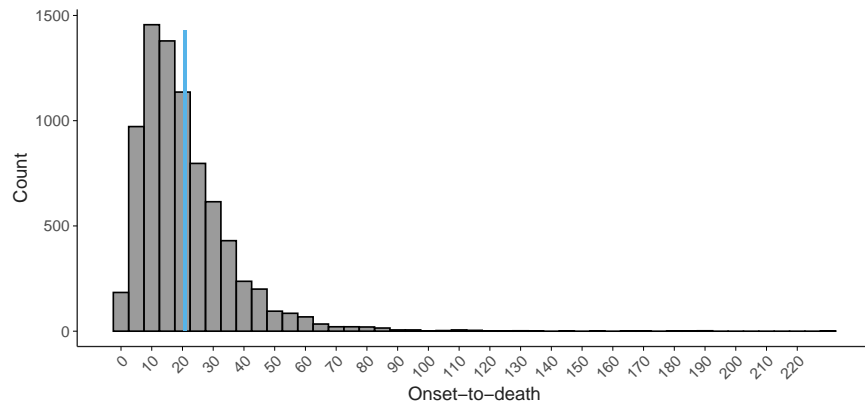


Figure S5: Distribution in days relative to the date of onset of first reported symptoms until date of death across Santa Catarina state in Brazil, according to data provided by Plataforma Boa Vista [27].

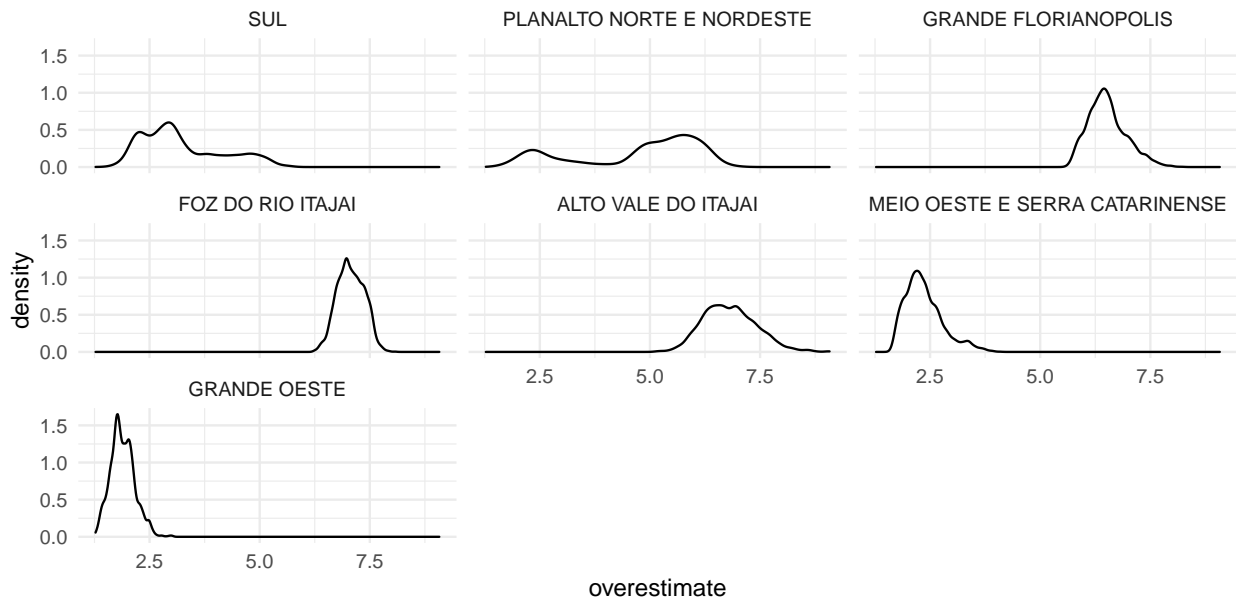


Figure S6: Distribution of the overestimate parameter in the last 600 iterations of all chains for the last base-run model. The multimodality present here is due to the fact that we ran 4 independent chains, which generated different distributions that, when combined, produce a multimodal distribution.