Pandemic Resilience

Developing an Al-calibrated ensemble of models to inform decision making

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Executive summary

Report overview

This report explores the use of ensemble modeling of infectious diseases to enable better data-driven decisions and policies related to public health threats in the face of uncertainty. It demonstrates how Artificial Intelligence (AI)-driven techniques can automatically calibrate ensemble models consistently across multiple locations and models. The ensembling, calibration, and evidence-generation reported here was conducted by an interdisciplinary team recruited by the Pandemic Resilience project team via the Global Partnership on Artificial Intelligence (GPAI) Pandemic Resilience living repository. This diverse team co-developed and tested a collaborative ensemble model that assesses the level of use of Non-Pharmaceutical Interventions (NPIs) and predicts the consequent effect on both epidemic spread and economic indicators within specified locations. The disease of interest was COVID-19 and its variants.

The development of the ensemble model was undertaken in five main phases from June 2022 to October 2023: 1. Definition of a standardized set of inputs and outputs; 2. Adaptation of individual models to the standard; 3. Development of a calibration framework for the ensemble; 4. Deployment and testing of the ensemble across different different locations; 5. Automated calibration of the ensemble using a Genetic Algorithm (GA) metaheuristic optimization approach.

Having constructed and tested the ensemble, the study team has prepared this report to share key findings about the use of such models and communicate key recommendations for governments and policymakers about their development and support:

Key findings

- Collaborative ensemble models developed by interdisciplinary teams offer unique opportunities for rapid, data-based policy development and responsible policy implementation by strengthening the modeling evidence base and permitting scenario evaluation under conditions of uncertainty.
- The collaborative ensemble model developed here reduced mean average prediction errors by at least 50 percent compared to its individual model components.
- An initial ensemble model that sampled at random from the two Cognizant Long Short-Term Memory network (LSTM) models produced lower errors than each of the individual models. This indicates the potential for giving more weight to different models depending on the stage of epidemic progression, e.g., when case numbers are low and beginning to rise versus when case numbers are high and dropping.
- The study team speculates that underexplored aspects of model generalizability, lack
 of computational expertise, and limited funding for modeling collaboratives has led to
 the underuse of ensemble models in policy laboratories and scenario analysis, despite
 the higher accuracy and bias reduction demonstrated here.

Recommendations

Connect decision makers to modelers

 Establish forums in the pre-pandemic period to develop and facilitate connections between policy makers and teams capable of developing and running models. Set up collaborative communication channels to enable information flow between policymakers and the international scientific community. Bridging the gap between scientific expertise and decision-makers is essential for effective utilization of models. The GPAI Pandemic Resilience Living Repository is a good example of such an effective forum.

• Explore opportunities for modeling and leverage the potential of ensembling

Explore opportunities where the use of models and other new data-driven technologies could inform evidence-based policy and decision making. When different models are available for the same system, consider ensembling to reduce model-to-model variability and therefore permit more robust decision making. Ensure there is diversity in model ensembles to validate model performance and embed different perspectives and approaches.

Anchor decision support systems in Responsible AI

 Make sure that the models and data used for supporting decision making are anchored in principles of human-centric, responsible AI and data justice. Decisions can have a more positive impact on the common good when supported by responsibly developed and deployed data-driven models. Decisions should be made by humans, who remain responsible and accountable.

· Build capacity for model-enhanced decision making

– Allocate adequate resources to build capacity within the public sector to understand models (model translation) and integrate them into the policy/decision making framework. In an ideal situation, teams within democratic governments would have the technical expertise to build and operate models directly and safely. An alternative approach is to have trusted modelling teams from, e.g., the academic or consulting sector, that are resourced to work alongside government as and when needed – but this approach should be tested to ensure it operates appropriately, i.e., it is fit for purpose (see Test the readiness of the models in real-life).

Establish policy review and model maintenance mechanisms

 Establish a feedback mechanism that allows for constant collaborative exploration and adjustment of policy decisions based on model outcomes (e.g., iterative scenario modeling vs. solely predictions and prescriptions). Periodically engage collaborative teams to review models for alignment with current policies, training, and calibration.

Integrate ensemble modeling into pandemic preparedness toolkits

Incorporate this methodology into existing frameworks and collaborate with teams
of modelers to adapt it to specific needs. The models can be brought to the data
which means that governments do not have to share their data outside of their
jurisdiction but still can benefit from model insights.

• Test the readiness of the models in real-life

 Initiate a structured testing process for governments to test and evaluate the whole life-cycle of the decision support system before a real life event needs to be addressed. This testing should include simulations of real-world scenarios, such as responding to new variants in the context of the COVID-19 pandemic. This enables building of trust and the optimization of models and policies in stable times so that the whole structure is live and ready to react when necessary.

Create a standard public data pipeline

Implement a standardized pipeline for collecting, processing, and sharing the required public data for modeling. This would enable different modeling teams to collaborate and innovate, as well as foster consistency and accuracy in the information used for decision making. Consider contributing data to a global data cooperative to enable cross-location learnings and the detection of global patterns. Having the right data ready for use is key for a timely response to threats.

Glossary

- AI An Artificial Intelligence (AI) system is "a machine-based system that can, for a given set of human-defined objectives, make predictions, recommendations, or decisions influencing real or virtual environments." (OECD, 2019). 1, 35
- **CDC** The Centers for Disease Control and Prevention (CDC) is "one of the major operating components of the Department of Health and Human Services" in the United States (CDC, 2023). 23
- CFR In epidemiology the Case Fatality Rate (CFR), "also called case fatality risk or case fatality ratio", is "the proportion of people who die from a specified disease among all individuals diagnosed with the disease over a certain period of time." (Harrington, n.d.). 32
- **CTMC** A Continuous Time Markov Chain (CTMC) is "a continuous stochastic process in which, for each state, the process will change state according to an exponential random variable and then move to a different state as specified by the probabilities of a stochastic matrix." (Chen and Mao, 2021). 2, 7, 10, 35
- **GA** Mitchell, 1996 states that no rigorous definition of Genetic Algorithms (GAs) is "accepted by all in the evolutionary-computation community that differentiates GAs from other evolutionary computation methods. However, it can be said that most methods called "GAs" have at least the following elements in common: populations of chromosomes, selection according to fitness, crossover to produce new offspring, and random mutation of new offspring". 1
- **GPAI** The Global Partnership on Artificial Intelligence (GPAI) is "a multi-stakeholder initiative which aims to bridge the gap between theory and practice on AI by supporting cutting-edge research and applied activities on AI-related priorities." (GPAI, 2021). 1, 2, 26
- **LSTM** A Long Short-Term Memory network (LSTM) is a recurrent neural network approach that uses "a novel, efficient, gradient based method" (Hochreiter and Schmidhuber, 1997). 1, 10, 35
- **MAE** The Mean Absolute Error (MAE) (Willmott and Matsuura, 2005) is defined as

$$\mathsf{MAE} = \frac{\sum_{i=1}^{n} |y_i - x_i|}{n}$$

where $y_i, x_i, i = 1, ..., n$ are *n* predicted and observed values respectively. 36

- NPI Non-Pharmaceutical Intervention (NPIs) are "actions, apart from getting vaccinated and taking medicine, that people and communities can take to help slow the spread of illnesses." (CDC, 2022). 1, 9, 33
- **OxCGRT** Oxford Covid-19 Government Response Tracker (OxCGRT) "provides a systematic cross-national, cross-temporal measure of how government responses have evolved over the full period of the disease's spread." (Hale et al., 2021). 10, 17, 36

- **RMSE** The Root Mean Square Error (RMSE) is the square root of the mean (a.k.a. average) of the square of the errors between predicted and actual values. 8
- SEIR Susceptible-Exposed-Infected-Recovered (SEIR) processes are compartmental models used for epidemiology with four compartments (a.k.a. state): 1) Susceptible: individuals that may become infected if they come into contact with infectious individuals;
 2) Exposed: individuals that are infected, but have not become infectious yet; 3): Infectious: individuals that are infected and may spread the disease, i.e., are infectious;
 4): Recovered: individual that have recovered, are no longer infectious and (in many cases) have immunity to the disease. 21, 34

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1 Introduction

From pandemics (diseases that spread globally) to natural disasters and emerging threats exacerbated by climate change, public healthcare systems across the globe continue to face a variety of uncertainties. Meanwhile, most of these uncertainties have strong interdependencies and interconnections that lead to significant adverse outcomes from the household level to country level (Joseph, Yan, and Oguche, 2021; Ru, Yang, and Zou, 2021; Salin et al., 2020). Furthermore, the COVID-19 pandemic created cascading and significant adverse effects beyond the health industry to impact higher education, tourism, accommodation and food industries (Joseph, Yan, and Oguche, 2021; H. Zhang et al., 2021; Revoredo-Giha and Dogbe, 2023). These unanticipated ripple effects of pandemics demonstrate a growing need for innovative approaches to scenario planning that enable resilient public healthcare systems, both locally and globally (Youn, Geismar, and Pinedo, 2022). This report addresses challenges in responding to public healthcare scenarios when faced with exceptional events that are often devastating, causing substantial mortality and economic damage.

The recent COVID-19 pandemic provides a good opportunity to consider how policymakers, faced with the task of building resilience, can take an evidence-based and forward-looking approach to decision making. Scenario planning, as a method of futures thinking in policy making, addresses these uncertainties by considering the socio-spatial dimensions of pandemics and exploring ways to build resilience (Banai, 2020). Traditional scenario planning can offer normative or descriptive alternatives that expand decision makers cognitive limitations and formulate relatable and plausible future narratives. However, it is important to note that developing credible and rigorously tested scenarios can be time consuming, as it requires drawing on robust data and diverse perspectives. Therefore, it is important to recognize the limitations of traditional scenario planning approaches and to explore the potential benefits of multi-modal data-driven (a.k.a. evidence-based) approaches.

In this research we offer ensemble modelling, a multi-modal approach that builds on historical data, using multiple machine learning and predictive AI models to cope with uncertainty in scenario planning for policy making. By framing our work as a means of improving a specific decision support tool for policy making, we believe that the audience for Al-enabled modelling can be expanded and the impact will be much greater. Ensembles of models provide a natural way to address sources of uncertainty which are unavoidable when the scientific method is applied to spatial socio-economic systems. From imperfections and injustices in data collection processes to flawed assumptions and insufficient resolution, we must first acknowledge the fact that all models are inadequate. The father of statistical modelling, George Box, famously said that "All models are wrong but some are useful". Ensemble modelling is offered as a workable solution for coping with uncertainty. Hence, we set out to achieve three objectives in our endeavor: (1) Describe why data-driven (evidence-based) decision making should be prioritised in scenario planning for resilient healthy futures; (2) Create a collaborative framework that enables multiple countries to combine data, science and expertise in the fight against global risks; and (3) Standardize data requirements for pandemic modeling so that all nations can easily benefit from international efforts towards data-driven (evidence-based), participatory policy making and more easily share research findings.

By using a modular design with standardized data for the calibration framework we enable the plug-and-play integration of models and we hope that our work here on the COVID-19 pandemic can inspire further partnerships to tackle some of the greatest challenges of the 21st century. Policymakers can visualise future scenarios from selected simulations and,

hence, actively participate in the use of the ensemble of models to investigate the consequences of decisions. This active participation makes the entire exercise more transparent, less intimidating, and most importantly builds trust. By demonstrating the advantages of combining models and integrating evidence from each individual country, it is hoped that a large community of knowledge sharing will emerge which will have mutual benefits across the globe.

In Section 2, this report starts by precisely defining the problem and objective of our research. It describes the need for a multi-model approach to account for uncertainty, enabling decision-makers to support their decisions with more accurate predictive scenarios of the future. Section 3 describes in detail the development of a calibration framework that leveraged a standardized interface to combine and compare three different but complementary modelling approaches: (1) a Cyber-Physical model; (2) a LSTM model, i.e., a type of neural network; and (3) a stochastic model based on Continuous Time Markov Chains (CTMCs). The definition of standard inputs and outputs, including data, enabled each model to take advantage of the same data and create compatible and comparable predictions. We demonstrate that an ensemble of models can be utilised to generate more accurate scenarios of how the future is likely to unfold. In section 4, we make a call for action for the development of a standardized public data pipeline, thereby facilitating collaborative, timely, inclusive, and accurate responses to global crises. In section 5, we delve into a reflection around the values-based Al principles developed by the OECD. We explore how the ensembling methodology benefits from the development of Responsible AI practices. We also explore its limitations and emit recommendations to address the challenges. Then, section 6 returns the focus to the policymakers by working through how this data-driven approach can answer a series of important questions for decision makers. We explore three use-cases: (1) Forecasting; (2) Scenarios; and (3) Policy laboratory. Finally, in section 7, we reflect on possible ways to build on the foundation established by this project in future work.

2 Context and Problem Definition

Given a wide variety of modeling approaches, this project aims to bring a systematic approach to model development, in particular through standardization and ensembling. It also aims at identifying ways in which the advantages of modeling can be communicated to decision-makers.

2.1 Motivation

The 21st Century has witnessed two pandemics (2009-10 pH1N1 and ongoing COVID-19), and with: global natural habitat destruction; populations; and transportation; all increasing, the stage is set for such outbreaks to be the future norm rather than the exception. Public health officials and political leaders alike require tools to rapidly assess the potential impact of novel health threats and to provide scenario analyses to consider initial response and ongoing management options (Borchering et al., 2021). Having multiple viewpoints to inform such efforts is valuable, especially in the setting of scientific uncertainty about the characteristics of new pathogens and their impact on society. Collecting, adjudicating, and managing multiple potentially conflicting sources of information, however, can make outbreak response unwieldy. Recent efforts attempting to provide guidance for this process in the context of COVID-19 have specifically addressed what has been termed the "multiple model" problem for policy makers: the simultaneous but uncoordinated production of multiple, sometimes conflicting modeling approaches and outputs for identical scenarios (Shea, Runge, et al., 2020). One example of this "corralling" approach to pandemic model analysis attempts to

integrate 17 different model outputs into a coherent policy-relevant narrative (Shea, Borchering, et al., 2020).

Hu et al., 2020 provide a suggestion on how to proceed in this situation: First, "Generalizing AI models to unseen data (inference), data coming from different distributions (domain adaptation, transfer learning) and data with limited or no labels (semi- or unsupervised learning) are all priority areas in the technical development of AI." Then, "Despite time pressures, rigorous validation is key to ensuring that safety and efficacy are tested; models must be validated before initial deployment and continuously monitored and adapted when implemented in local healthcare environments and as outcome likelihoods change due to evolving patient management strategies." Leading to the suggestion, "New international cross-disciplinary collaborations, carefully identifying time-, course- and region-dependent clinical actions in response to COVID-19 can benefit from scientifically sound AI model development, validation and deployment to support local healthcare providers."

In other words, the alternative to post-hoc efforts to integrate modeling outputs is to flip the process on its head and design an integrated suite of models that operate within a common operating environment that standardizes inputs, parameters, and output formats. This is the approach taken in this research and described in §3.

2.2 Model Ensembling

The use of ensemble modelling has appeared to varying degrees in many different disciplines. In 1907, Sir Francis Galton asked 787 villagers to guess the weight of an ox. None of them arrived at the correct answer. When Galton averaged their guesses, however, he arrived at a near perfect estimate (Galton, 1907). This is a classic demonstration of the phenomenon known as the "wisdom of the crowds", popularised in the book by Surowiecki (2005). Contrary to traditional deterministic models, ensemble models or multi-modal ensembles leverage the collective intelligence of multiple models or the "wisdom of crowds" to address uncertainty and improve the accuracy and interpretability of predictions in genomics (Lin, Langfelder, and Horvath, 2013), climate modeling (Merrifield, Brunner, Lorenz, Medhaug, et al., 2020; Merrifield, Brunner, Lorenz, and Knutti, 2020), weather forecasting (Tippett and Barnston, 2008; Roebber, 2015), sentiment analysis (Tran and Phan, 2019), and optimization problems (Xu et al., 2021).

Researchers have found that ensemble modeling applied in the context of pandemics, such as the COVID-19 pandemic, performed better than single models since they were less likely to be influenced by the assumptions of an individual model. For example, Paireau et al. (2022) used an ensemble model to forecast the number of Intensive Care Unit (ICU) admissions, bed occupancy in general wards, and bed occupancy in ICUs. The researchers first developed twelve individual models which use meteorological, epidemiological and mobility predictors to forecast the number of hospital admissions at both national and regional levels, up to 14 days ahead. The researchers compared the performance of these models based on Root Mean Square Error (RMSE) for point forecast error and the weighted interval score (WIS) to assess probabilistic forecast accuracy in order to select the six best-performing models. These six top-performing individual models were then combined into a single ensemble forecast. The ensemble model was then used to derive three other targets: (1) the number of ICU admissions; (2) bed occupancy in general wards; and (3) bed occupancy in the ICU; from the number of hospital admissions and its performance was evaluated against new observed data to mimic real time analysis. The researchers found that although the performance of individual models decreased with the prediction horizon, the ensemble model adjusted to variations in prediction horizon and performed well in all regions (i.e., the ensemble model provided an inter-region mobility predictor).

Ensemble approaches to numerical weather prediction were proposed originally by Epstein

(1969) and are now the state-of-the-art in weather forecasting (Palmer, 2019). Various empirical forecast comparisons have established the added accuracy of ensemble weather forecasting for various applications such as wind power (Taylor, McSharry, and Buizza, 2009).

The forecasting community has long recognized the power of combining forecasts. Makridakis and Hibon (2000) organized several forecast competitions to arrive at some key findings that are relevant for the Pandemic Resilience project: (1) Statistically sophisticated or complex methods do not necessarily provide more accurate forecasts than simpler ones. (2) The relative ranking of the performance of the various methods varies according to the accuracy measure being used. (3) The accuracy when various methods are combined outperforms, on average, the individual methods being combined and does very well in comparison to other methods. (4) The accuracy of the various methods depends on the length of the forecasting horizon involved.

In the field of machine learning, the benefits of ensembles are well documented and offer a means of building robust approaches for classification and regression (Hastie et al., 2009). For example, an ensemble of decision trees is now popularly known as a Random Forest, based on an initial proposal by Ho (1995) and eventually trademarked by Breiman (2001).

On the other hand, although ensemble modelling offers improved prediction accuracy and robustness for scenario planning, it is limited by computational complexity, interpretability challenges, and dependence on the quality of individual models. Doblas-Reyes, Hagedorn, and Palmer (2005) found that ensemble modelling requires combining diverse sets of individual models for specific predictors using complex statistical calibration. Also, the researchers found that predictions from ensembles can be affected by biased and inaccurate predictions of the individual models in the ensemble. Weller et al. (2020) also found that the combination of multiple models can make it challenging to understand the underlying relationships and mechanisms driving the predictions for decision making in socio-ecological systems where pathogens interact with other system agents. As a part of this project, a new method of ensembling will be proposed, addressing some of these issues. However, ensembling is still an active area of machine learning. One key point of this report is that the ensemble model presented can already be used effectively in pandemic prediction, and further advances in such prediction can be incorporated into the ensemble approach.

3 Developing, testing and deploying an ensemble of models for decision making on NPIs

In this project, an ensemble model was proposed, developed, calibrated and tested in supporting decision making for the COVID-19 pandemic. The key decisions being evaluated by the ensemble model were the level of use of Non-Pharmaceutical Interventions (NPIs) and the consequent effect on both epidemic spread and economic indicators within specified locations. Model inputs and outputs were standardised and kept consistent across locations and models as appropriate, e.g., the same reproduction number for COVID-19 variants was used across multiple locations but the proportion of the variant present could vary at each location.

3.1 Description of the architecture

The standardised, consistent architecture for the ensemble model provides two main benefits: (1) Shared inputs, e.g., variant reproduction numbers could be calibrated using datasets from multiple locations simultaneously; and (2) New locations and models can be easily added to modelling scenarios, i.e., the architecture is easily scalable to new locations and modelling approaches. The architecture, implementation – including an automatic calibration framework – and preliminary results of the ensemble model are described in this section.

The fundamental "building block" of the ensemble model and associated calibration framework is a particular model that was developed during the pandemic to describe epidemic spread and/or the time series of economic indicators under a schedule for NPI levels. Figure 3.1 shows two different models (1 and 2) being developed in two different locations (A and B respectively). These models may have been calibrated separately for their particular locations and, hence, may be using different values for the same parameter, e.g., the reproduction number of the α variant of COVID-19.



Figure 3.1: Individual Models with Calibration

Three models were selected for the initial development of the ensemble model/calibration framework. These models all used different mechanisms to evaluate the effect of NPIs on epidemic spread:

- 1. The Cyber-Physical model was developed in Aotearoa | New Zealand and uses a plantcontroller mechanism – see §A.1;
- The Cognizant model was developed in the United States and uses a Long Short-Term Memory network (LSTM) mechanism for not only the United States but for locations around the world – see §A.2;
- 3. The Continuous Time Markov Chain (CTMC) model was developed in Aotearoa | New Zealand and uses a CTMC mechanism see §A.3.

The input data for the models was standardised to the Oxford Covid-19 Government Response Tracker (OxCGRT) which contains a schedule of NPIs for many countries and locations across the world as well as information on epidemic spread, i.e., the number of confirmed cases and number of confirmed deaths (Hale et al., 2021). The Cognizant model only uses this data for training, but the other two models use input parameters at three levels (also shown in Figures 3.1 and 3.2):

- 1. Global parameters that should be consistent across multiple locations globally, e.g., the "raw" reproduction number of each of the COVID-19 variants;
- 2. Location parameters that should be consistent across multiple models in a single location, e.g., the proportion of variants at that location;
- 3. Model parameters that are model-specific, e.g., the extra transition rates for the CTMC model which describes how patients transition into/out of wards and ICUs. Note that these parameters might be different in different locations.



Figure 3.2: Ensemble Model with Calibration

The global, location and model parameter inputs are combined with the input data within a single, standardised input structure as defined in §B.1. Figure 3.2 shows how, in the ensemble model and associated calibration framework, models 1 and 2 are being used in an ensemble model across both locations A and B. The same global parameter values are shared across all the models at every location. Location parameters are shared across all the models within each location. Finally, model parameters can be different for each model at each location.

3.1.1 Calibration framework architecture

The standardised input/output – see B.1 – across all the models in the ensemble also provides an opportunity to automatically calibrate the entire ensemble. Figure 3.2 shows: how individual model parameters within given locations are calibrated for that specific model in that specific location; how location parameters are calibrated for the ensemble model, i.e., all models concurrently, at that specific location; and how global parameters are calibrated for the ensemble model across all locations concurrently.

This integrated calibration approach in the Pandemic Resilience project uses a multi-objective GA called NSGA-II (Deb et al., 2002). Various input parameters are allowed to change – see §B.2 for details – with two objectives for the ensemble to match the 7-day moving average for new daily cases and new daily deaths respectively. Parameter changes might be as simple as the reproduction number for the alpha variant being within [2.29, 3.29] or as complex as determining the variant proportions for a given country. Note that the latter is achieved using a irredundant approach where:

- 1. the last variant proportion, i.e., omicron, is removed from the GA variables;
- 2. all other variant proportions have bounds [0.0, 1.0];
- 3. the sum of the other variant proportions is constrained to be \leq 1.0;
- 4. the last variant proportion is then calculated as 1.0 the sum of the other variant proportions before all the proportions are used within the Cyber-Physical or CTMC models.

The GA for the calibration framework is configurable to try multiple different parameter sets concurrently, i.e., the number of individuals for the GA, and to evolve these parameter sets over time, i.e., the number of generations for the GA. Typically, the number of parameter sets/individuals is the order of 10s (e.g., 20, 50) and the number of generations is order of 100s (e.g., 100, 500).

3.2 Summary of the implementation

All three models were previously implemented in Python 3. They were adapted to run a single problem instance from a run.py file which uses the standard inputs and outputs see §B.1 – defined in two JSON files. The calibration framework was developed in Python 3 using the pymoo: Multi-Objective Optimization in Python library (Blank and Deb, 2020). The input parameters that the GA could calibrate were defined in a third JSON file – see §B.2. The Cognizant model is run once at the beginning of the calibration (since it does not use input parameters, only input data) and the Cyber-Physical and CTMC models are run with each set of parameters for each defined location and for each generation, i.e., when calibrating for 3 countries using 20 individuals and 100 generations both the Cyber-Physical and CTMC models will be run $3 \times 20 \times 100 = 6,000$ times during calibration. A Jupyter notebook, adapted from a previous version by Cognizant to evaluate XPRIZE Pandemic Response Challenge (XPRIZE, 2021) submissions, is used to visualise the performance – in terms of predicting daily new cases and daily new deaths. Multiple sets of parameters can be included in the interactive visualisations. Some initial results for a problem instance looking at Aotearoa | New Zealand, Kenya, Italy and the United Kingdom from 31 March 2020 to 30 June 2020 are shown in Figure 3.3.

Figure 3.3a shows the overall 7-day moving average for new cases. Note that the predictions from all of the models are far greater than the Ground Truth. Note also though that the predictions are moving towards the Ground Truth after more generations of the calibration framework. In Figure 3.3b the accuracy of the two Cognizant models and the best performing Cyber-Physical model is shown. The LSTM prediction is a reasonable match in April (2020), but then drifts away for later months. The conditional LSTM defaults to no new cases – not a great match – and the best Cyber-Physical model (after 500 generations of parameter evolution) matches the Ground Truth in a few places but also has large inaccuracies, e.g., in early April (2020). The same pattern of initial inaccuracy that improves as the calibration framework evolves the models is observed in Figures 3.3c-3.3f. There are some notable differences, e.g., CyberPhysical_2_early for Kenya that predicts a second surge of new cases.



Figure 3.3: Initial Calibration Results

Although they cannot be seen in Figures 3.3c-3.3f due to the scale, the Cognizant model predictions are closer to the Ground Truth, albeit only for the LSTM_0 model.



Figure 3.4: Best Calibration Results for 7DMA of Daily Deaths after 500 generations

Figures 3.4a-3.4d show the best results (from 500 generations of parameter evolution) for predicting the 7DMA of Daily Deaths with some reasonable matches in the surge of new deaths and the shape of the curve in the United Kingdom as well as low mismatches in Kenya and Aotearoa | New Zealand (less than 8 and 4 respectively). Note that Sweden is problematic and more exploration into appropriate parameters for the Cyber-Physical model in the location of Sweden is needed.

Figure 3.5 depicts the improvement in prediction for the United Kingdom for the first parameter sets, through to those produced after 42 generations, then those resulting from 158 generations through to the final parameter sets from 500 generations. There is a clear decrease in predicted 7DMA cases towards the Ground Truth.

Note that Cognizant's interactive plots within a Jupyter Notbook have been a key part of analysing the initial calibration results/performance. Also note that a relatively simple change to the calibration framework, namely bounding initial populations numbers to not move too far from historical estimates has helped speed up the improvement of the models being calibrated.

Once the models have been calibrated satisfactorily, they provide an ensemble of calibrated models for predicting pandemic spread. The use of this ensemble is discussed next.





3.3 Using the ensemble model

The different models may predict different outcomes given the same set of context information, so the various predictions are integrated into an ensemble to formulate a higher quality prediction. We evaluated two ensembling techniques: (1) a daily prediction sampling applied during rollout of the statistical models, and (2) a more general residual estimation system that can be applied to all models. The second ensembling technique is new and a contribution of this project in its own right.

3.3.1 Sample ensemble

A well-studied property of deep learning systems is that the model that results from fitting parameters to the training data varies depending on the random initialization of the model parameters. Thus repeated runs of the training procedure result in a multitude of different models, a phenomenon studies refer to as the bias-variance tradeoff. We designed a system to integrate the various predictions of an ensemble of such models during the prediction rollout procedure. This method, called the *sample ensemble*, works by, at each day, randomly selecting a predictive model in the ensemble and taking its prediction for that day to be the daily prediction of the ensemble. The process is iterated for each day during the prediction rollout period, resulting in a prediction trajectory which weighs the votes from each model in the ensemble.

3.3.2 Residual estimation ensemble

We introduce Residual Estimation with an I/O Kernel (RIO; Qiu, Meyerson, and Miikkulainen, 2020) to serve as the ensembling technology. The various models described in this report have different performance characteristics, offering greater or lesser accuracy in different settings. The RIO technology assigns a level of confidence to each model based on how the model performed in similar settings in the past. It works by fitting a Gaussian process model to fit the error residuals of each model given the context inputs. The result is an estimate of the model's predictive capabilities, conditioned on the contextual information available. RIO has previously been leveraged to generate confidence bounds for LSTM-based statistical models predicting the number of disease cases in COVID-19 (Miikkulainen et al., 2021). Here it is used as a basis for ensembling predictions from a diverse set of models.

3.4 Technical conclusions/ preliminary results



Figure 3.6: The mean average prediction error of number of cases per 100,000 people in a sample scenario (Argentina, March 1, 2021-April 30, 2021)

Results seen in Figure 3.6 indicate that the sample ensembling technique dramatically reduces the prediction error. The prediction error for the ensemble is significantly less than any given model taken alone, demonstrating that integrating the results of multiple different models offers superior performance. During the rollout phase of predictions, the LSTM-based systems consume the previous day's output to inform their prediction for the following day. However, the self-feedback can result in a positive feedback loop in which the model's estimate of an increase in cases one day informs a prediction of a further increase in cases the following day, cascading in high case predictions. The sample ensemble was designed to ameliorate this positive feedback problem by introducing model uncertainty into the case rollout procedure. Indeed, the sample ensemble system tends to produce more noisy and less extreme predictions more in line with the observed data.

Results from the RIO-based ensemble method will follow in a subsequent publication.

4 A call for a data standardization

The Oxford Covid-19 Government Response Tracker (OxCGRT) – Hale et al., 2021 – serves as an example of how standardized data can be a pillar in harmonizing the global pandemic response. This public data set, shared by the team at the University of Oxford, played a pivotal role in our collective fight against the virus.

It provided a common framework for modeling teams across the world to work cohesively; a homogeneous structure of data points on the same period of time for different locations that enabled teams of modelers and decision makers to share a common reference and "speak the same language". It paved the way for the Pandemic Resilience project team to agree on a standard set of inputs and outputs for the different models – see §B.1, and significantly facilitated the creation of the calibration framework – see §3 and §B.2. By having access to standardized data from different locations, teams of modelers could also learn interesting patterns about the COVID-19 virus and pandemic spread that were useful at the global level.

Despite all the benefits resulting from access to the OxCGRT, it also has a number of limitations. The mechanism for creating the OxCGRT means that, if a new pandemic occurred, the models built using the OxCGRT would not be immediately useful. The creation of the Ox-CGRT required a significant amount of laborious, manual – predominantly volunteer – effort to collect and curate publicly accessible data. The creation process involved the meticulous extraction of variable information from a variety of, sometimes unstable, sources including journals, news websites, etc. Even with diligent work, this mechanism potentially leads to a loss of precision and bias in data. There also were significant delays before stakeholders had access to crucial data, creating a lag in the generation of pandemic spread scenarios and, consequently, pandemic response. For a timely and effective pandemic response – i.e., pandemic preparedness, models have to be trained, calibrated and updated with the most recent data on a regular basis.

4.1 Our proposition: Two levels of data sharing

Now that the pandemic is effectively over, the team maintaining the OxCGRT has been dismantled and there is no existing capacity to sustain it. Looking forward, if humanity faces similar pandemic-related global challenges and threats, the same process performed by the OxCGRT team and their "army" of volunteers would need to be started and a similar dataset built again. The current models would have to be retrained using this new dataset, so any delays would delay model training and calibration, hence delaying the usefulness of the models in informing pandemic response the next time the world is faced with a pandemic.

This significant gap in pandemic preparedness, i.e., the lag until an accurate model-informed response can be actioned, is the main reason why the Pandemic Resilience team proposes that governments consider the creation of a standard public data pipeline for public health information. Having direct access to standardized and regularly updated public health data (that has been appropriately aggregated and deidentified) would greatly enhance and accelerate pandemic response in locations where this standardized data is available, i.e., it would significantly enhance pandemic preparedness in these locations. It would enable modeler teams to access key metrics from public health; thus realising the potential of models to make precise and timely predictions and generation of possible future scenarios.

We propose a 2-level approach for this standard public data pipeline. These levels are in recognition that not all jurisdictions have the same vision in terms of open data.

The first level is the aggregation, deidentification and standardization of public health data

internally, i.e., within a jurisdiction. This enables the public health system with that jurisdiction to utilize models trained on their standardized data to inform local pandemic response. However, this localized training means that learnings from other jurisdictions are not available to the local models. For example, the Cognizant model based on LSTMs is more accurate when incorporating data from multiple locations.

The second level is the sharing and aggregation of standarized data from multiple jurisdictions, at a level of privacy, i.e., aggregation and deidentification, deemed appropriate by the contributing jurisdictions. This is the approach in the OxCGRT in that high level, aggregated metrics such as national NPI schedules and confirmed cases are joined together into a single dataset across all contributing jurisdictions (a.k.a. locations). This cooperative dataset enables learnings from multiple jurisdictions to be part of model training, leading to models that are more accurate across all jurisdictions than those trained on datasets from individual jurisdictions. For example, effectiveness of NPIs in one location can be (at least partially) informed by learning from the NPI's earlier observed effectiveness in another location.

In addition to sharing learnings by sharing data, adhering to data standards both within and across jurisdictions promotes innovation and a diverse range of models. Working with the same data, modeler teams (from the same location or dispersed across the world) can challenge and learn from each other. The resulting diverse range of models can provide different ways of interpreting data, generating scenarios and informing decisions. As we discussed earlier in this report, enabling diverse modelling via standardized data also facilitates model ensembling which in turn significantly increases the accuracy of the predictions, leading to better decisions.

Adhering to a data standard also enables models developed in different locations to be rapidly deployed and utilised in new locations, i.e., new locations can quickly implement and then benefit from innovations in modeling. This is especially true for low and middle income countries that don't necessarily have the capacity to build multiple models to inform their decision making. We can make the analogy to chargers for laptops or mobile phones. In many cases the part of the charger that plugs into the phone or laptop is standardized (at least by brand), but the part that plugs into the wall comes with multiple different attachments for the different mains plugs in the wall, e.g., between the United States, United Kingdom, Aotearoa | New Zealand, etc. When changing jurisdiction, a quick change of attachment for the mains plug is all that is required for the charger to work seamlessly. With standardized data formats, the data will be different but it will work with the ensemble model in a similar way, producing appropriate pandemic response information for the new location.

The development of a mutual data standard enables models to learn patterns aggregated between different contexts. Such diversity of training data allows for models to perform in new unseen contexts, as the models avoid overfitting to a narrow band of information available from one region. In fact, such a rich training set is essential to the training of machine learning models, which form a statistical distribution that explains the available training data. If the LSTM model were given only one country of training data, it would not learn many interesting patterns. Thus cross-location, cross-context, training data is powerful and necessary for the LSTM model.

When the dataset is rich with detail, including context information from each region, then the history of one region can be leveraged to inform the response of other regions experiencing similar conditions. The context information helps to characterize how each unique region may experience a pandemic. As an analogy, if you have only the speed of a car, you also need to know what's going on with the acceleration pedal and brake to make predictions. The standardized data portal would act as a central hub for giving insights to sovereign nations of what they should look at and what tools are available for them to enhance their data-driven (evidence-based) decision making.

Note that, in the future, other types of data could be included in standardized, shared pandemic datasets (with appropriate privacy protection in place). Of special interest for pandemic spread is the mobility data such as aggregated data on travel within (e.g., commuting and public transport data) and between (e.g., flight information) jurisdictions (Aung et al., 2023).

4.2 Extended benefits

There are extended benefits to data standardization and ensemble modeling beyond the immediate benefits for global pandemic preparedness described in the previous section. By creating a collaborative, interoperable process for sharing data and developing innovative modeling approaches, governments can foster digital ecosystems that promote problem solving for complex problems. These ecosystems not only provide access to both the research and innovation communities within a jurisdiction, but enable international cooperation, collaboration and learnings to be easily shared – in fact embedded into the model training pipeline – between jurisdictions and, hence, interesting patterns that persists across the globe to be recognised (e.g., the efficacy of school closure for reducing COVID-19 spread). Standardized data and associated ensemble modeling pipelines – with previously described benefits of innovative, diverse modeling approaches and robust modeling outcomes – could help to address complex, global issues such as: climate change – and its consequences like forest fires, severe weather events, etc; housing; and education.

Note that for both pandemic preparedness and the other global issues mentioned in this section, there is no requirement for governments to share data. The first level of data standardization – see §4.1, which is appropriate for the extended data/modeling ecosystems described here, recommends that governments standardize their own internal data first and, in doing so, can access and use models from other jurisdictions that have been developed for the data standards. The Pandemic Resilience team believes that further insights for many global issues can be realised by sharing data globally, but these insights must be balanced against the data sovereignty implications of data sharing.

5 Benefits and limitations of ensemble modelling for responsible AI development (RAI)

Ensemble modeling, as a collaborative and multidisciplinary approach, offers several benefits for fostering responsible AI practices, but it also comes with limitations and risks. In this section, we reflect on these benefits and limitations and delve into the implications for responsible AI development. This reflection – presented in the following section – compares the ensemble modeling technique to the five values-based AI principles developed by the OECD, also typically referred to as the OECD AI Principles for Trustworthy AI(OECD, n.d.). Although we recognize that the OECD also proposes five complementary recommendations for policymakers, this exercise focuses on the values-based principles only, providing a benchmark to these principles from a technical and applied point of view. Our intention is to recognise benefits and limitations, and inform recommendations based on our practical experience with ensemble modeling. Note that each subsequent section corresponds to one of the five values-based AI principles:1) Inclusive growth, sustainable development and well-being; 2) Human-centred values and fairness; 3) Transparency and explainability; 4) Robustness, security and safety; 5) Accountability.

5.1 Inclusive growth, sustainable development and well-being

Benefits (of ensemble modeling) Data standardization and ensemble modeling is good for inclusive growth and sustainable development because it encourages innovation and provides access to diverse groups. It also enables "plug-n-play" modeling in which new models can be easily added to the ensemble and, hence, diverse perspectives on modeling can be easily included. The Pandemic Resilience team is diverse in geography, ethnicity, background and expertise. We have noticed and appreciated this diversity in terms of the contribution of individual researchers and how the team has collaborated as well as how it has shaped the research Pandemic Resilience research, e.g., the use of 3 quite different modeling approaches from different locations, and the standardization the model interface (inputs and outputs) so that all models could work in unison.

Limitations (of ensemble modeling) The "entry point" for understanding and contributing to the models in the Pandemic Resilience project was quite high, so despite the diversity (described in **Benefits**) there was still some (default) exclusion due to the level of expertise required to engage in this project. This accessibility issue could be overcome in the future via deeper engagement with affected communities and/or co-production of future models.

Recommendation(s) (from ensemble modeling) The ensemble modeling approach is inherently diverse and, hence, encourages innovation and supports robustness. However, careful consideration of the composition of contributors to the ensemble model is needed and important to safeguard inclusion and accessibility for those affected by the model outputs, e.g., policy decisions.

5.2 Human-centred values and fairness

Benefits Ensemble modeling as used within the Pandemic Resilience project is focused on providing decision making support. It provides models for predicting the effect, i.e., evaluating, making decisions and, even through future research could extend these models to become prescriptive, i.e., recommend decisions, the intention is for the ensemble model to inform decision makers, hence human values will underpin any decisions. The standardization of the ensemble modeling approach in the Pandemic Resilience project aims to provide easy access to models and data for those jurisdictions that do not currently have the resources to develop such models themselves. This approach attempts to democratise modelling across nations and provide fair access to the necessary expertise in terms of pandemic preparedness.

Limitations Human-centred values are not explicitly included in the Pandemic Resilience approach. If the extension to prescriptive models is combined with automated decision making then human-centred values could be omitted from the decision making process. Fairness is only present in the Pandemic Resilience approach as fairness of opportunity, i.e., ease of access, but is still dependent on countries having the necessary expertise or resources to gain access to the data/modeling pipeline.

Recommendation(s) Providing AI and modeling tools as decision making support rather than direct decision making systems is important for maintaining human-centred values in decision making, which is especially important for public health policy such as pandemic preparedness and response. Enabling easy access to such tools is important for fairness, but extra consideration as to the resources and/or expertise required to effectively access and use those tools is also key when ensuring fairness of Al/modeling tools.

5.3 Transparency and explainability

Benefits Both the Cyber-Physical – see §A.1 – and CTMC – see §A.3 – models are customised versions of the Susceptible-Exposed-Infected-Recovered (SEIR) approach and, as such, are both transparent and explainable. They are transparent because the effect of input parameters/data on the outputs are clearly defined by mathematical equations. They are explainable because, e.g., an increase in the peak of pandemic spread can be traced back to an increased reproduction number of a COVID-19 variant, a reduction in NPI levels, etc.

Limitations The LSTM models provided by Cognizant are neural nets and, as such, are not transparent or explainable. Changes in the NPI schedule will lead to consequent changes in confirmed cases, etc, but the reverse is not clear, i.e., a change in confirmed cases can not necessarily be directly linked (a.k.a. explained) by an aligned change in NPIs.

Recommendation(s) Combining transparent/explainable models with non-transparent/nonexplainable models in an ensemble means that a degree of transparency/explainability is retained and complex behaviour, that may not be easily captured by the explainable models, can also be included albeit in a non-transparent way. The choice of models for the Pandemic Resilience project intentionally combined data heavy, opaque (a.k.a. non-transparent) models with models that rely on well defined mathematical mechanisms. This choice was not only because of the diversity of models and situations in which they are effective, but also to ensure that there was a degree of transparency/explainability when both calibrating and experimenting with the ensemble model.

5.4 Robustness, security and safety

Benefits Ensemble modeling – as used in the Pandemic Resilience project – provides robustness by combining multiple diverse models, created by teams with different perspectives, into a single ensemble model that, hence, addresses a variety of possible inputs and gives robust outputs. Security of data was provided within the Pandemic Resilience research by only using the publicly available dataset OxCGRT. Security and safety of the ensemble model outputs were ensured by using these outputs for decision support, so the humans are kept in the decision making process, i.e., the Pandemic Resilience project aims to provide Al-enhanced decision making.

Limitations Robustness, safety and security are provided by the Pandemic Resilience methodology, but not embedded directly into any of the models or data processing.

Recommendation(s) The Pandemic Resilience methodology design provides a level of robustness (in particular, due to the ensemble modeling approach), security and safety, but it may be worth having an expert review of this methodology to see if other steps could be taken to improve robustness, security and/or safety in the Pandemic Resilience research.

5.5 Accountability

Benefits Thus far, the Pandemic Resilience project outputs are limited to prediction and so the decision making and hence, accountability remains with the human decision makers using the Pandemic Resilience ensemble model.

Limitations The next step is to expand towards providing prescriptions, i.e., suggestions/recommendations for decisions. The final decision making will remain with a human, so accountability will stay with the decision makers but poor prescriptive outputs could lead to poor decisions and erode public trust in Al-driven decision making. **Recommendation(s)** Ensure that the final decision making and accountability is in the hands of human decision makers, but implement prescription in the Pandemic Resilience ensemble model. Take steps to ensure these prescriptive outputs are 'fit for purpose" to build/maintain public trust in decision making supported by Pandemic Resilience research.

6 Policy Implications

Policymakers require simplicity yet the assurance that a sufficient amount of the world's complexity has been appropriately taken into account by experts and practitioners. Our collaborative platform is designed to be easy to use, transparent and facilitates the generation of actionable insights that will facilitate decision making by policymakers. We strive to extract insights that are directive, relevant and solution-focused.

While some policymakers are skeptical about using models for decision making, others are ready to immediately trust models without proper interrogation, knowledge of limitations, or consideration of potential risks. Neither of these extremes is ideal and we encourage a participatory approach to using models for supporting decisions that enhances awareness of the challenges and opportunities. By providing more reliable predictions and greater confidence in health outcome predictions, ensemble models play an assuring role by mitigating data integrity risks in insights-driven health policy development and decision making (M. E. Smith et al., 2017; Ray, Wattanachit, et al., 2020; Ray and Nicholas G. Reich, 2018). This GPAI report showcases the benefits of ensemble modelling for policymaking by considering three specific use-cases – described in the following sections – when managing pandemics.

6.1 Use case 1: Forecasting

The ability to accurately forecast the future has obvious potential. For managing pandemics, the focus is usually on short-term (weeks) to medium-term (months) forecasting of cases, hospital admissions and deaths. Mechanistic models such as epidemiological models can quickly learn about the evolution of the virus and offer a means of predicting how serious an emerging pandemic might become in the near future.

The use of ensemble models in public health forecasting has implications for policymakers. These models can quantify the impact of delays in data availability and variable reporting practices on the accuracy of current epidemic assessment (Moss et al., 2018). By considering uncertainties and variabilities that influence infectious disease dynamics such as: population demographics; changes in policies and behaviours over time; healthcare infrastructure; and socio-economic conditions; ensemble models provide policymakers with more comprehensive and realistic predictions of the future (Doms, Krämer, and Shaman, 2018).

One way to use a forecasting ensemble model in public health policy is to incorporate it into decision-making processes for resource allocation and response planning. This can help to ensure that resources are allocated efficiently and effectively, and that the public health system is prepared to respond to potential outbreaks or other public health emergencies. For example, the United States Centers for Disease Control and Prevention (CDC) organized a collaborative seasonal influenza forecasting ensemble model that enabled real-time insights-driven public health decision-making against the largest outbreak in 15 years since 2002 (Nicholas G. Reich et al., 2019). Nonetheless, modellers must clearly communicate the limitations and uncertainties associated with models to policymakers and stakeholders to enhance the accuracy and reliability of forecasting ensemble models in public health (Swedo et al., 2023). This communication can be achieved through visualizations, probability distributions, or confidence intervals to help decision-makers understand the potential limitations and risks associated with the forecasts (Ray, Wattanachit, et al., 2020).

6.2 Use case 2: Scenarios

The longer the forecast horizon the greater the uncertainty and unfortunately the larger the forecast error. This degradation of forecast skill presents a challenge for policymakers as they seek facts, scientific understanding and certainty. Scenarios arising from ensembles of models can help to guide a participatory conversation about what is most likely to happen in the future. Different modelling approaches and even a variety of critical parameters (relating to the virus or the model in general) can be encapsulated so that all opinions are reflected. Even more importantly, scenarios can help to manage risk and avoid disastrous consequences. A platform with an ensemble of models therefore accounts for uncertainty and demonstrates possible outcomes, helping to visually explore uncertain versions of the future.

Mitigating against forecast error within ensemble models that use scenarios involves incorporating scenario-based analysis, using model averaging or weighted averaging, applying data assimilation techniques, and employing post-processing techniques (Kuhl et al., 2007; Cawood and Zyl, 2021; Rayner and Bolhuis, 2020). Incorporating scenario-based analysis into the ensemble modelling process involves developing multiple scenarios that represent different possible future conditions or events and running the ensemble model for each scenario to capture the uncertainty and variability in future outcomes, reducing the impact of forecast errors. Giving more weight to the more accurate or reliable models within the ensemble can help mitigate the impact of individual forecast errors. Data assimilation involves combining observational data with model predictions to update the initial conditions of the ensemble model. Employing post-processing techniques can help refine the ensemble forecasts and reduce systematic errors or biases in the ensemble by applying statistical methods or machine learning algorithms to the ensemble output to further adjust or calibrate the forecasts. Note that, as well as mitigating against forecast error, the use of scenarios with model ensembles also provides decisions makers with a measure of forecast variability and enables them to plan, e.g., for unlikely, but severe forecasts. The use of a variety of scenarios when planning, e.g., a pandemic response, adds robustness to the decision makers' plans.

6.3 Use case 3: Policy laboratory

A policy laboratory (a.k.a. policy lab) refers to a space or platform or controlled environment where interdisciplinary teams, including policymakers, researchers, and stakeholders, come together to test and evaluate different policy interventions, strategies, and approaches before large scale implementation (Lunn and Choisdealbha, 2018). Policy labs are used to identify risks, vulnerabilities, and unintended consequences, and evaluate the effectiveness and feasibility of different policy measures(Saam and Kerber, 2008). The platform offers a means of safely exploring different policies and better understanding the costs and benefits (economic and health).

During the pandemic, Oxford University established the OxCGRT – Hale et al., 2021 – which collected information on policy measures over the period 2020-2022. As an example of the utility of integrating diverse datasets, Agyapon-Ntra and McSharry, 2022 combined OxCGRT with Google mobility data to quantify compliance at the country level and evaluate the efficacy of different policies in reducing cases. A policy lab can integrate data from OxCGRT – a global panel of policy responses for 19 policy areas – with the ensemble of models (see §3) to explore how government responses relate to a number of social, political, and economic factors. The Pandemic Resilience project is prototyping such a policy lab and envisages that it will have impactful implications for understanding and responding to future pandemics or global emergencies.

7 Future work

The experiments in this report demonstrate the value of establishing a common interface and calibration framework for different kinds of pandemic prediction models so that they can be compared and ultimately brought together through ensembling. This approach enables the combination of various kinds of human domain expertise, local knowledge, and global data-based machine learning in order to obtain more robust predictions across different geographical regions as well as time phases of the pandemic. It is possible to build on this foundation in several ways in future work:

Ensembling: Thus far in this report, the effect of ensembling was demonstrated across variations of the same (Cognizant) model and across two different kinds of LSTM models. The next step is to extend it to the Cyber-Physical and CTMC models as well. The interface and calibration framework makes it straightforward; it will be interesting to see how each of these different models will be used in the ensemble, i.e., across different geographic locations and time periods. In the future, other types of models can be added to the ensemble, eventually leading to a theory of what models are most useful in various situations, and how they can be best combined.

What-if simulations: Each model, as well as the ensemble of models, can be used by decision makers to evaluate NPI schedules and simulate their impact on, e.g., the number of cases, hospital admissions, and deaths. Understanding the accuracy of such what-if simulations is an important step towards deploying them in this role, e.g., as part of a policy lab – see §6.3.

Prescriptions: This report focused on predictive models as the first step. An important follow-up is to go one step further. Once accurate predictive models are available, it is possible to optimize NPI scenarios according to different objectives such as the number of cases and economic impact. Given a desired tradeoff between the objectives, such prescriptive models can suggest NPI schedules to decision makers and help them make more informed choices. Decision makers also have the possibility to constrain the prescriptive model to search only for specific scenarios: for instance, "close schools for a maximum of 2 weeks", "do not recommend full lockdown", etc. Furthermore, it will be possible for the decision makers will work. Prescriptive models can thus serve an important role in empowering decision makers to discover better solutions that they can trust.

Extension to other diseases: Using the same methodology but different data, the framework can be adapted to other diseases. For instance, given available data for influenza, respiratory syncytial virus (RSV), monkey pox, and adenovirus, predictive and prescriptive models could be developed for them, possibly even jointly for several of them. Eventually the approach could be extended to a comprehensive ongoing intervention policy for public health officials.

Impact on decision-making: A close collaboration with governments/decision makers and computational experts is needed to take advantage of the technology described in this report. Researchers build the technology, software engineers develop the tools, and decision makers use them and provide feedback and requirements to the researchers and engineers. Such an ecosystem does not yet exist but GPAI is in a pivotal role to realise such an ecosystem in the future.

Scientific publication: This is a progress report on the current state of the project. The team is working on extending the study in order to publish it as a scientific research paper

for technical audiences.

8 Conclusion

This report describes progress of the Global Partnership on Artificial Intelligence (GPAI) Pandemic Resilience project and learnings from the research work undertaken by the project team. Some of the alignment with responsible AI has been intentional, such as the design of the calibration framework to extend pandemic modeling to more, diverse models. Other alignment has been serendipitous or discovered during the project, such as the inherent robustness of the ensemble model. This section summarises the key learnings from the Pandemic Resilience project (so far) and how they align with key principles of responsible AI. It also summarises how this project aims to support policy decision makers and provide an exemplar for (ensemble) model-informed, evidence-based decision making in government (and other organisations).

In our exploration of ensemble modeling and responsible AI practices, it becomes abundantly clear that this collaborative, multidisciplinary approach offers immense promise for addressing complex global challenges. The strength of ensemble modeling lies in its ability to bring together a multitude of technologies and teams, each contributing their unique expertise and perspective to a collective effort. Working and learning together is not only socially worth-while but also scientifically invaluable. This synergistic methodology leads to better and more accurate model predictions. To achieve this, ensemble models require modular calibration frameworks and data standardization. In this global context, organizations like the GPAI can contribute to this dialogue, assisting stakeholders in defining international standards by offering a technical perspective in the standards creation process.

We must emphasize the important potential of well-informed, data-driven decision making, free from biases and misinformation. However, to fully realize this potential, governments and other stakeholders must actively participate in shaping the responsible AI landscape. Decision makers must stay responsible and accountable for the model-informed decisions they take. Thus, responsible AI must be anchored in the core of decision support systems, ensuring that ethics, transparency, and accountability guide every decision.

As we've witnessed with the COVID-19 pandemic and climate change, the next global crisis may involve a complex web of interconnected challenges. Decision makers will probably increasingly rely on models to navigate these multifaceted issues. Therefore, human-centered AI and modeling, with humans in the loop, becomes invaluable for responsible and effective decision support systems. Governments, with their power to enact impactful decisions, have a significant role to play in this endeavour. We must collectively ensure that AI development adheres to responsible and safe practices, with the common good in mind, leaving no one behind.

The Pandemic Resilience project's research is aligned with responsible AI principles and has provided an ecosystem of ensemble modelling, standardized interfaces/data and AI to improve model performance. This ecosystem is a paradigm for bringing together diverse perspectives and AI technology into a modelling environment that provides robust decision making.

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A Model Summaries

This appendix contains summaries of each of the models – in section §A.1-A.3 respectively – used in the calibration framework:

- the Cyber-Physical model;
- the Cognizant model; and
- the CTMC model.

A.1 Model 1 summary: Cyber-Physical Model

This model consists of two parts: the plant (epidemiological model) and controller (NPI strategy). This model, including some predefined scenarios, is available online on GitHub at https://github.com/PRETgroup/ccpe-covid19 (Compositional Epidemiology of COVID-19) and is explained in full detail in the associated paper https://www.nature.com/articles/s41598-020-76507-2.

Note that the Cyber-Physical model was developed by Prof Partha Roop, Dr Nathan Allen – one of the authors, Mr Sobhan Chatterjee – another one of the authors, all from the University of Auckland in Aotearoa | New Zealand.

A.1.1 Plant (Epidemiological Model) – Inputs and Outputs

The model follows a basic Suspected-Exposed-Presymptomatic-Infected-Recovered (SEPIR) implementation, with modifications to allow for different reproduction numbers for confirmed cases (e.g., to capture enforced isolation requirements), and testing rates.

A.1.1.1 Model inputs

- Reproduction number (R_0) for the general population [initial: 2.5]
 - Initial values are for an uncontrolled setting
 - Note that this is an input to allow for it to be changed by the controller, could also be set to a constant value
 - In the calibration framework this has been modified to the reproduction number for each variant (which is fixed over all locations) along with the proportion of each variant present in each location
- Reproduction number $(R_{0.c})$ for confirmed cases that are then isolated [initial: 0.02]
 - Note that this is an input to allow for it to be changed by the controller, could also be set to a constant value
- Testing rate (c) [initial: 0.10]

A.1.1.2 Model outputs

- Susceptible Population (S)
- Population (E)
- Pre-symptomatic Population (*P*)
- Infected (untested cases) (I_u)

A.1.2 Plant – Parameters

- Infected (confirmed cases) (*I_c*)
- Recovered (untested cases) (R_u)
- Recovered (confirmed cases) (R_c)
- Deaths (D)

This section describes the parameters of the "Plant" in the Cyber-Physical model, i.e., the component of the model that describes the epidemiological spread. These parameters have been categorised into: global, i.e., those that will have the same value at any location; location, i.e., those that will differ by location, but should be consistent across models; and model, i.e., those that are specific for the Cyber-Physical model.

A.1.2.1 Global parameters

- Transition Rate from Exposed to Pre-Symptomatic (α) [default: 0.25]
 - This is the reciprocal of the average incubation time
- Transition Rate from Pre-Symptomatic to Infected (δ) [default: 1]
 - This is the reciprocal of the average pre-symptomatic time
- Transition Rate from Infected to Recovered (γ) [default: 0.1]
 - This is the reciprocal of the average infectious time
- Relative Infectiousness when Pre-Symptomatic (*e*) [default: 0.15]
- Case Fatality Rate (CFR) with ICU Availability (CFR₀) [default: 0.01]
- CFR without ICU Availability (*CFR*₁) [default: 0.02]
- Proportion of cases requiring ICU (p_{ICU}) [default: 0.0125]

A.1.2.2 Location parameters

- Population Size (population)
- Initial Cases
 - Number of Initial Cases (*initial_cases*)
 - Distribution of Initial Cases Between (Model) States, i.e., Suspected, Exposed, etc. (*initial_case_distribution_factor*)
- ICU Capacity (n_{ICU})

A.1.2.3 Model parameters

- Step Size (in days)
- Simulation Length (in days)
- Logging Rate

A.1.2.4 Input data

Since the Cyber-Physical model is an epidemiological model based on physics, no model training, hence input data, is required. However, the number of initial cases (i.e., *initial_cases*) is sourced from input data.

A.1.2.5 Output data

The model outputs were compared against the Johns Hopkins CCSE COVID-19 data set – obtainable from GitHub https://github.com/CSSEGISandData/COVID-19 – to evaluate the model accuracy.

A.1.3 Controller (NPI Strategy) – Inputs and Outputs

A controller is implemented as a Hybrid Automata which can contain one or more "states" of control. This controller was used to capture the four-level structure implemented in New Zealand, but different control strategies can be implemented accordingly. This model is created by the person testing out a strategy and so the following is just an example for the New Zealand four-level controller.

Note that – in the calibration framework – the controller is informed by a Non-Pharmaceutical Intervention (NPI) schedule.

A.1.3.1 Location parameters

- R0 for isolated cases (R_{0,lso})
- R0 for each control level ($R_{0,L0}$ through $R_{0,L4}$)
- Testing Rate for each control level (c_{L0} through c_{L4})
- Thresholds for shifting up levels based on rate of change of cases (k_{L1} through k_{L4})
- Thresholds for shifting down levels based on confirmed cases (dk_{L1} through dk_{L4})
- Minimum times at each level before shifting down (t_{L1}^{\min} through t_{L4}^{\min})

A.1.3.2 Model parameters

- Number of confirmed cases (*I_c*)
- Rate of change of confirmed cases (c_dot)

- Step Size (in days)
- Simulation Length (in days)
- Logging Rate

A.1.3.3 Input data

• The controller was designed to mimic the operation and alert-level switching of the New Zealand approach, including minimum times at each level before control can be switched to a lower level, using the Johns Hopkins Center for Systems Science and Engineering (CSSE) data as a control.

A.1.3.4 Model outputs

- R0 for general population (R₀)
 - This can be adjusted based on the NPIs that are present at any point in time
- R0 for confirmed cases ($R_{0,c}$)
 - This can be adjusted based on the NPIs that are present at any point in time
- Testing rate (c)

A.1.4 Strengths and Weaknesses

A.1.4.1 Model strengths

- 1. Computationally efficient
- 2. Large time-horizon of predictions
- 3. Able to "test out" various control strategies with relative ease
- 4. Not dependent on data availability for predictions once initial data-points are present

A.1.4.2 Model weaknesses

- 1. Requires NPIs to be quantified in terms of R_0 impact
- 2. Does not "create" control strategies, only tests provided ones
- 3. Changes to transmission rates of variants requires changing parameters of model
- 4. Since Susceptible-Exposed-Infected-Recovered (SEIR) models are continuous models, Cyber-physical has issues with values tending towards (but never reaching) zero
- 5. Only one prediction provided, not a range of possible scenarios (i.e., not stochastic).

A.2 Model 2 summary: LSTM Model

Two distinct Long Short-Term Memory network (LSTM) models were provided by Pandemic Resilience team members from Cognizant Artificial Intelligence (AI) Labs and both model the dynamics of the epidemic. These models are trained to predict the daily number of new cases reported, given a case history and regional metadata such as population. The models involve machine learning to fit the model to historical data. While they incorporate little modeling information about how epidemics ought to progress in theory, they are able to flexibly learn a statistical distribution that fits the observed data. The first version of the model is explained in full details in a paper (Miikkulainen et al., 2021) and was used in the XPRIZE Pandemic Response Challenge (XPRIZE, 2021). The second version was developed later to adapt to changes in the pandemic. Both versions are available online on GitHub at https://evolution.ml/demos/npidashboard/.

A.2.1 Inputs and Outputs

Unlike the Cyper-Physical – see §A.1 – and Continuous Time Markov Chain (CTMC) – see §A.3 – models, the Cognizant models do not have parameters based on epidemic spread. The spread is modelled directly from training using the data, the parameters for the Cognizant models determine how the data is used and the underlysing structure of the Long Short-Term Memory network (LSTM) models.

A.2.1.1 Global parameters

- Moving average length, to smooth noisy data [default: 7 days]
- Lookback period [default: 3 weeks (of 7 days moving averages)]
- Number of cases can be normalized by 100K residents to improve "fairness" of comparisons

A.2.1.2 Location parameters

- · Population size for the region/country
- Total number of recorded cases by day, n, for the region/country. **Note** the model is assuming that recovered cases are fully immune

A.2.1.3 Model parameters

- LSTM layer size [default: 32 units]
- Testing set [default: last 14 days fo the input data]
- Training set [default: 90% of remaining data (random split)]
- Validation set [default: 10% of remaining data (random split)]
- (Later version) Max dataset size, to account for changes in the data introduced by delta and omicron variants, and vaccinations [default: last 365 days]

A.2.1.4 Input Data

For a given country/region, 3 weeks of 7 days moving averages – from 4 weeks of data on number of cases, along with 8 (later 12) NPIs restrictiveness values (NPIs stringency level). See Oxford Covid-19 Government Response Tracker (OxCGRT) codebook for definitions (Hale et al., 2021):

- C1_School closing
- C2_Worplace closing
- C3_Cancel public events
- C4_Restrictions on gatherings

• C5_Close public transport

- C6_Stay at home requirements
- C7_Restrictions on internal movement
- C8_International travel controls

Later versions also include:

- H1_Public information campaigns
- H2_Testing policy

- H3_Contact tracing
- H6_Facial coverings

A.2.1.5 Model Outputs

• The predicted number of cases 1 day in the future. Note that the Cognizant models can make predictions arbitrarily far into the future, given a schedule of NPIs, by autore-gressively feeding the predicted number of cases back into the model as input.

A.2.2 Evaluation Metrics

- Mean Absolute Error (MAE) for predicted day
- MAE with respect to new cases over the 14 test days summed over 20 test countries (countries with most deaths)
- Normalized Case MAE, i.e., MAE normalized by population size, to aggregate countries with different population size
- Rank (to compare with other models)

A.2.3 Strength and Weaknesses

A.2.3.1 Model strengths

- 1. No epidemiological assumption. Works even when nothing is known about the virus, starts learning even with limited data (e.g., 2 or 3 months)
- 2. Fast to train: less than 24 hours
- 3. Fast to predict: fast to make predictions: a few seconds
- 4. Retrained daily, with 1 day of additional data. Gets better and picks up new trends (delta, omicron, vaccinations, etc.)

A.2.3.2 Model weaknesses

- 1. Data is noisy and unreliable
- 2. Data can be politically manipulated (some countries officially reported 0 cases)
- 3. The model assumes that recovered cases are fully immune (which we now know is **not** true)
- 4. The model assumes NPIs always reduce the number of cases, and more NPIs reduce the number of cases more (which is NOT proven)
- 5. Model does not work well for countries with a very small number of cases (e.g., New Zealand)

A.2.4 The Conditional LSTM Model

The Cognizant team iterated on the initial design of the LSTM Model to form the Conditional LSTM Model, in order to address the changing setting of the COVID-19 pandemic. During the later stages of the pandemic in late 2021, vaccines were put into widespread usage, which affected the epidemic dynamics and motivated architectural changes to the model. In addition to re-fitting hyperparameters to the new training setting, here are the key innovations made to create the Conditional LSTM Model:

- 1. The format of the predicted data was changed. The first model predicted the ratio of new cases on one day divided by the number of new cases on the previous day. In this architecture, a constant positive prediction repeated over several days results in exponential growth of the number of predicted cases. We overcame this limitation by switching the data format to the number of new cases per 100,000 population, a measure that still has consistent meaning between different countries but has an additive, rather than multiplicative, interpretation. All data is converted back to daily predicted new cases in accordance with the standardized data pipeline.
- 2. The model layers were rearranged. In the first model, the actions (NPIs) and context (cases) are fed into separate layers before being combined to inform the final prediction. In the revised model, the output of the context layer flows into the action encoding layer. Thus the representation of the action is conditioned on the recent context so that the action representation has some information about the recent effects of previous actions and the country status.

A.3 Model 3 summary: Auckland: Stochastic Markov Chain Model

The CTMCs model consists of a base CTMCs model of epidemic spread with two extensions:1) adding hospitalization; and 2) adding intensive care units. Similar to the Cyber-Physical model – see §A.1 – the CTMCs model predicts the number of individuals that are susceptible, exposed, infected, hospitalized, in Intensive Care Unit (ICU), etc. The model is modified to allow for testing different control scenarios by adjusting various parameters such as the initial number of individual in each state. The CTMCs model was developed from initial SEIR modelling from Hendy et al., 2021 .Control scenarios that can be tested under this model are the same as those for the Cyber-Physical model and these control effects, such as school closures, are modelled using shared, common code in the Pandemic Resilience code repository. The CTMCs model was developed by Assoc Profs. Cameron Walker, Ilze Ziedins and Mike O'Sullivan.

A.3.1 Inputs and Outputs

The model follows compartmental approach which can be summarised as Suspected-Exposed-Presymptomatic-Infected-Wards-ICU-Recovered and predicts cases in each state (a.k.a. compartment) during lockdown. The Wards state refers to individuals who are confirmed to be infected (tested or untested cases) and transition into hospital, i.e., are hospitalized, before being escalated into the ICU or moving to the Recovery/Deceased states. Note that there are actually 2 Ward states that repesent a ward stay before and after an ICU stay. The ICU state refers hospitalized individuals that have transitioned into ICU and thereafter transition to becoming Deceased or further hospitalization in the second ward state. Note that the CTMC model also includes data on cases from immigration of confirmed infected people (i.e., arrivals from overseas to the Infectious and Untested, I_0 , state).

A.3.2 Inputs and Outputs

A.3.2.1 Global parameters

- *R*₀, basic reproduction number for the COVID-19 (i.e., number of people that an infected person will infect before recovery) [default: 2.5]
 - Note that this value was adjusted for Aotearora | New Zealand, so was adapted within the calibration framework to consider location effects, i.e., proportion of each variant present in the location's population.
- *ϵ* relative infectiousness while presymptomatic [default: 0.5].Note that the transmission
 rates defined here are set to be the same fro both the Cyber-Physical and CTMC mod els when the states begin moved between are present in both models, e.g., Presymp tomatic to Infected.
- α , rate of change from Exposed to Presymptomatic [default: 0.25]
 - Approximately 4 days in Exposed, i.e., not showing symptoms or being infectious, state.
- δ , rate of change from Presymptomatic to Infectious and Untested, I_0 [default: 1]
 - 1 day in Presymptomatic state
- γ , rate of change from Infectious and Untested, I_1 , to Recovered or Deceased [default: 0.1]
 - 10 days in I_0 state
- θ , rate of change from patients admitted to hospital (W_1) to Recovered or Deceased [default: 0.2]
 - 5 days in W_1 state
- η , relative infectiousness while in hospital, i.e., in either of the Ward states [default: 0.1]
- ψ , rate of change from in ICU to Recovered or Deceased [default: 0.2]
 - 5 days in ICU.
- ω , Relative infectiousness while in ICU [default: 0.01]

A.3.2.2 Location Parameters

- Level 4 interval = day 25 to day 53 (28-day lockdown from 25 March). This is the NPI that was initially used in Aotearoa | New Zealand. This is superseded by the adjusted R_0 for each location, NPI and NPI level.
- $R_C = 0.84$, reduced reproduction number (reduced number of expected infections given alert level 4). This was adjusted for Aotearoa | New Zealand and superseded by a shared, common approach to modeling NPI effects within the calibration framework.
- Start date [default: 1 March 2020]
- Population size, the number of people in the population being modeled [default: for Aotearoa | New Zealand 5,000,000]
- Number of ICU beds, N_{ICU} (i.e., estimated number of ICU beds available in Aotearos | New Zealand) [default: 500]
- Average household size the average number of people in a household
- Test rate, rate of testing infectious patients [default: 0.6]
- Parameters estimated for decision making in New Zealand's health system:
 - $\rho_{I_1 W_1}$, proportion of infected patients that go to the ward [default: 0.18]
 - $\rho_{W_1 ICU}$, proportion of admitted infected people needing ICU [default: 0.019]
 - $\rho_{I_1 D}$, proportion of infected patients that die [default: 0.16]
 - $\rho_{I_1 R_0}$, proportion of infected patients that recover [default: 0.63]
 - $\rho_{W_1R_1}$, proportion of (pre-ICU) ward patients that recover [default: 0.09]
 - $\rho_{W_1 ICU}$, proportion of infected (pre-ICU) ward patients requiring ICU [default: 0.65]
 - ρ_{W_1D} , proportion of (pre-ICU) ward patients that die [default: 0.25]
 - ρ_{ICUW_2} , proportion of ICU patients that go to (post-ICU) ward [default: 0.63]
 - ρ_{ICUD} , proportion of ICU patients that die [default: 0.34]
 - ρ_{ICUR_1} , proportion of ICU patients that recover [default: 0.02]
 - $\rho_{W_2 R_1}$, proportion of (post-ICU) ward patients that recover [default: 0.54]
 - ρ_{W_2D} , proportion of (post-ICU) ward patients that die [default: 0.46]
- Infection Fatality Rate [default: 0.01 when ICU is under capacity, 0.02 when ICU is over capacity]
 - This provides input for a calculation of deaths based on what happens in Aotearoa | New Zealand.

A.3.2.3 Model Parameters

The model is parameterised for New Zealand and the default scenario is initialized using current case data.

• Model duration [default: 300 days]

A.3.2.4 Input data

• Initial counts [default: Exposed = 60, Susceptible = 5,000,000 - 60, others = 0]

A.3.2.5 Model outputs

- Susceptible Population (Sus)
- Exposed Population (*Exp*)
- Pre-symptomatic Population (*Pre*)
- Infected but not infectious (untested cases) (*I*₀)
- Infected and Infectious(confirmed cases) (*I*₁)
 - A.3.3 Strength and Weaknesses

A.3.3.1 Model strengths

- 1. Allows for a range of possible scenarios (i.e,. stochastic)
- 2. Able to test various control strategies to recommend improvements
- 3. Not dependent on data availability for predictions once initial data points are present
- 4. Since initial data points are set based on actual data from a country, it enables different country situations to be tested
- 5. Computationally efficient
- 6. Large time-horizon of predictions
 - The model is, however, sensitive to large data sets (i.e., large datasets can creates awkward outcomes for some outputs)
- 7. Does not require a large amount real data to run

A.3.3.2 Model weaknesses

- 1. Unable to differentiate regional disparities in outputs due to regional differences in healthcare infrastructure
- 2. Unable to consider the probability of an individual in one location directly infecting an individual in another location because of physical distance or mobility
 - The R_0 and local parameters capture transmissibility and how much contact a household (not individual) has with people but assumes the transmissibility will be the same irrespective of where individuals in the household are located

- Infected patients that are hospitalized (pre-ICU) (*W*₁)
- Infected patients that go to ICU(V)
- Infected patients that are hospitalized (post-ICU) (W₂)
- Recovered (untested cases) (R₀)
- Recovered (confirmed cases) (R₁)
- Deaths (D)

- 3. Takes a long time to run large computational "burden"
- 4. Does not "create" control strategies, only tests provided ones
- 5. Changes to transmission rates of variants requires changing parameters of model, although this has been adapted for the calibration framework
- 6. Sensitive to the initial data points, it is important to ensure that initial data points are objectively justified

B Inputs, Outputs and Calibration Definitions

B.1 Standardized inputs and outputs

This section catalogs the standardized inputs and output for the models and definitions of the terms that we will use for our ensemble of models.

B.1.1 Modelling Interface – Terms and Definitions

- 1. Transmission rate of COVID-19 variant "We define the transmission rate as the number of people infected in one close contact event over the number of people in that event." L. Zhang et al., 2021 The symbol R_0 is usually used. The following variables reflect the state of an individual in relation to the virus:
 - (a) Susceptible (*S*) an individual that could become infected with a COVID variant due to proximity to other infected and infectious (although possibly not symptomatic) individuals
 - (b) Exposed (E) an individual that has been exposed to a COVID variant, and is infected but is not yet infectious or symptomatic
 - (c) Pre-symptomatic (*P*) an individual that is infected with a COVID variant and is infectious, but not yet symptomatic
 - (d) Infected and Infectious (I_1) an individual that is infected with a COVID variant and is infectious and symptomatic
 - (e) Infected and not Infectious (I_2) an individual that is infected with a COVID variant and is symptomatic but no longer infectious
 - (f) Deceased (D) an individual who has died as a result of the infection
 - (g) Recovered (*R*) an individual that has been infected with COVID but is no longer symptomatic or infectious (they have received from the infection)
 - (h) In Ward Pre-ICU (W_1) an individual that is in a hospital ward, but has not been to the ICU
 - (i) In ICU (V) an individual that is in a hospital ICU
 - (j) In Ward Post-ICU (W_2) an individual that is in a hospital ward after staying in the ICU

urrently 4) /emment Response Tracker (OxCGRT) codebook. In the GitHub repository under data/timeseries ach NPI. Instead of Economic effects, the tracker monitored countries that used selected include:	E3_fiscal measures E4_international support	plement economic policy are assigned 0. Flags are used to determine if a policy applied to ion or not. However, economic policies and flags were not used because it was assumed nificant impact on confirmed cases and deaths for the countries that were being studied. g confirmed cases and deaths were the priority at this time. However, using the flags and we provided a more accurate view. It is helpful to take note of how some NPIs have cross of combining NPIs may lead to double changes to predictions. elta and omicron) -19 infection	Infected and Not Infectious; Recovered; Deceased; r stades. so this parameter is generic.	
 1.1. Global Inputs 1.1.1. Global Input Parameters 1.1.1.1. List of NPIs 1.1.1.1. NPI name/code 1.1.1.1.2. Max NPI level (integer, currently 4) See Oxford Covid-19 Government R there are CSV files for each NPI. Ir economic policies which include: 	E1_income support E2_debt/contract relief	Countries that did not implement ec a proportion of a population or not that it did not have a significant imp Predicting and controlling confirmec economic effects may have provide impacts and as a result of combining 1.1.1.2. List of variants (e.g., alpha, delta and on 1.1.1.3. Hierarchy of stages of COVID-19 infectit For example:	Susceptible; Exposed; Presymptomatic; Infected and Infectious; Other models. mav have other stages, s	1.1.1.3.1. Stage name/symbol

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B.1.2 Modelling Interface – Standard

1. Inputs

1.1.1.3.2. Transition rates between stage of COVID-19 infection For example, transition rate from Exposed to Presymptomatic has been estimated at $\frac{1}{4}$, i.e., it take on average 4 days for someone who has been infected to become infectious without displaving symptoms. This will be N/A for some
stages, e.g., Susceptible to Recovered, but this corresponds to a rate of 0. These rates determine how COVID-19 progresses and will be variant specific.
1.1.1.3.3. Relative infectiousness of Presymptomatic with respect to Infectious
1.1.1.4. Countries modelled List of countries to produce model outputs for
1.2. Location Inputs
1.2.1. Location Input Parameters
1.2.1.1. Proportion of variants
I he proportion of each of the variants at the locations, listed by country.
1.2.1.2. Effective transmission rates
I nis would be a model of function that estimates the effective transmission rates between COVID-19 stages at a particular location taking into account the transmission rate between stages and the levels of NPIs in place. It needs to be consistent
across models
1.2.1.3. Extra stages of COVID-19 infection for location's health system For example In Ward Pre-ICU In ICU In Ward Post-ICU
1.2.1.3.1. Stage name/symbol
1.2.1.3.2. Transition rates into and out of location's health system stages for COVID-19 cases
1.2.1.4. Estimates of total population size and number of population in each stage (including extra stages from 1.2.1.2)
1.2.1.5. Time periods for model horizon
1.2.1.6. NPI schedule - level of NPI for each time period in the model horizon
1.2.2. Location Input Data
1.2.2.1. Time periods for historical data
1.2.2.2. Case numbers for each time period for the previous 3 months-1 year depending on availability
1.2.2.3. Deaths for each time period for the previous 3 months-1 year depending on availability
1.2.2.4. Level of NPI for each historical time period
1.3. Model-specific (aka Model) Inputs
1.3.1. Model Input Parameters
1.3.1.1. List of models being used
1.3.1.2. Table of coefficients relating NPIs to effective transmission
1.3.1.3. Output locations for the models

2. Outputs

- 2.1. Location Outputs
- 2.1.1. Location Output Estimates
 - 2.1.1.1. Location information

- 2.1.1.2. Time periods for model horizon
 2.1.1.3. Case number estimates for each time period in the model horizon
 2.1.1.4. Daily new case number estimates, i.e., the difference each day
 2.1.1.5. (Optional) Recovered number estimates for each time period in the model horizon
 2.1.1.6. (Optional) Death estimates for each time period in the model horizon
 2.1.1.7. (Optional) Daily new deaths number estimates, i.e., the difference each day
 2.1.2. Location Output Data
 2.1.2.1. Time periods for historical data
 2.1.2.1. Time periods for historical data
 2.1.2.1. Time period for the previous 3 months-1 year depending on availability
 2.1.2.4. Level of NPI for each historical time period

B.1.3 Interface Notation

Interface Description	Interface Notation	Range
1.1.1.1. List of NPIs	$n \in N$	
1.1.1.1.2 Level of NPI for each historical	l _{nt}	$n \in N, t \in -T^H,, T^E$
time period and each time period in		
The model horizon		
1.1.1.3 Hierarchy of stages of COVID-19 in-	$s \in S$	
fection		
1.1.1.3.2 Transition rates between stage of	$Q_{S_1S_2}$	$(s_1, s_2) \in S \times S$
COVID-19 infection		
1.2.1.1 Effective transmission rates	$\hat{Q}_{s_1s_2t}(Q_{s_1s_2}, l_t)$	$(s_1 s_2) \in S \times S, t \in 1, \dots, T^E$
1.2.1.2 Extra stages of COVID-19 infection	$S' \supseteq S$	
for location's health system		
1.2.1.2.2 Transition rates into and out of lo-	$Q'_{S_1S_2}$	$(s_1s_2) \in S' \times S'$
cation's health system stages for COVID-19		
cases		
1.2.1.3 Effective transmission rates into and	$\hat{Q'}_{s_1s_2t}(Q'_{s_1s_2}, l_t)$	$(s_1s_2) \in S \times S, t \in 1, \dots, T^E$
out of location's health system		
1.2.2.1 Time periods for historical data	$t \in -T_H,, 0$	
1.2.2.2 Case numbers for each time period	I_t^E	$t \in -T_H,, 0$
for the previous 3 months-1 year depending		
on availability		
1.2.2.3 Recovered numbers for each time	R_t^E	$t \in -T_H,, 0$
period for the previous 3 months-1 year de-		
pending on availability		
1.2.2.4 Deaths for each time period for the	D_t^E	$t \in -T_H,, 0$
previous 3 months-1 year depending on		
availability		
2.1.1.1 Time periods for model horizon	$t \in 1,, T^E$	
2.1.1.2 Case number estimates for each	I_t^E	$t \in 1,, T^E$
time period in the model horizon		
2.1.1.3 Recovered number estimates for	R_t^E	$t \in 1, \dots, T^E$
each time period in the model horizon		
2.1.1.4 Death estimates for each time pe-	D_t^E	$t \in 1,, T^E$
riod in the model horizon		

B.2 Calibration framework

This section presents the how the calibration framework was developed from a generic multiobjective Genetic Algorithm (GA) approach including pseudocode for the "fitness" evaluation for a given set of parameters and a comparison of a generic metaheuristics framework versus the calibration framework.

B.2.1 Fitness Evaluation Method

The Fitness Evaluation Method (a.k.a. the Evaluation Function) is used to determine how close the model outputs, from a given set of input parameters and input data, to the actual output data. It assesses the value of an individual set of parameters.

```
Algorithm 1 Fitness Evaluation
```

Input: Global parameters P_G , location parameters P_L , L in locations \mathcal{L} , and 1: model parameters P_{LM} , $L \in \mathcal{L}$, M in models \mathcal{M}

Output: Evaluation metrics for \hat{E} ensemble parameters

2: for $L \in \mathcal{L}$ do

3: for $M \in \mathcal{M}$ do

- 4: Populate standard input JSON using parameters for P_G , P_L and P_{LM}
- 5: Run model *M* with JSON
- 6: Get outputs
- 7: Calculate evaluation metrics E_{GLM} using outputs
- 8: end for
- 9: end for
- 10: Calculate ensemble evaluation metrics \hat{E} using E_{GLM} for global parameters G, all $L \in \mathcal{L}$, $M \in \mathcal{M}$

B.2.2 Generic Metaheuristics versus Calibration Framework

Metaheuristics are strategies that guide the search process to find solutions that are close to ideal requires effective search space exploration. The calibration framework was based on a generic metaheursitics approach as shown in Table B.1.

B.2.3 Multi-Objective Genetic Algorithm Method (NSGA2)



Figure B.1: Multi-Objective Genetic Algorithm Method

B.2.4 NSGA2-based Calibration Method



Figure B.2: NSGA2-based Calibration Method

Table B.1: Generic Metaheuristics versus Calibration Framework

 put: Initial guess of (a set of) input(s) x while time/iterations remaining AND not converged do Evaluate objective function f for input(s) x 	Input: Initial values for (set of) input parameters $x_1,, x_P$ 1: while time / iterations remaining AND not converged do 2: Use Fitness Evaluation Method – see Algorithm 1 (i.e., run
3: Find x that are in the neighbourhood of x that improves the objective	models, get outputs and calculate ensemble evaluation met- rics) for each instance of input parameters to get evaluation
4: end while	metrics $\hat{E}_i, i = 1, \dots, P$ 3. Find new $x_i = x_i$ that are in the neichbourhood of
	x_1, \dots, x_P that (hopefully) improves the evaluation metrics
	4: end while

B.2.5 Inputs

The key functionality we need to define for using NSGA2 for calibration are: The variables that can change with bounds, i.e., our input parameters .

- 1. Inputs
- 1.1. Global Inputs
- 1.1.1. Global Input Parameters
 - 1.1.1.1. List of NPIS

1.1.1.1. NPI name/code The parameter used in the calibration (NSGA2) framework won't change during calibration, However the team will use available data of NPIs during the model horizon (31 March-30 June 2020) and currently available data of NPIs.

1.1.1.2. List of variants (e.g., alpha, delta and omicron)

Set lower and upper bounds, allow them to change to improve ensemble metrics alpha - [2.29, 3.29] delta - [4.58, 5.58] omicron - [9,10] 1.1.1.2.1. Estimated "true" reproductive numbers for variant

- 1.1.1.3. Hierarchy of stages of Covid infection
 - 1.1.1.3.1. Stage name/symbol
- The parameters Won't change during calibration

| NPI, location and variant. | 1.3.1.1. Table of coefficients relating NPIs to effective transmission
These are transformed using a linear model for the different levels of NPI, the slope of the model can change for each | 1.3.1. Model Input Parameters | .3. Model-specific (aka Model) Inputs | The parameters will change | 1.2.1.6. NPI schedule - level of NPI for each time period in the model horizon

 | The parameters won't change during calibration | 1.2.1.5. Time periods for model horizon | Initial number in each stage will change - need a constraint to make sure the sum of initial numbers = total?

 | Total population won't change | 1.2.1.4. Estimates of total population size and number of population in each stage (including extra stages from 1.2.1.2) | Won't change during calibration | 1.2.1.3.1. Stage name/symbol
1.2.1.3.1. Transition rationints and out of Ionation's hoalth evidem starting for Covid accord | 1.2.1.3. Extra stages of Covid intection for location's health system
 | The function won't change during calibration, but parameters that define it - see 1.3.1.1 - will change | across models | location taking into account the transmission rate between stages and the levels of NPIs in place. It needs to be consistent | 1.2.1.2. Effective transmission rates
This would be a model or function that actimates the officiative transmission rates between Covid states of a particular | The parameters will change - bounds should be [0,1] and these proportions should add to 1. | 1.2.1.1. Proportion of variants
The proportion of each of the variants at the locations | 1.2.1. Location Input Parameters | 2. Location Inputs | The parameters won't change during calibration | 1.1.1.4. Countries modelled
List of countries to produce model outputs for |
|---|--|---|--|--
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---|---|---|---|--|--|---|--|---|---|---|--|---|
| 1.1.1.4. Countries modeled 1.1.1.4. Countries nodeled 1.2.1.1.4. Countries to produce model outputs for
The parameters wort change during calibration 2. Location Input Parameters 1.2.1.1. Proportion of variants 1.2.1.1. Proportion of variants 1.2.1.2. Effective transmission rates 1.2.1.3. Effective transmission rate between Stages and the levels of NPIs in place. It needs to be consistent location taking into account the transmission rate between Stages and the levels of NPIs in place. It needs to be consistent location taking into account the transmission rate between Stages and the levels of NPIs in place. It needs to be consistent location taking into account the transmission rate between Stages and the levels of NPIs in place. It needs to be consistent location taking into account the transmission rate between stages of Covid infection for location's health system 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.4. Estimates of total population wort change during calibration 1.2.1.5. Transiton rates into and out of location's health system 1.2.1.6. Pla stanetion sourt change during calibration 1.2.1.6. MPI schedule - level of NPI for each time period in the model horizon 1.2.1.6. MPI schedule - level of NPI for each time period in the model horizon 1.2.1.6. MPI | 1.1.1.4. Countries modelled 1.1.1.4. Countries to produce model outputs for
List of countries to produce model outputs for
The parameters wont change during calibration 2. Location Input Parameters 1.2.1.1. Proportion of variants 1.2.1.1. Proportion of variants 1.2.1.1. Proportion of variants 1.2.1.1. Proportion of variants 1.2.1.2. Effective transmission rates 1.2.1.2. Effective transmission rates 1.2.1.2. Effective transmission rates 1.2.1.2. Effective transmission rates 1.2.1.3. Extra stages of or function that estimates the effective transmission rates between Covid stages at a particular oction taking into account the transmission rate between stages and the levels of NPIs in place. It needs to be consistent across models 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.3. Tansition rates into and out of location's health system stages for Covid cases Won't change during calibration 1.2.1.3. Estimates of fortal population action and under of population in each stage for 1.2.1.2. It me periods for model horizon 1.2.1.5. Time periods for model horizon 1.2.1.6. API schedule - level of NPI for each time period in the model horizon 1.2.1.6. API schedule - level of NPI for each time period in the model horizon 1.2.1.6. API schedule - level of NPI for each time period in the model horizon 1.2.1.6. API schedule - level of NPI for each time period in the model horizon 1.2.1.6. API schedule - level of NPI for each time period in the model horizon 1.2.1.6. API schedule - level of NPI for each time period in the model horizon 1.2.1.6. API schedule - level NPI for each time period in the model horizon 1.2.1.7. Model Input Parameters | 1.1.1.4. Countries modelled List of countries to produce model outputs for | 1.1.4. Countries modelled List of countries to produce model outputs for The parameters won't change during calibration Location lipputs Location lipputs Location lipputs I.2.1. Excation lipput Parameters 1.2.1. Excation lipputs I.2.1. Proportion of variants I.2.1. Effective transmission rates between Covid stages at a particular me parameters will change - bounds should be [0,1] and these proportions should add to 1. I.2.1. Effective transmission rates I.2.1.2. Effective transmission rates between Covid stages at a particular iconstion taking into account the transmission rate between Stages and the levels of NPIs in place. It needs to be iconstion taking into account the transmission rate between Stages and the levels of NPIs in place. It needs to be constituent across models The function won't change during calibration, but parameters that define it - see 1.3.1.1 - will change 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.3. Extra stages of Covid infection for location's health system 1.2.1.3. Transition rates into and out of location's health system 1.2.1.3. Transition rates into and out of location's health system 1.2.1.3. Transition rates into and out of location's health system 1.2.1.3. Transition rates into and out of location's health system 1.2.1.3. Transition rates into and out of location's health system 1.2.1.3. Transition rates into and out of location's health system 1.2.1.3. Transition rates into and out of location's health system 1.2.1.4. Estimates of total population 1.2.1.5. The perindentian lipse and 1.2.1.5. The popul | 1.1.1.4. Countries modelled 1.1.1.4. Countries to produce model outputs for The parameters won't change during calibration 2. Location liputs 2. Location liputs 1.2.1. In Proportion of variants 1.2.1. Location liputs 1.2.1. Location liput Parameters | 1.1.1.4. Countries modelled 1.1.1.4. Countries to produce model outputs for
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1.2.1.2. Effective transmission rates 1.2.1.2. Effective transmission rates 1.2.1.3.1. Effective transmission rates between Covid stages at a particular location taking into account the transmission rate between stages and the levels of NPIs in place. It needs to be consistent across models 1.2.1.3.1. Stage name/symbol 1.2.1.4. Estimates of total population 1.2.1.5. Transition rates into and out of location's health system stages for Covid cases 1.2.1.4. Estimates of total population work change unimer of population in each stage (including extra stages from 1.2.1.2. Total population work change unimer of population in each stage (including extra stages from 1.2.1.2. Total population work change unimer of population in each stage (including extra stages from 1.2.1.2. Total population work change unimer of population in each stage (including extra stages from 1.2.1.2. Total population work change unimer of population in each stage (including extra stages from 1.2.1.2. Total population work change uniper accosing to make sure the sum of initial numbers = total? 1.2.1.5. Time periods for model horizon
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