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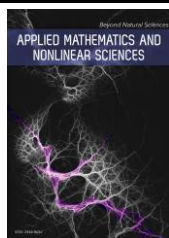


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## Adaptation of the COVASIM model to incorporate non-pharmaceutical interventions: Application to the Dominican Republic during the second wave of COVID-19

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### Abstract

We adapt the Covasim agent-based model for predicting new COVID-19 cases by tuning the transmissibility rate with information on the impact of the most common non-pharmaceutical interventions (NPIs) obtained through machine learning models. Such impact has been estimated thanks to the information on applying pools of NPIs worldwide from the Oxford COVID-19 Government Response Tracker.

This approach permits the simulation of a whole country or a smaller region, providing information about asymptomatic, recovery, severe, and critical new cases and enabling governments and authorities to set NPIs plans to cope with the pandemic.

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**Keywords:** COVID-19; agent based modeling; non-pharmaceutical interventions.

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## 1 Introduction

Since the beginning of the COVID-19 pandemic, the mathematical modeling of the pandemic has permitted to forecast its evolution and determine whether sanitary services would eventually collapse. There was not a typical pattern for all patients. Moreover, there could be asymptomatic people and severe cases who finally die [1]-[3]. The application of different non-pharmaceutical interventions (NPIs) resulted in being the only kind of measures governments could take to contain the illness spreading and avoid collapses in health services. Meanwhile, a vast amount of medical research started in order to develop effective treatments based on existing drugs, and the appearance of new vaccines reduced mortality and illness severity [4]-[7].

The rapid and massive increase in cases has been forecasted using mathematical and computational base epidemic models [8],[9]. Most of these models, such as compartmental models, are tuned to predict the evolution in the number of cases and deaths [10],[11]. These models admit incorporating population vaccination [12]-[14]. However, the effect of the application of different combinations of NPIs is challenging to incorporate them into these models. Nevertheless, we can address statistical and artificial intelligence-based models [15]-[17] to estimate each NPIs contribution to modify the infection rates.

Agent-based models (ABM) arise as an alternative to these approaches. In these models, people are considered agents. The NPIs are incorporated to modify the population's behaviors and simulate future scenarios of the disease spreading after the applications of different pools of NPIs. More than a decade ago, they started to be used to simulate the spread of influenza across metropolitan areas and the continental United States of America [18]. That model was used at the pandemic's beginning to simulate COVID-19 disease spreading in Singapore, accounting for geographical, demographic, and epidemiological data [19]. In [20], an ABM was used to model the French population integrating demographic and social contact data extracted from population statistics on age, household size and composition, workplace and school size, smartphone penetration, and commuting fluxes. Later, it was extended to incorporate the effect of vaccination policies [21]. In Australia, anonymized demographic information was completed with near real-time SARS-CoV-2 virus genome sequencing in order to identify infection outbreaks where traditional epidemiological models could not find these links, simulating indoor spreading of the virus [22] and permit to evaluate of different strategies to control the virus spreading inside care homes [23]. Such an approach was also considered to model the COVID-19 spread in small [24] and big cities [25]. In this last case, data from mobile phone tracking, census, and building characteristics were combined with NPIs, such as contact tracing, compulsory mask usage and early testing.

Beyond the simulation and prediction of the virus expansion, ABMs let researchers test the effect that different pools of NPIs can have in the control of the pandemics, deciding how to set postlock down NPIs in order to predict the number of deaths, new cases, and intensive care units (ICU) occupancy [26] or for deciding that it was better to prioritize the first dose of the vaccine to almost the whole population instead of completing the vaccination scheme with a second dose [27] for a part of the population. See also [28] for another use case of ABMs to determine vaccination policies among other NPIs. ABMs let us also study the impact of different NPIs applications on economic activities [29]. Early volunteer accomplished lockdowns resulted in a strategy with more negligible economic damage to stop the virus from spreading at an early stage. The impact increases as long as the percentage of the population who need to work for a living or depend on social services increases. In a similar line, in [30] it was shown that the dichotomy between deaths and economic costs is false. Scenarios simulated with no implemented NPIs to preserve the economy resulted in higher deaths, eventually negatively affecting a country's economy. Besides, ABMs permit to

simulate the supply chain recovery process shows that a rapid increase in production permits a sooner economic recovery [31].

Remarkable ABM models have been used in Australia [22], Singapore [22], the United Kingdom [32] and the United States [33],[34]. Among all ABMs, Covasim was one of the most widely used agent-based modeling tools [35]. It is flexible and allows to be adapted to incorporate estimations on the effect of different NPIs.

Since the beginning of the pandemic, two open data repositories have aided researchers and governments in coping with the pandemic. On the one hand, the John Hopkins Coronavirus Resource Center<sup>1</sup> has gathered information on the number of cases, deaths, tests, hospitalizations, and vaccinated people since January 22<sup>nd</sup>, 2020, in order to help governments and healthcare professionals around the world to respond to the pandemic. On the other hand, the Oxford Covid-19 Government Response Tracker (OxCGRT) [36] has collected information on policy measures, and NPIs applied by governments in 180 countries worldwide to tackle COVID-19. These NPIs have systematically been coded on 23 indicators, such as school closing level, gathering restrictions, or vaccination policies. The NPIs scheme and data can be downloaded from<sup>2</sup> the official GitHub repository.

Although Covasim allows modeling non-pharmaceutical interventions using different layers, some NPIs that have commonly been applied are not included. Besides, an estimation of the effect on the population of these NPIs is not considered. To do so, we have adapted the Covasim model to incorporate information on the different application levels of NPIs. Our work is organized as follows: In Section 2, we describe how Covasim can model different populations and how it implements NPIs that can be applied to control the spread of COVID-19. We also introduce how we implement the usage of the Oxford Covid-19 Government Response Tracker of non-pharmaceutical interventions to extract accurate information about the NPIs application worldwide. Later, in Section 3, we show the results obtained and we present the conclusions in Section 4.

## 2 Methodology

There are three population network models already implemented in Covasim to simulate people interactions. These models simulate contacts among people in different situations. When an agent is infected with the virus, some of her interactions with other agents result in newly infected people.

- **Random networks.** Each person can get in touch, transmitting or catching the COVID-19 disease, with any other person in the simulated population. This basic model considers no other information like demographics or contacts at schools or workplaces, making it the less realistic model but the fastest one to be computed.
- **SynthPops.** SynthPops<sup>3</sup> is an open-source model which allows the creation of realistic contact networks for synthetic populations. This model permits setting contact patterns for different age groups in different environments like households, schools, workplaces, and the whole community. A Poisson distribution simulates the contacts.
- **Hybrid networks.** This is a hybrid method of the random and SynthPop models. It inherits part of the realism from SynthPops but requires fewer input data. As in SynthPops, every

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<sup>1</sup> <https://github.com/govex/COVID-19>

<sup>2</sup> <https://github.com/OxCGRT/covid-policy-tracker>

<sup>3</sup> <https://www.synthpop.org.uk/>

person in the population is assigned to contacts in her household, school (children), workplace (adults), and community. The initial population is created following the selected location age distribution. Each person is randomly assigned to a household, considering specific location information about households. All people between six and twenty-two years old are assigned to schools and universities, while all individuals between twenty-three and sixty-five are assigned to workplaces. Nevertheless, household population age distribution is not considered when distributing the individuals. In our experiments, we have used this model for reducing computational costs, without committing the accuracy in the predictions.

We can also model intervention policies that can affect how COVID-19 spreads, which helps us to understand their impact on spreading the disease. The basic default interventions included in Covasim are the following ones:

- **Physical distancing, masks, and hygiene.** This intervention is modeled by reducing the propagation rate ( $\beta$ ) or by reducing the number of links (edges) between individuals, depending on which population model we are using.
- **Testing and diagnosis.** Testing can be modeled by the user providing a daily number of tests to be done or by establishing probabilities for an individual to get a test depending on symptoms or risk factor level.
- **Contact tracing.** When an individual is tested positive, another individual who has been in contact with her should be traced to be set under quarantine, tested, and, if needed, change their state to positive.
- **Isolation of positives and contact quarantine.** Isolation applies to an individual who has tested positive, while quarantine refers to someone who has been in contact with someone who has tested positive.
- **Vaccines and treatments.** This intervention can be implemented in Covasim by modifying the probability of an individual infecting others and developing symptoms after receiving the vaccine.

These interventions can be parametrized and estimated ad hoc. However, to facilitate its comprehension and generalization, we propose to tune the Covasim model with information from Oxford Covid-19 Government Response Tracker (OxCGRT) [36], whose database is the result of gathering information from monitoring the application of NPIs around the world. Other alternatives are discussed in [37], such as the Health Intervention Tracking for COVID-19 (HIT-COVID) [38], the Complexity Science Hub COVID-19 Control Strategies List (CCCSL) project, the Response2covid19 project [39], the CoronaNet Research Project (CoronaNet) [40], or the COVID-19 Economic Stimulus Index [41].

In this work, we will rely on the OxGRCT, whose use was widely extended and was the base of the Pandemic Response Challenge organized by the XPRIZE Foundation. The real impact of each of these interventions was studied in great detail there, to use the subsequent analysis to study the period between December 22nd, 2020, and January 22nd, 2021, during the second wave of cases in the Dominican Republic.

## 2.1 Tuning the model with OxGRCT interventions

Let us tune the parameters. We can start setting a default COVID-19 infection rate ( $\beta$ ) of 0.016, which was estimated at the beginning of the pandemic (*Primal* variant) when no intervention policies were set [35], see also [11]. In this work, we will use the default value, although it can be increased for high-transmission environments and reduced for low-transmission ones. Modifying the interventions mentioned above can restrict the value of  $\beta$  to a minimum value of 0.001 since there is no viable way to prevent in-house contact. There will always be a minimal residual spread rate among families and close contact groups.

In December 18<sup>th</sup>, 2020, the World Health Organization (WHO) included the *Alpha* variant (lineage B.1.1.1, henceforth VOC 202012/01) among the variants of concern due to its high transmissibility. It was firstly estimated to have an increase in the infection rate of a 77% (95% CI, 73 to 81%) in the United Kingdom, 55% (95% CI, 45 to 66%) higher in Denmark, 74% (95% CI, 66 to 82%) higher in Switzerland, and 59% (95% CI, 56 to 63%) higher in the United States [42] because of mutations in the spike protein. As an average of the current results, we consider for our simulations that it is 66% more transmissible, see [42] [Table 1], resulting in a value for  $\beta$  of 0.02656.

In both cases, we have estimated that the infection rate is reduced due to the application of NPIs informed in the OxGRCT database. Some were the basis of one of the most successful models in short and long-term predictions of the pandemics [15], which was developed by the Valencia IA4COVID team that won the Pandemic Response Challenge organized by the XPRIZE Foundation.

Confinement intervention policies (C1 to C8) were used to predict COVID-19 cases of [15],[43], which were running during the period between December 2020 and February 2021. Confinement and public health interventions (H1, H2, H3, and H6) were considered in the prescriptor of NPI plans of [15]. The application of these NPIs is tagged with different levels as shown in Table 1, being 0 the lower level of application and the highest level the most restrictive one. Further details on the description of these NPIs can be found in the codebook of the OxCGRT dataset [44]. The vaccination policy (H7), with five levels, was later incorporated into both the predictor and prescriptor models, but this is outside the scope of this work since, during this period, no vaccines were administered in Dominican Republic.

**Table 1.** NPIs selected from the OxCGRT [36].

NPI name	Values	NPI name	Values
C1. School closing	[0,1,2,3]	C7. Internal movement restrictions	[0,1,2]
C2. Workplace closing	[0,1,2,3]	C8. International travel controls	[0,1,2,3]
C3. Cancel public events	[0,1,2]	H1. Public information campaigns	[0,1,2]
C4. Restrictions on gatherings	[0,1,2,3,4]	H2. Testing policy	[0,1,2,3]
C5. Close public transport	[0,1,2]	H3. Contact tracing	[0,1,2]
C6. Stay at home requirements	[0,1,2,3]	H6. Facial coverings	[0,1,2,3,4]

The importance of each NPI was estimated using a gradient-boosting algorithm, see [45], [Supplementary Material]. Their relative importance has been rescaled to add 100%. For completeness, we present this information in Table 2 regarding their relative importance.

**Table 2.** NPIs relative importance from [45]. The sum of all of them is 100%.

NPI name	Import.	NPI name	Import.
C2. Workplace closing	32.2%	H1. Public information campaigns	5.6%
C1. School closing	16.0%	C6. Stay at home requirements	3.9%
H2. Testing policy	10.3%	C7. Internal movement restrictions	3.3%
C8. International travel controls	7.7%	H3. Contact tracing	2.9%
C4. Restrictions on gatherings	7.0%	H6. Facial coverings	2.7%
C5. Close public transport	6.0%	C3. Cancel public events	2.4%

According to those above  $\beta$  range values, the minimum stringency (all NPIs set to 0) corresponds to the maximum  $\beta$  value of 0.016 for the Primal variant and 0.02656 for the Alpha variant, and the maximum stringency (all NPIs set to their respective maximum value) produces the minimum  $\beta$  value of 0.001. Given a policy plan determined by the application of some of these policies at certain levels  $L_{C_1}, L_{C_2}, \dots, L_{C_8}, L_{H_1}, \dots, L_{H_6}$  gives the following estimation of the parameter  $\beta$ .

$$\beta = \beta_0 - \left( \sum_{i=1}^8 w_{C_i} L_{C_i} + \sum_{i=1,2,3,6} w_{H_i} L_{H_i} \right) \cdot \left( \frac{\beta_0 - 0.001}{100} \right). \quad (1)$$

where  $\beta_0 = 0.016, 0.0256$ , depending on the variant (Primal/Alpha),  $w_{C_1}, \dots, w_{H_6}$  are the values with the relative importance of each NPI as stated in Table 2 and  $L_{C_i}, L_{H_i}$  are the levels of the applied NPIs divided by the maximum level of application of each one.

NPIs are usually combined at different levels, so it is impossible to correctly determine the importance of each one in the reduction of the number of cases. In [17], the importance of each NPI is estimated through the weight of the regression coefficients in the model. Both estimations agree that school and workplace closings are among the most effective NPIs. There are also other measures, such as testing policy and contact tracing, in which both models differ in the assigned importance but are usually jointly applied.

In the period under consideration, the NPIs were set almost all the days to the following levels:

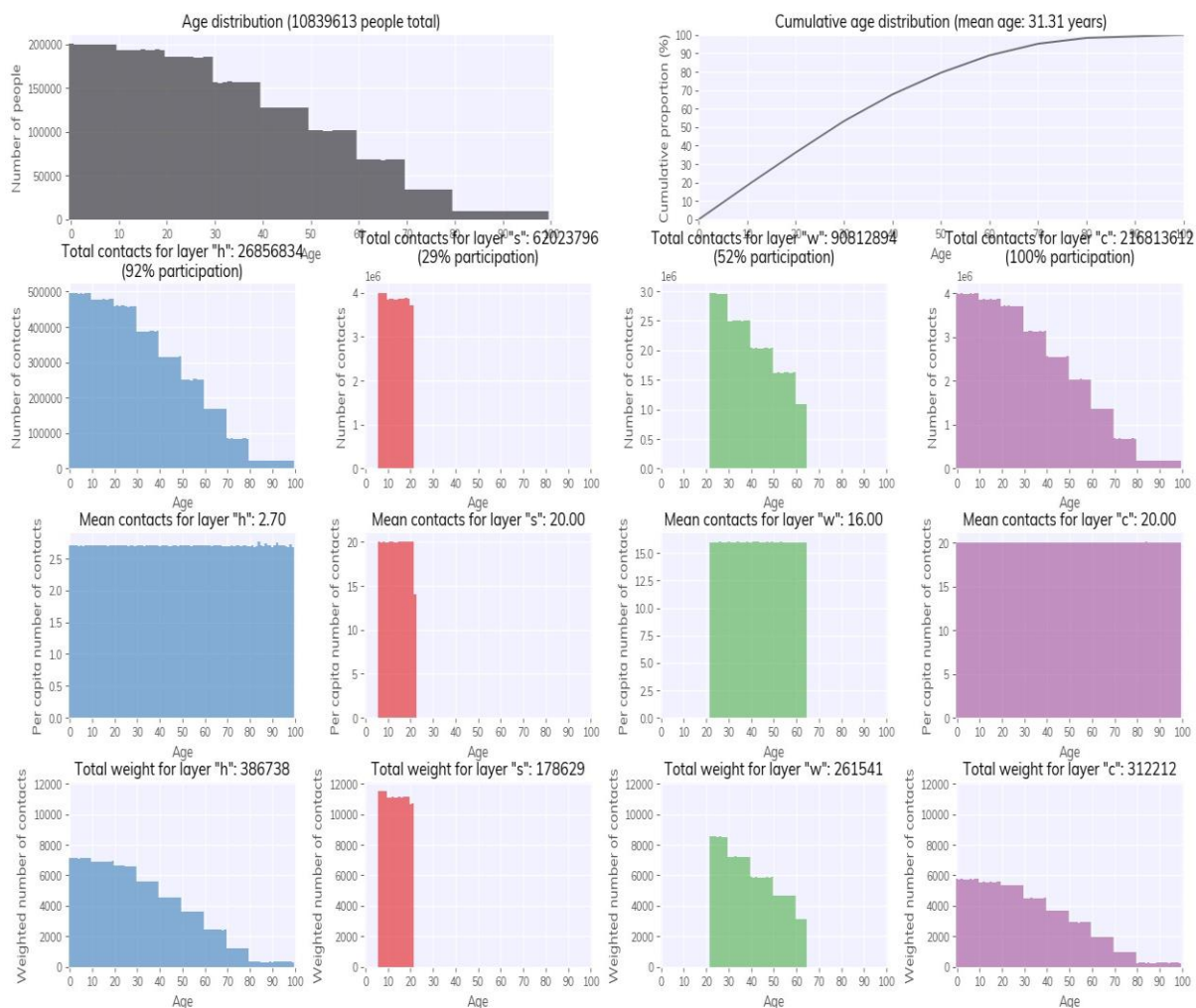
- C1 (3 - require closing all school levels),
- C2 (2 - require closing (or work from home) for some sectors or categories of workers),
- C3 (2 - require canceling public events),
- C4 (3 - restrictions on gatherings between 11-100 people),
- C5 (1 - recommend closing (or significantly reduce volume/route/means of transport available)),
- C6 (2 - require not leaving the house with exceptions for daily exercise, grocery shopping, and 'essential' trips),
- C7 (0 - no restrictions on movement between regions),
- C8 (3 - ban arrivals from some countries),
- H1 (2 - coordinated public information campaign (e.g., across traditional and social media)),

- H2 (2 - testing of anyone showing COVID-19 symptoms),
- H3 (1 - limited contact tracing; not done for all cases),
- H6 (3 - facial coverings required in all shared/public spaces outside the home with other people present or all situations when social distancing is not possible).

It is worth pointing out that this information merely shows the willingness to fulfill them, and it does not convey its efficacy. Nevertheless, as we will see in the next section, they are extremely helpful for simulating the evolution in predicting new COVID-19 cases.

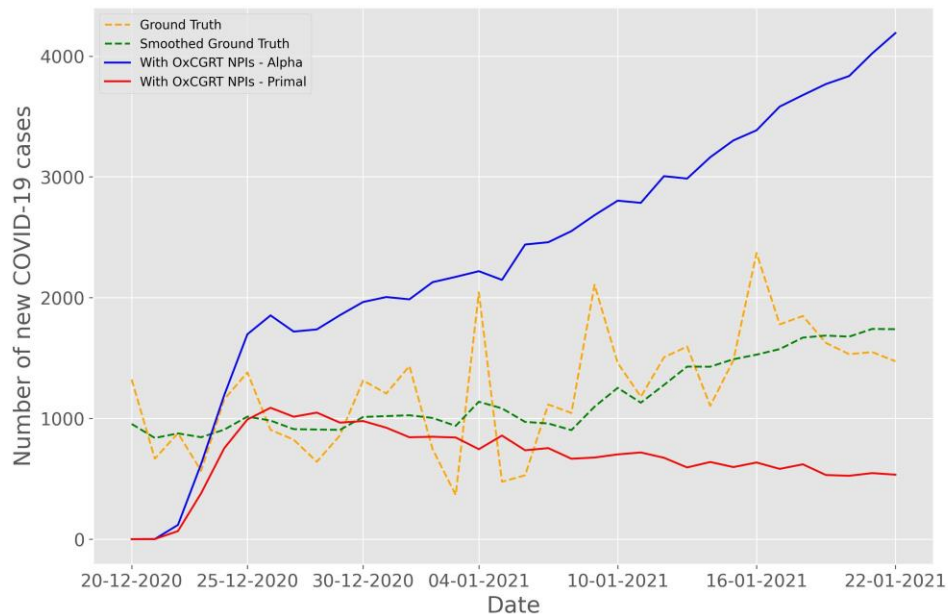
### 3 Results

In this work, we will test the model with data from the Dominican Republic. We have considered a population of 1,099,664 people and the age distributions and household sizes reported by the UN Population Division 2019 [46], see Figure 1 for the results under the Primal variant scenario. This number is assumed to be constant during the period under analysis. Besides, since the pandemic's beginning up to December 21st, 2020, were 160,386 people already infected, who were discounted from the total population for performing the simulations.



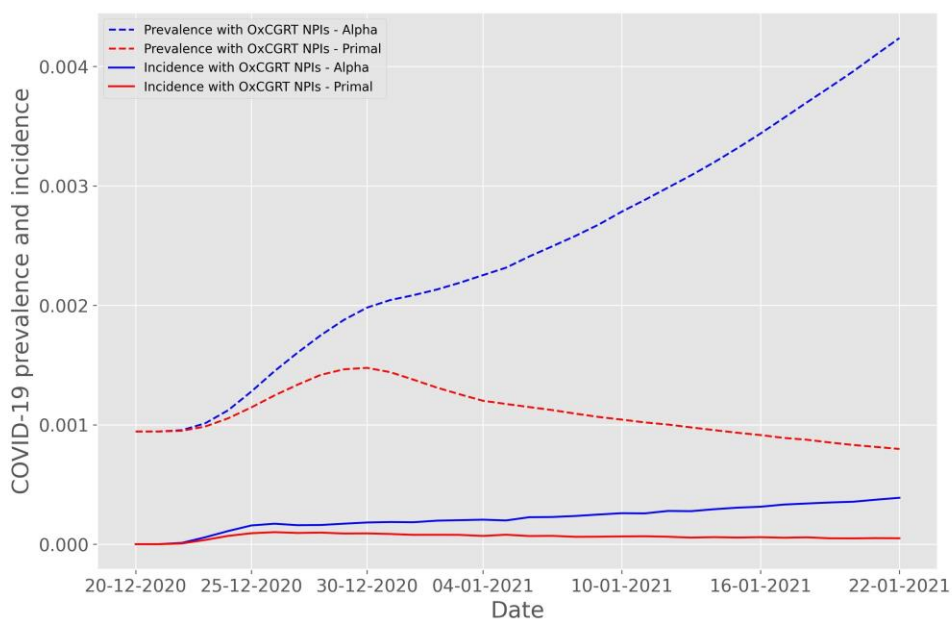
**Figure 1.** Population statistics for the Primal strain from the Dominican Republic between Dec. 22<sup>nd</sup>, 2020 and Jan. 22<sup>nd</sup>, 2021.



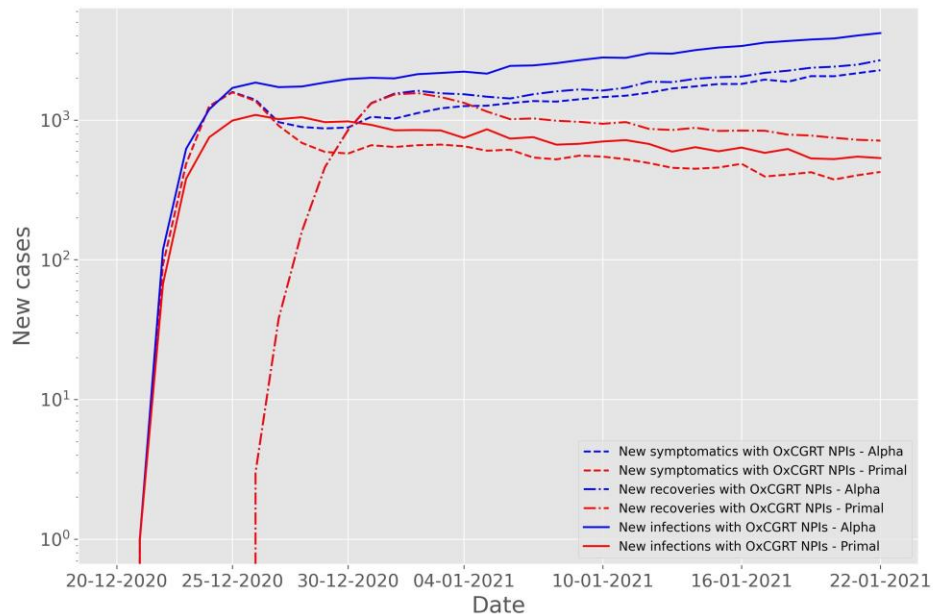


**Figure 2.** Comparison of new COVID-19 cases predictions for the Dominican Republic under the existence of just the Primal/Alpha variants vs. the real number of new COVID-19 cases between Dec. 22<sup>nd</sup>, 2020, and Jan. 22<sup>nd</sup>, 2021.

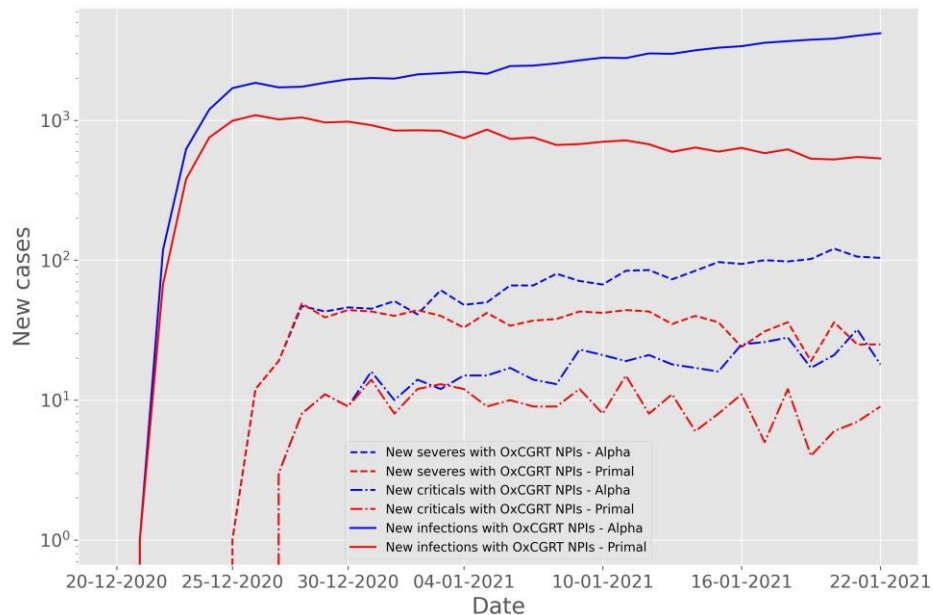
One of the advantages of ABMs is that they easily permit the extraction of data in order to forecast the prevalence and incidence of an illness, as we can see in Figure 2 and Figure 3 from the simulations run for the Primal/Alpha variants under the application of the actual NPIs.



**Figure 3.** Comparison of the estimated COVID-19 prevalence and incidence under the existence of just the Primal/Alpha variants for the Dominican Republic between Dec. 22<sup>nd</sup>, 2020, and Jan. 22<sup>nd</sup>, 2021.



**Figure 4.** Comparison of symptomatic and recovery cases under the existence of just the Primal/Alpha variants for the Dominican Republic between Dec. 22<sup>nd</sup>, 2020, and Jan. 22<sup>nd</sup>, 2021.



**Figure 5.** Comparison of new severe and critical cases for Primal/Alpha variants for the Dominican Republic between Dec. 22<sup>nd</sup>, 2020, and Jan. 22<sup>nd</sup>, 2021.

Besides, it also permits estimating the number of asymptomatic cases and recoveries, see Figure 4, and the number of severe and critical cases, see Figure 5, beyond the total number of new cases of infected people. This information is extremely helpful in order to forecast the occupancy of health facilities, and in particular intensive care units.

## 4 Conclusions

ABMs models show the effectiveness of NPIs in containing the virus spreading and reducing the number of COVID-19 infections. These models permit incorporating different data sources such as demographics, geographical, and mobile data information [47]. These models permit the simulation of scenarios with different NPIs configurations to evaluate the best policies to stop the pandemic spread.

These models can be deployed with low computational cost since simulations can be run over a small population subgroup for later inferring the results for the whole group. It is also worth mentioning that it permits customized populations and contact networks down to the level of a university campus [48] or a city [49].

In this work, we have combined the ABM framework of Covasim with the information provided by the OxGRCT dataset. This shows that despite the simplifications in the description of the most common NPIs, the model can provide pretty accurate forecasts for several weeks, even considering the existence of different strains with different transmissibility rates.

Despite managing ordinal information that illustrates the NPIs application, a satisfactory estimation of each NPI impact level through a machine learning model has permitted to set a fine-tuning of the model. This has been possible due to the abundance of data about how such NPI has been applied worldwide and the actual impact on the number of new COVID-19 cases. Besides, we can also estimate asymptomatic, recoveries, severe, and critical cases only with the information on the number of new cases. This information enables governments, policymakers, and health authorities to forecast the impact on the health facilities of an increment in the number of cases, as it commonly happens with the appearance of a new virus or a new variant of an existing one.

Finally, it is also worth mentioning that with such an approach, it is straightforward to predict possible scenarios of pandemics under the application of different NPIs plans.

### Ethics declarations

The authors declare no conflict of interest.

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