Supplementary Materials for

Behavioral dynamics of COVID-19: estimating under-reporting, multiple waves, and adherence fatigue across 92 nations

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S1 MODEL STRUCTURE AND KEY FORMULATIONS

The model simulates the evolution of COVID-19 epidemic, risk perception and response, testing, hospitalization, and fatality at the level of a country, and couples all countries in the parameter estimation step. Here we explain key equations and structures in each sector, followed by complete listing of model equations and parameters in S9. Full model, data, and analysis code is available online at https://github.com/tseyanglim/CovidGlobal.

Population Groups and Transmission Dynamics

The model is a derivative of the well-known SEIR (Susceptible, Exposed, Infectious, Recovered) framework for simulating infection dynamics. Figure S1 provides an overview of key population groups and the population movements among them[1].

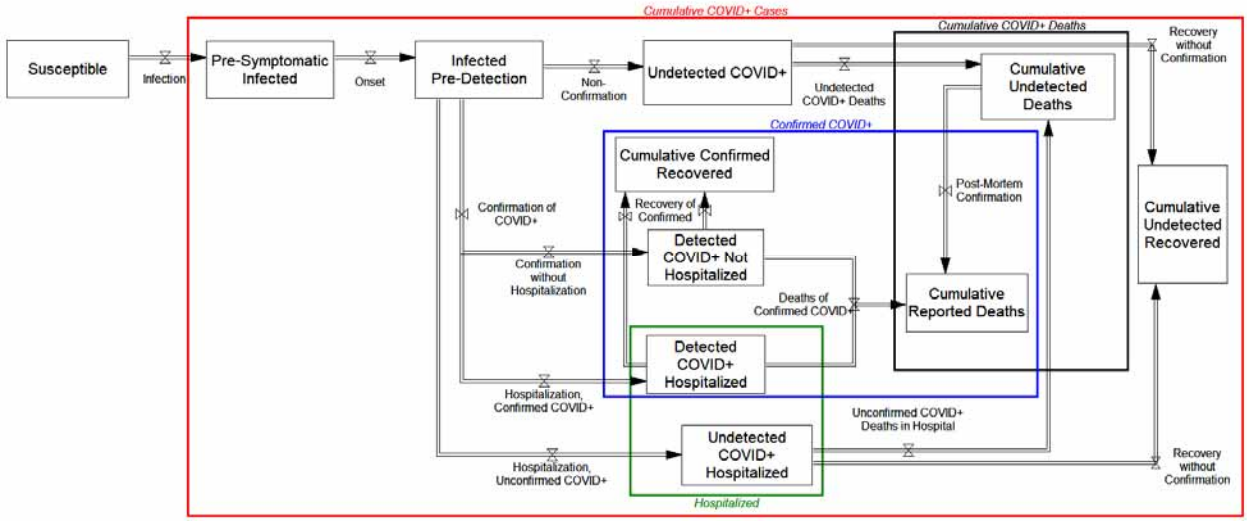


Figure S1- Key population stocks and flows. Rectangles represent stocks (state variables), while arrows and valves represent the flows between them (state transitions). Some in the *Susceptible* population (S) flow into the *Pre-Symptomatic Infected* stock (P) based on the *Infection Rate* (r_{SP}). After an average *Incubation Period* (τ_P), these pre-symptomatic infected flow into the *Infected Pre-Detection* (I_P) stock. After a further average *Onset to Detection Delay* (τ_T), this group splits among multiple pathways. First, if tested positive for COVID-19, they flow into either *Infectious Confirmed Not Hospitalized* (I_C) or *Hospitalized Infectious Confirmed* (I_{CH}). Anyone not tested positive, whether for lack of testing or erroneous test results, transitions into either *Hospitalized Infectious Unconfirmed* (I_{UH}) or *Infectious Unconfirmed Post-Detection* (I_U). We assume demand for testing and hospitalization are driven by symptoms, so all asymptomatic patients will be in the latter category.

From these Infectious categories, resolution flows ($r_{...}$) take individuals to either Recovered (R...) or Dead (D...) states, with corresponding subscripts $_U$, $_C$, $_{CH}$, and $_{UH}$ for stocks and $_{UU}$, $_{UHCH}$ etc. for flows. Given the differences in severity and potential survival extension due to hospitalization, we distinguish

[1] In the equations below we use short-hand to simplify mathematical notations. The full model documentation uses full variable names. Table S1 provides the mapping between the short-hand and the full names, as well as the sources and equations for the variables and parameters discussed below.

between resolution delay for those in hospital (*Hospitalized Resolution Time;* τ_H) and those not hospitalized (*Post-Detection Phase Resolution Time*; τ_R). We use first order exponential delays for all lags, though sensitivity analyses showed very little impact of using higher order delays.

The *Infection Rate* (r_{SP}) controls the flow from S to P and depends on *Infectious Contacts* (C_I), fraction of total *Population* (N) that is susceptible, and *Weather Effect on Transmission* (W). The latter is a function of R_W, the country-level projections for impact of weather on COVID-19 transmission risk year-round developed by Xu and colleagues (*1*) and a parameter, *Sensitivity to Weather* (s_W), to be estimated:

$$r_{SP} = C_I W \left(\frac{S}{N}\right) \quad (1)$$

$$W = R_W^{sw} \quad (2)$$

Infectious contacts depend on the *Reference Force of Infection* (β), various infectious sub-populations (and their relative transmission rates; m_a for asymptomatic and m_T for confirmed), and *Contacts Relative to Normal* (F_C), which captures behavioral and policy responses as a fractional multiplier to baseline infectious contacts:

$$C_I = \beta F_C(m_a(P^a + I_P^a + I_U^a) + I_P^s + I_U^s + P^s + I_{UH} + m_T(I_{CH} + I_C)) \quad (3)$$

In this equation we separate various stocks (of I and P) into asymptomatic (a superscript) and symptomatic (s superscript). That distinction is treated analytically using a zero-inflated Poisson distribution that is discussed in the next section. In light of evidence on the short serial interval for COVID-19, likely below the incubation period (*2, 3*), we do not distinguish the infectivity of pre-symptomatic individuals from those post onset. Contagion dynamics start from *Patient Zero Arrival Time*, T_0, another estimated parameter. The key mechanisms regulating the population flows among these stocks are discussed below, and a schematic of important relationships is provided in Figure S2.

Five parameters are estimated in the equations discussed above. One of them (s_W) is global (i.e. assumed identical across countries; see the estimation section below for details on the distinction between global and country-specific parameters) and the remaining four are country-specific: β, m_T, m_a, *and* T_0.

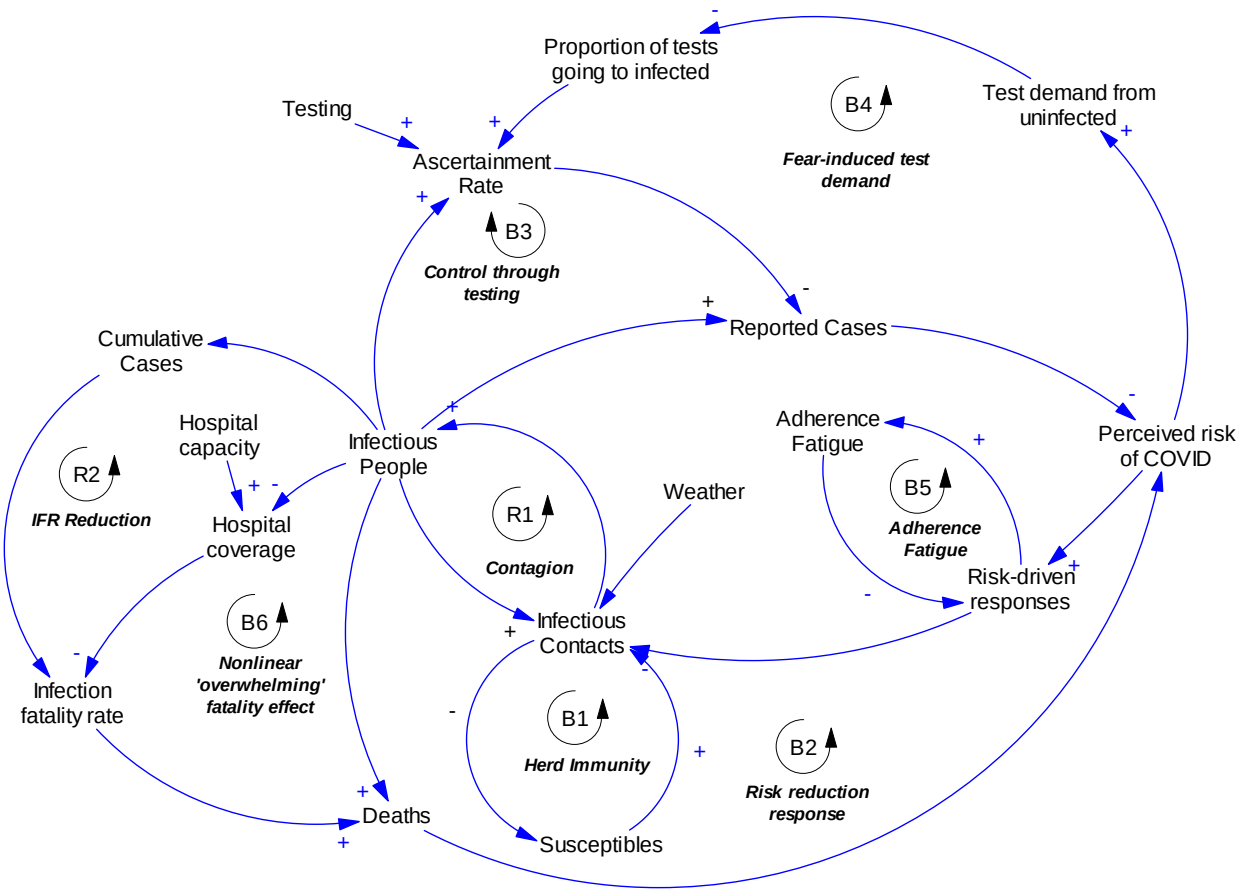


Figure S2- Overview of model's mechanisms. Major feedback loops are identified as Balancing (Negative feedback; B) and Reinforcing (Positive feedback; R).

Modeling the Severity of Symptoms

COVID-19 infection varies in acuity, from asymptomatic to life-threatening. Disease acuity affects fatality risk and also testing and hospitalization decisions, which in turn affect official records of infection and fatality rates. Since movement between population groups via testing or hospitalization is itself a function of acuity, to allow for consistent inference of mean acuity across different population groups, we use an analytical framework to track acuity levels. The framework, which we adapted from prior research (*4*), obviates the need to disaggregate the population by different acuity levels (which would prohibitively raise the computational costs for estimation).

Specifically, we represent acuity using a zero-inflated Poisson distribution. This distribution combines two subpopulations – one with Poisson-distributed acuity levels with mean *Covid Acuity* (α_C), and another *Additional Asymptomatic Fraction* with zero acuity, which is the zero-inflated component. The sum of those with zero acuity from the Poisson part of the population and the second group is the *Total Asymptomatic Fraction* (p_a). We assume this asymptomatic group is not given priority in testing or hospitalization, and is not at risk of death. Thus they will always follow the $S \xrightarrow{r_{SP}} P \xrightarrow{r_{PP}} I_P \xrightarrow{r_{IU}} I_U \xrightarrow{r_{UU}} R_U$ pathway. The pathways for the remaining population depend on acuity and its impacts on testing, hospitalization, and death. Note that the concept of acuity defined here only needs to have a

monotonic relationship with tangible symptoms and risk factors and it does not have a one-to-one relationship with any real-world measure of acuity, and as such is better seen as a mathematical construct that informs modeling rather than a real-world variable with clinical definition.

From this framework two parameters, *a* and α_C, are estimated as country specific parameters with limited variability across countries.

Testing

The testing sector reads the *Active Test Rate* (T_t) for each country as exogenous input data (see appendix S3 for pre-processing details for this data). A fraction of the total test rate, typically small, is allocated to post-mortem testing of COVID-19 victims who have not been previously confirmed (*Post Mortem Tests Total*, T_{PM}). Specifically, of the deaths of unconfirmed infectious individuals (whether hospitalized or not), a certain *Fraction of Fatalities Screened Post Mortem* (n_{PM}) will be identified true post-mortem tests. We anchor the n_{PM} to *Fraction Covid Death In Hospitals Previously Tested* (n_{DCH}). The rationale for this anchoring is that on the margin if there are many unidentified COVID patients in hospitals, the chances are that the system lacks enough testing capacity and thus post-mortem testing should also be less thorough:

$$n_{PM} = n_{DCH} \tag{4}$$

We experimented other functional forms with a free parameter connecting the two constructs, but following our conservative estimation principle decided against including that free parameter in the final model. We feared that absent clear observables to identify this additional parameter (e.g. on country-specific policies regulating post-mortem testing) the degree of freedom would improve the fit but potentially for the wrong reason.

The remaining *Testing Capacity Net of Post Mortem Tests* ($T_{Net} = T_t - T_{PM}$) is allocated to test demand from two sources. First, symptomatic COVID patients leaving the pre-detection (I_P) phase may seek testing (*Positive Candidates Interested in Testing Poisson Subset*: $M_C = \frac{I_P}{\tau_T}(1 - p_a)$). Second, COVID-negative individuals may seek testing due to various perceived risks and other conditions with overlapping symptoms such as common cold and influenza-like illnesses (M_N, *Potential Test Demand from Susceptible Population*). This "negative" demand includes a *Baseline Daily Fraction Susceptible Seeking Tests* (n_{ST}) of the population not previously tested positively (N_U), and increases with the *Recent Detected Infections* (T_{PIR}), which is an exponentially weighted moving average of *Positive Tests of Infected* (T_{PI}). COVID-positive and COVID-negative sources of demand add up to create the overall *Testing Demand* (M_T):

$$M_N = n_{ST} N_U + m_{IT} T_{PIR} \tag{5}$$

$$M_T = M_N + M_C \tag{6}$$

Where the *Multiplier Recent Infections to Test* (m_{IT}), captures the sensitivity of negative test demand to recent infection reports.

To allocate the available tests (T_{Net}) between these two sources of demand, we use an analytical logic that allocates testing based on symptom severity. Via self-selection and screening by testing centers, people who have more symptoms or other signals that correlate with COVID infection (e.g., high exposure risk) are more likely to be tested. We assume each unit of acuity increases the likelihood that an individual gets tested, based on a variable *Prob Missing Symptom*, p_{MS}. This variable represents the probability that each acuity unit fails to convince the testing decision process to test a given individual, i.e. how selectively and sparingly tests are conducted. Specifically, in this model an individual with k acuity units is tested with probability:

$$p(test|k\ symptoms) = 1 - p(missing\ k\ symptoms) = 1 - p_{MS}^{k} \quad (7)$$

We assume the negative test demand is coming from a population with a Poisson-distributed, unit average acuity level (α_N=1) for symptoms of non-COVID influenza-like illnesses. The test demand from COVID patients also comes from a Poisson distribution of acuity, but with mean α_C. With the Poisson distribution and given a level of α and p_{MS}, one can calculate the fraction of each demand source that would be tested:

$$p(getting\ test) = 1 - p(not\ being\ tested) = 1 - \sum_{k=0}^{k=\infty} \frac{e^{\alpha}\alpha^{k}}{k!} p_{MS}^{k} = 1 - e^{-\alpha(1-p_{MS})} \quad (8)$$

We therefore need to find the p_{MS} that allows test supply to match demand that is satisfied, specifically, by solving the following equation for p_{MS}*:

$$T_{Net} = M_N(1 - e^{-\alpha_N(1-p*_{MS})}) + M_C(1 - e^{-\alpha_C(1-p*_{MS})}) \quad (9)$$

Figure S3 provides a graphical summary of the zero-inflated Poisson symptom and testing framework. In this figure testing outcomes are graphed for a population where 10% are COVID-positive, assuming that *Covid Acuity*, α_C, is 6, and with two different levels of p_{MS} (=0.8 and 0.95). For this figure we also assume a 55% asymptomatic fraction for COVID patients. Even with testing that prioritizes patients with more symptoms, and despite the large difference in symptom frequency between COVID patients and negative cases, the majority of tests are allocated to negative cases with a few symptoms. COVID patients with multiple symptoms are likely to be identified if P_{MS} is not very large, but when total demand for testing (i.e. the sum of all bars with symptoms>0) is large, P_{MS} , found from solving equation 9, may be close to 1, excluding many COVID patients with multiple symptoms and thus higher risks of fatality.

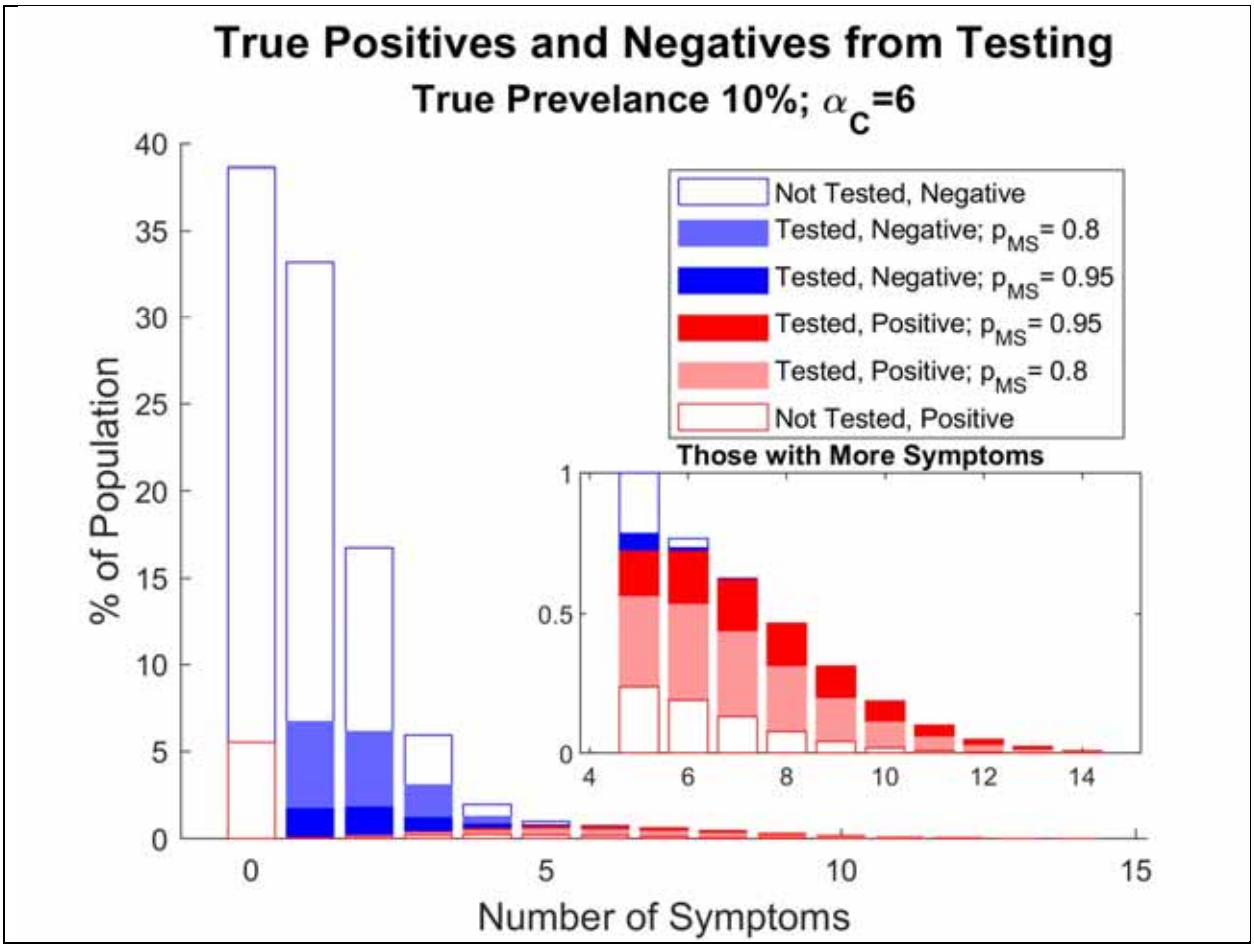


Figure S3- Schematic overview of zero-inflated Poisson process and test allocation. Red bars represent COVID-positive individuals and blue ones are COVID-negative. Asymptomatic fraction is assumed to be 55% for COVID patients with the symptomatic cases following a Poisson distribution with mean 6. Color coded bars signal fraction of tested individuals with different levels of probability of missing symptoms, P_{MS}.

Having solved for p^*_{MS} (numerically), we analytically calculate the average acuity level for those positively tested (α_{CP}: *Average Acuity of Positively Tested*) and those either not tested or having received a false negative result (α_{CN}). Specifically, if test sensitivity was 100%, the average acuity for those not tested would be:

$$\alpha_{Not\ Tested} = \sum_{k=0}^{k=\infty} k \frac{e^{\alpha}\alpha^k}{k!} {p^*_{MS}}^k = \alpha p^*_{MS} e^{-\alpha(1-p*_{MS})} \quad (10)$$

The acuity level for those tested could then be found based on the conservation of total acuity across those positively tested and those not. Starting with this basic specification we further account for the *Sensitivity of Covid Test (s_T)* to calculate the values of α_{CP} and α_{CN}. We parametrize sensitivity at 70%, which is the estimated sensitivity for the PCR-based tests used as the primary diagnosis method of current infections of COVID-19 (*5, 6*).

Overall, the testing rates that are determined by solving for p^*_{MS}, combined with sensitivity of tests, inform the fraction of COVID positive individuals transitioning from pre-detection (I_P) to confirmed

vs. unconfirmed states (I_C or I_{CH} vs. I_U or I_{UH}), while the calculated α values inform the likelihood of hospitalization and fatality rates, as discussed next.

The testing sector includes the following two country level parameters that are estimated: n_{ST}, m_{IT}.

Hospitalization

The hospitalization sector of the model starts with each country's *Nominal Hospital Capacity* (h_N) in total hospital beds. In practice, geographic variation in hospital density and demand creates imperfect matching of available beds with cases of COVID-19 at any point in time, e.g. because some potential capacity is physically distant from current COVID hotspots. This imperfect matching means some of the nominal hospital capacity is effectively unavailable at any time, especially in larger, less densely populated countries. We therefore calculate *Effective Hospital Capacity* (h_E) by considering geographic density of hospital beds (*Bed per Square Kilometer;* d_H):

$$h_E = h_N \left(\frac{d_H}{d_H^*}\right)^{s_{DH}} \tag{11}$$

Where the d_H^* represents a large *Reference Hospital Density* of 6.06 beds per km^2 (which is the value of d_H for South Korea). The parameter s_{DH} (*Impact of Population Density on Hospital Availability*) is estimated.

Effective capacity is allocated between *Potential Hospital Demand* (H_{CD}) from COVID-19 cases and the regular demand for hospital beds from all other conditions (which we assume equals pre-pandemic effective hospital capacity). We assume that COVID-19 patients will have higher priority for hospitalization compared to regular demand. Specifically, we assume that fraction of regular demand allocated (m_{HR}) would be the square of that for COVID demand (m_{HC}), $m_{HR} = m_{HC}^2$, and solve the resulting hospital capacity allocation problem analytically:

$$h_E = h_E m_{HR} + H_{CD} m_{HC} \Rightarrow m_{HC} = \frac{-H_{CD} + \sqrt{H_{CD}^2 + 4h_E^2}}{2h_E} \tag{12}$$

We determine the COVID demand for hospitalization based on a screening process similar to that for testing. Two types of COVID patients may seek hospitalization: those with confirmed test results and those without. The former are more likely to seek hospital treatment. We first calculate a parameter analogous to p_{MS} in the testing sector that informs the demand from confirmed COVID patients for hospitalization. This parameter, the *PMAS Confirmed for Hospital Demand* (p_{MHC}) is determined based on acuity level of confirmed (α_{CT}) and *Reference COVID Hospitalization Fraction Confirmed* (r_H), an estimated parameter capturing the overall need for hospitalization among COVID patients:

$$p_{MHC} = (1 - r_H)^{\frac{1}{\alpha_{CT}}} \tag{13}$$

For unconfirmed COVID patients we scale the analogue of this parameter (p_{MHU}) based on how much priority non-COVID patients generally receive:

$$p_{MHU} = p_{MHC} + (1 - p_{MHC})(1 - m_{HR}) \tag{14}$$

This formulation ensures that: 1) Confirmed COVID patients are more likely to be hospitalized, but also that 2) if there is ample hospital capacity (m_{HR}~1), then confirmed and unconfirmed COVID patients will receive similar priority for the same level of acuity. In short, the $p_{M.}$ values determine hospital demand by confirmed and unconfirmed COVID patients, which add up to H_{CD}. The latter determines the fraction of hospital demand that is met. Analogous to the testing sector, this fraction along with demand determines the flow of individuals from the pre-detection (I_P) state to hospitalized vs. non-hospitalized states (I_{CH} or I_{UH} vs. I_C or I_U). Matching demand to allocated capacity also allows us to calculate the realized *Probability of Missing Acuity Signal at Hospitals* (p^*_M) for confirmed and unconfirmed patients. As in the testing sector, those probabilities let us approximate for the expected acuity levels for COVID patients in and out of hospital, as well as tested vs. not-tested, i.e. α_{CT}, α_{CH}, α_U, and α_{UH}. These average acuity levels in turn inform fatality rates for each group.

The hospital sector includes two country level estimated parameter with limited variation across countries: s_{DH} and r_H.

Infection Fatality Rates

For patients in each of the $_U$, $_C$, $_{CH}$, and $_{UH}$ groups we specify the *Infection Fatality Rate* (f), as:

$$f_{(.)} = f_b \alpha_{(.)}^{s_f} s_{HF}(.) g_{Ag} v_f \quad (15)$$

The parameter *Base Fatality Rate for Unit Acuity* (f_b) sets the baseline for fatality rate. *Sensitivity of Fatality Rate to Acuity* (s_f) determines how fatality changes with estimated acuity levels; more severe cases are expected to have higher fatality rates. Hospitalization reduces fatality rates, expressed as the relative *Impact of Treatment on Fatality Rate* (s_{HF}); Finally, IFR reduction due to heterogenous responses (e.g. high risk groups becoming more cautious as cases accumulate), improved treatment with learning curves, and other drivers is captured in *Time variant change in fatality* (v_f).

The g_{Ag} function incorporates the impact of age distribution on fatality rates. For age effect, we calculate a risk factor for each country. We use data from the World Bank on the age distribution of each country's population in 10-year age strata to calculate an age-weighted average of the IFRs for COVID patients by 10-year age group reported in prior work (*7*). We normalize this age-weighted average IFR against its value for China, where the data on IFRs by age group were originally recorded. Normalizing in this way means the age effect is not sensitive to any systematic over- or under-estimation of the IFR in prior work, only to the relative risk by age group. The resulting normalized age effect ranges from 0.271 (Kenya, median age ~20 years) to 2.368 (Japan, median age ~48 years). Given the well-established impact of age on fatality, this factor is directly multiplied into the infection fatality equations.

Finally, we formulate the v_f factor as a function of cumulative cases to-date in each country using a standard learning curve formulation, bounded by a minimum multiplier that is 10% baseline, and starts to operate after cases reach 0.5% of population. The *Learning and Death Reduction Rate*, l_{IFR}, is estimated for each country. Specifically:

$$v_f = \text{Max}(0.1, \text{Max}\left(1, \frac{\text{Cumulative Cases}}{0.005*\text{Population}}\right)^{-l_{IFR}}) \quad (16)$$

Overall, the fatality sector includes three parameters that are estimated at the country level, with limited variance across countries, those are: f_b, s_{HF}, and s_f. A fourth country-level parameter, l_{IFR}, is allowed to very more widely across different nations.

Note on comorbidities and fatality: We also explored including three comorbidities but found the estimates unreliable and therefore they are not included in the main specification of the model. Those comorbidities include obesity, chronic disease, and liver disease. The effects we explored for each were: $g_{(.)} = d_{(.)}^{s_{(.)f}}$, where we used the following country-level indicators from the World Health Organization (*8*), normalized by the average across all countries ($d_{(.)}$):

For obesity: Prevalence of obesity among adults, BMI ≥30 (age-standardized estimate) (%)

For chronic health issues: Probability (%) of dying between age 30 and exact age 70 from any of cardiovascular disease, cancer, diabetes, or chronic respiratory disease

For liver disease: Liver cirrhosis, age-standardized death rates (15+), per 100,000 population

Risk Perception, Behavioral Responses, and Adherence Fatigue

In equation 3 we noted that *Contacts Relative to Normal* (F_C) regulates infection rates. This factor ranges between a minimum (*Min Contact Fraction*; c_{Min}) and 1 as a function of the impact of perceived risk on behaviors, F:

$$F_C = (1 - c_{Min})F + c_{Min} \quad (17)$$

$$F = \text{e}^{-\max(0, \lambda L_R a_F - \frac{s_C}{a_F})} \quad (18)$$

The impact of perceived risk on response uses an exponential function (eq 18) with exponent informed by *Perceived Risk of Life Loss* (L_R), which is then moderated by a multiplier (*Dread Factor in Risk Perception*, λ) and *Impact of Adherence Fatigue* (a_f). This moderated risk is compared to a Risk *Threshold for Response* ($\frac{s_C}{a_F}$), which itself responds to adherence fatigue.

L_R adjusts to an underlying *Indicated Risk of Life Loss* (L_R^*) with a time constant that is asymmetric, i.e. *Time to Upgrade Risk* (τ_{RU}) could be different from *Time to Downgrade Risk* (τ_{RD}). The L_R^* itself depends on *Perceived Hazard of Death* (Z_{DP}) and a discount rate to turn daily costs to life-long ones (γ=0.03/year):

$$\frac{dL_R}{dt} = \frac{L_R^* - L_R}{\tau_{R.}} \quad (19)$$

$$L_R^* = \frac{Z_{DP}}{\gamma} \quad (20)$$

The *Perceived Hazard of Death* (Z_{DP}) is an average of reported daily hazard of death (with the weight *Weight on Reported Probability of Infection,* w_R) and true hazard for death which individuals may perceive through word of mouth and their social networks.

Finally, we formulate the *Impact of Adherence Fatigue* based on a 100-day exponential average of relative contacts, *Recent Relative Contacts* (F_R) and a country-specific estimated parameter, *Strength of Adherence Fatigue* (s_a):

$$\frac{dF_R}{dt} = \frac{F_C - F_R}{100} \tag{21}$$

$$a_f = F_R^{s_a} \tag{22}$$

Overall, the risk perception and response sector includes the following six country-specific parameters that are estimated: c_{Min}, τ_{RU}, τ_{RD}, λ, w_R, *and* s_a.

Vaccination

We include a simple vaccination sector in the model to inform policy analyses. This sector was not active in the estimation of the model and most of the analyses reported in the paper, but is operational for vaccination scenarios reported in future projections. It is formulated using the following assumptions:

- Vaccines are perfect in stopping transmission to vaccinated. Therefore they move individuals from the "Susceptible" stock to "vaccinated" where they remain for the rest of simulation.
- Individuals may opt not to vaccinate. A user of the model can specify a fraction of population not accepting the vaccine, and those individuals are assumed to be represented with the same fraction across different population stocks. The scenarios simulated in the paper assume this fraction is zero but the online simulator allows for changing that fraction.
- All individuals willing to vaccinate will get vaccinated regardless of their prior COVID infection status. However, vaccines are effective only on susceptible individuals, so those actively infected at the time of vaccination will not be affected by vaccine.
- Vaccination rate is set based on a user-specified vaccination period. The rate will ramp up linearly for a given fraction of this period, and then will remain constant for the remainder. The final rate is specified such that everybody will get the vaccine within the specified vaccination period. In the reported simulations, the ramp-up is assumed to be fast and the overall period is set to one year, starting from January 2021. In the online simulator the ramp up period is assumed to be half the overall vaccination period, and users can input the overall period.
- Vaccination could follow a priority plan in which higher-risk individuals are vaccinated first. In the model this mechanism is implemented by tracking a co-flow of acuity for all susceptible individuals. Vaccination is allowed to drain this acuity coflow with a rate that exceeds average acuity in the susceptible population by a user-specified ratio. In the reported scenarios we use a draining factor 1.5 times the average acuity in the stock of susceptibles. The average acuity in susceptible population would then be the α_C used in the formulations above (with initial α_C starting from the empirically estimated value), and will change dynamically in response to vaccination of elderly and other high-risk groups and the potentially faster draining of acuity coflow.

Summary of Key Equations and Parameters

Table S1 summarizes the main equations discussed in S1, providing the mapping between full variable names and the short forms. It also includes all estimated model parameters, as well as those specified based on prior research.

Table S1- Mapping between full variable names and their short form for the subset of variables and parameters discussed in S1. Also included are equations explained above and sources for other variables.

Short form	Full variable name	Equation/Source
T_t	Active Test Rate	Data (See S4 for pre-processing details)
m_{HC}	Allocated Fraction COVID Hospitalized	$\frac{-H_{CD}+\sqrt{H_{CD}^2+4h_E^2}}{2h_E}$
m_{HR}	Allocated Fration NonCOVID Hospitalized	m_{HC}^2
α_{CP}	Average Acuity of Positively Tested	See full documentation
f_b	Base Fatality Rate for Unit Acuity	Estimated
n_{ST}	Baseline Daily Fraction Susceptible Seeking Tests	Estimated
d_H	Bed per Square Kilometer	Data (*8*)
m_T	Confirmation Impact on Contact	Estimated
F_C	Contacts Relative to Normal	$e^{-\max(0,\lambda L_R a_F-\frac{s_C}{a_F})}(1-c_{Min})+c_{Min}$
α_C	Covid Acuity	Estimated
R_W	CRW	Use estimates from (*1*)
g_{AG}	Demographic Impact on Fatality Relative to China	Use estimates based on (*8, 9*)
γ	Discount Rate per Day	$8.2e^{-5}$ /Day
λ	Dread Factor in Risk Perception	Estimated
h_E	Effective Hospital Capacity	$h_N\left(\frac{d_H}{d_H^*}\right)^{s_{DH}}$
n_{DCH}	Fraction Covid Death In Hospitals Previously Tested	See full documentation
n_{PM}	Fraction of Fatalities Screened Post Mortem	n_{DCH}
I_{CH}	Hospitalized Infectious Confirmed	See full documentation
I_{UH}	Hospitalized Infectious Unconfirmed	See full documentation
τ_H	Hospitalized Resolution Time	20 Days
s_a	*Impact of Adherence Fatigue*	$F_R^{s_a}$
s_{DH}	Impact of Population Density on Hospital Availability	Estimated
s_{HF}	Impact of Treatment on Fatality Rate	Estimated
τ_P	Incubation Period	5 days
L_R^*	Indicated Risk of Life Loss	$L_R^*=\frac{Z_{DP}}{\gamma}$
I_P	Infected pre Detection	See full documentation
I_U	Infected Unconfirmed Post-Detection	See full documentation

f(.)	Infection Fatality Rate (.)	$f_b \alpha_{(.)}^{s_f} s_{HF}(.) g_{Ag} v_f$
r_{SP}	Infection Rate	$C_I W\left(\frac{S}{N}\right)$
I_C	Infectious Confirmed Not Hospitalized	See full documentation
C_I	Infectious Contacts	$\beta F_C(m_a(P^a + I_P^a + I_U^a) + I_P^s + I_U^s + P^s + I_{UH} + m_T(I_{CH} + I_C))$
l_{IFR}	*Learning and Death Reduction Rate*	Estimated
c_{Min}	Min Contact Fraction	Estimated
m_{IT}	Multiplier Recent Infections to Test	Estimated
h_N	Nominal Hospital Capacity	Data
τ_T	Onset to Detection Delay	5 Days
T_0	Patient Zero Arrival Time	Estimated
Z_{IP}	Perceived Hazard of Infection	See full documentation
L_R	Perceived Risk of Life Loss	$\frac{dL_R}{dt} = \frac{L_R^* - L_R}{\tau_R}$
N	Population	Data (*10*)
M_C	Positive Candidates Interested in Testing Poisson Subset	$\frac{I_P}{\tau_T}(1-a)$
T_{PM}	Post Mortem Tests Total	See full documentation
τ_R	Post-Detection Phase Resolution Time	10 Days
H_{CD}	Potential Hospital Demand	See full documentation
M_N	Potential Test Demand from Susceptible Population	$n_{ST} N_U + m_{IT} T_{PIR}$
T_{PI}	Positive Tests of Infected	See full documentation
P	Pre-Symptomatic Infected	See full documentation
p_{MHC}	PMAS Confirmed for Hospital Demand	$(1 - r_H)^{\frac{1}{\alpha_C}}$
p_{MHU}	PMAS Unconfirmed for Hospital Demand	$p_{MHC} + (1 - p_{MHC})(1 - m_{HR})$
p_{MS}	Prob Missing Symptom	From solution to equation 9
T_{PIR}	Recent Detected Infections	See full documentation
r_H	Reference COVID Hospitalization Fraction Confirmed	Estimated
β	Reference Force of Infection	Estimated
d_H^*	Reference Hospital Density	Data (*8*)
m_a	Multiplier Transmission Risk for Asymptomatic	Estimated
F_R	*Recent Relative Contacts*	$\frac{dF_R}{dt} = \frac{F_C - F_R}{100}$
s_T	Sensitivity of Covid Test	0.7
s_f	Sensitivity of Fatality Rate to Acuity	Estimated
s_C	Sensitivity of Contact Reduction to Utility	Estimated
s_W	Sensitivity to Weather	Estimated
s_a	*Strength of Adherence Fatigue*	Estimated

S	Susceptible	See full documentation
T_{Net}	Testing Capacity Net of Post Mortem Tests	$T_t - T_{PM}$
M_T	Testing Demand	$M_N + M_C$
τ_{RD}	Time to Downgrade Risk	Estimated
τ_{RU}	Time to Upgrade Risk	Estimated
v_f	Time Variant Change in Fatality	$\text{Max}(0.1, \text{Max}\left(1, \frac{\text{Cumulative Cases}}{0.005*\text{Population}}\right)^{-l_{IFR}})$
p_a	Total Asymptomatic Fraction	Estimated
U_L	Utility from Limited Activities	$e^{0.5s_C}$
U_N	Utility from Normal Activities	$e^{s_C a_f (1-L_R)}$
w_R	Weight on Reported Probability of Infection	Estimated
W	Weather Effect on Transmission	R_W^{sw}

S2 ESTIMATION METHOD

Overview of the Approach

The model we estimate is nonlinear and complex, and any estimation framework is unlikely to have clean analytical solutions or provable bounds on errors and biases. Therefore, in designing our estimation procedure we apply 3 guideposts: 1) Being conservative by incorporating uncertainties. 2) Avoid over-fitting; and 3) Enhance generalizability and robustness of estimates and projections. To these ends: we use a likelihood function that accommodates overdispersion and autocorrelation (negative binomial); we utilize a hierarchical Bayesian framework to couple parameter estimates across different countries which reduces the risk of over-fitting the data; and we use the conceptual definitions of parameters and their expected similarity across countries to inform the priors for the magnitude of that coupling across countries. Compared to more common choices in similar estimation settings (e.g. use of Gaussian likelihood functions), these choices tend to widen the credible regions for our estimates and reduce the quality of the fit between model and data. In return, we think the results may be more reliable for projection, more informative about the underlying processes, and better reflective of uncertainties in such complex estimation settings. We also conduct a validation test of our estimation framework using synthetic data in section S3.

The model is a deterministic system of ordinary differential equations with a set of known and unknown parameters. The known parameters are those specified based on the existing literature and do not play an active role in estimation. The unknown parameters can be categorized into those that vary across different countries and those that are the same across all countries (i.e. "general" parameters). The estimation method is designed to identify both the most likely value and the credible regions for the unknown parameters, given the data on reported cases and deaths (and for a subset of countries, the excess deaths). This is done through a combination of estimating the most likely parameter values in a likelihood based framework, and using Markov Chain Monte Carlo simulations to quantify the uncertainties in parameters and projections.

We first introduce the 3 different components of the likelihood function we use: the fit to time series data, the random effects component coupling country-level parameters, and the penalty for excess mortality. Then we explain the implementation details.

The Fit to Time Series for Cases and Deaths

Define model calculations for expected reported cases and deaths for country i as $\mu_{ij}(t)$ (with index j specifying cases and deaths) and the observed data for those variables as $y_{ij}(t)$; the country-level vector of unknown parameters as $\boldsymbol{\theta_i}$ and the general unknown parameters as $\boldsymbol{\phi}$. Note that $\boldsymbol{\theta_i}$ vector includes several parameters, each specifying an unknown model parameter, such as Impact of Treatment on Fatality, or Total Asymptomatic Fraction, for country i. The model can be summarized as a function f that produces predictions for expected cases and deaths for each country given the general and country-specific parameters:

$$\mu_{ij}(t) = f(\boldsymbol{\phi}, \boldsymbol{\theta_i}) \tag{23}$$

We use a negative binomial distribution to specify the likelihood of observing the y values given $\boldsymbol{\theta}$ and $\boldsymbol{\phi}$. Specifically, the logarithm of likelihood for observing the data series y given model predictions $\mu(\boldsymbol{\theta}, \boldsymbol{\phi})$ is:

$$LT(t|\boldsymbol{\phi},\boldsymbol{\theta}) = \sum_{ij} L1_{ij}(t) + L2_{ij}(t) + L3_{ij}(t) \quad (24)$$

where (dropping time index for clarity):

$$L1_{ij} = -\sum_{y_{ij}=0} \frac{\ln(1+\varepsilon_i\mu_{ij})}{\varepsilon_{ij}} \quad (25)$$

$$L2_{ij} = \sum_{y_{ij}>0} \sum_{k=0}^{y_{ij}-1} \ln(k + \frac{1}{\varepsilon_{ij}}) \quad (26)$$

$$L3_{ij} = \sum_{y_{ij}>0} [-\ln(y_{ij}!) - \left(y_{ij} + \frac{1}{\varepsilon_{ij}}\right)\ln(1 + \varepsilon_{ij}\mu_{ij}) + y_{ij}\ln(\varepsilon_{ij}) + y_{ij}\ln(\mu_{ij}) \quad (27)$$

Summing the LT function over time provides the full (log) likelihood for the observed data given a parameterization of the model. The negative binomial likelihood function includes two parameters, μ and ε which determine the mean and the scaling/shape of the observed outcomes. The second parameter, ε, provides the flexibility needed fit outcomes with fat tails and auto-correlation. This parameter could itself be subject to search in the optimization process. Specifically, we assume that:

$$\varepsilon_{ij} = \varepsilon_i \varepsilon_j \quad (28)$$

Thus we create a (set of) country specific parameter(s) (ε_i) and two general parameters (ε_j) which should be estimated along with the conceptual model parameters. The country level scale (ε_i) implicitly assesses the reliability and inherent variability in country level reports, and the general ones inform the variability in case data vs. deaths. We augment the vectors $\boldsymbol{\phi}$ and $\boldsymbol{\theta}$ to include these scaling parameters as well.

Incorporating the coherence of parameters across countries

Up to this point we have not included any relationship among country specific parameters, $\boldsymbol{\theta_i}$. This independence assumption would allow parameters representing the same underlying concept to vary widely across different countries. Such treatment, by providing more flexibility, enhances the model's fit to historical data. However, it ignores the conceptual link that exists for a given parameter across countries, potentially allowing the model to fit the data for the wrong reasons (i.e. using parameter values that do not correspond to meaningful real world concepts). The result would likely be less reliable and also not robust for future projections. We therefore define a Hierarchical Bayesian framework to account for the potential dependencies among model parameters. Specifically, we assume the same conceptual parameters (e.g. Impact of Treatment on Fatality), across different countries, are coming from an underlying normal distribution with an unknown mean (to be estimated) and a pre-specified prior for the standard deviation. This assumption is similar to the use of "Random Effect" models common in regression frameworks, though we deviate from canonical random effect models by pre-specifying the standard deviation. In fact it is possible to estimate the standard deviation across countries as well (and to obtain better fits to data by including the additional degrees of freedom), but adding those degrees of freedom ignores qualitatively relevant insights about the level of coupling across different countries for each parameter, and thus results may fit the data better but for the wrong reasons. For example, some parameters, such as Patient Zero Arrival Time, could be very different across countries, whereas parameters reflecting innate properties of the SARS-CoV-2 virus itself (e.g. *Total Asymptomatic Fraction* (*a*)) or those determining fatality (e.g. *Base Fatality*

Rate for Unit Acuity (f_b)) should be very similar across different countries. Allowing the model to determine the variance for the latter will lead to better fits: the model can find baseline fatality rates that easily match fatality variations across countries, and would expand the corresponding variance parameter accordingly. However, as a result the estimation algorithm will have too easy a job: it will not require a precise balancing between hospitalization, impact of acuity on fatality, and post-mortem testing decisions to fit fatality data. Thus, the estimates may well be less informative, or further from true underlying processes and the general characteristics of the disease which we care about. Overall, our implementation of a hierarchical Bayesian estimation framework to account for the coupling among the variables may reduce the apparent quality of fit but offer more robust results better informing the underlying mechanisms.

The implementation of this random effect introduces another element to the overall likelihood function:

$$LC(\boldsymbol{\theta}) = -\sum_{ik} \frac{(\theta_{ik}-\bar{\theta}_k)^2}{2\sigma_k^2} \quad (29)$$

Here θ_{ik} represents the k^{th} parameter for country i, and $\bar{\theta}_k$ is the (estimated) average across countries for the k^{th} parameter. σ_k is the pre-specified allowable variability for the k^{th} parameter across different countries.

In setting these factors we chose small values for factors representing biological and natural processes, while adding more room for variation when human behaviors and perceptions were involved (See Table S2 for those settings). Specifying these standard deviation priors adds a subjective element to the estimation process. We note that subjective elements are ultimately indispensable in any modeling activity: from specifying the model boundary to the level of aggregation, use of various functional forms, and choice of likelihood functions, these choices are built on subjective assessments that experts bring to a modeling project. Absent our conceptually informed variability factors, we would need to make the assumption that country-level parameters are independent, or that our complex estimation process would correctly identify the true dependencies among those parameters. We think both those alternatives are inferior in the chosen method. So here we focus on transparently documenting and explaining those assumptions, and Supplement S3 provides a validation experiment. Table S2 summarizes the estimated model parameters, their estimated values (mean across countries and mean of Inter-Quartile Range) and the assumed variability factor (σ_k) for each.

Table S2- Estimated model parameters, their estimated values (mean and standard deviation (std) across countries and the mean of Inter-Quartile Range (MIQR). Last column reports the variability allowances used to specify the coupling among country-level estimates. See equation 29 and related discussions above.

Parameter Name		Mean	StDev	MIQR	Variability Factor, σ_k
f_b	Base Fatality Rate for Unit Acuity**	5.74E-04	7.30E-06	1.27E-05	1.00E-05
n_{ST}	Baseline Daily Fraction Susceptible Seeking Tests	8.36E-04	5.70E-04	1.72E-04	0.0005
m_T	Confirmation Impact on Contact	1.73E-01	1.24E-01	9.90E-02	0.1
α_C	Covid Acuity**	5.92E+00	1.21E-03	1.29E-02	0.01
λ	Dread Factor in Risk Perception*	6.14E+03	1.28E+04	3.74E+03	$10^{0.8}$

s_{DH}	Impact of Population Density on Hospital Availability	1.70E-01	1.62E-01	9.23E-02	0.1
s_{HF}	Impact of Treatment on Fatality Rate	4.58E-01	2.17E-01	6.65E-02	0.1
l_{IFR}	Learning and Death Reduction Rate	7.07E-01	7.42E-01	1.67E-01	0.5
c_{Min}	Min Contact Fraction	7.91E-02	4.99E-02	2.28E-02	0.03
m_{IT}	Multiplier Recent Infections to Test	4.49E+01	2.38E+01	9.47E+00	30
m_a	Multiplier Transmission Risk for Asymptomatic**	2.93E-01	2.55E-03	1.29E-02	0.02
T_0	Patient Zero Arrival Time	9.90E+01	2.98E+01	4.59E+00	Uniform
β	Reference Force of Infection	4.07E-01	2.19E-01	3.34E-02	0.2
r_H	Reference COVID Hospitalization Fraction Confirmed	6.32E-01	1.25E-01	8.65E-02	0.1
s_f	Sensitivity of Fatality Rate to Acuity**	2.14E+00	2.35E-03	6.42E-03	0.005
s_C	Sensitivity of Contact Reduction to Utility	3.17E+00	5.27E+00	1.35E+00	6
s_a	Strength of Adherence Fatigue	1.24E+00	1.07E+00	1.91E-01	0.5
τ_{RD}	Time to Downgrade Risk*	2.45E+02	1.88E+02	6.43E+01	$10^{0.3}$
τ_{RU}	Time to Upgrade Risk*	3.83E+01	5.34E+01	1.33E+01	$10^{0.2}$
a	Total Asymptomatic Fraction **	4.99E-01	9.15E-03	1.28E-02	0.03
w_R	Weight on Reported Probability of Infection	4.52E-01	2.62E-01	2.05E-01	0.2
s_W	Sensitivity to Weather	2.64E+00	(not applicable for global parameter)		

*Given the wide range and potential long tail for these parameters the Log_{10} transformation is used in specifying the dispersion penalty (equation 27) and variability factors are reported as 10^{σ}, where σ is used in equation 27.
** These parameters are expected to be less variable across countries and thus are assigned small variability allowances compared to their mean.

Excess mortality penalty

Finally, we include a likelihood-based penalty term to allow model predictions be informed by excess mortality data collected by various news agencies and researchers for a subset of countries in our sample. These data provide snapshots of excess mortality (compared to a historical baseline) for a window of time in each country. Subtracting from total excess mortality the COVID-19 deaths officially recorded in that window offers a data point for excess mortality not accounted for in official data (e_i). We can calculate in the model the counter-part for this construct: the simulated mortality that is not included in the simulated reported COVID-19 deaths ($\bar{e}_i$). There is uncertainty in these excess mortality data: the historical baselines used by various sources do not adjust for demographic change, excess mortality may be due to factors other than COVID-19, and some of it may be due to changes in healthcare availability and utilization motivated by COVID-19 but not directly attributable to the disease (for example when surgeries are delayed, hospitalization is avoided, or heart conditions are ignored). Excess mortality may also be reduced due to reduced traffic accidents (in light of physical distancing policies) and pollution related deaths. Given these uncertainties, we use the following penalty function to keep the simulated unaccounted excess mortality close to data:

$$LE = -\sum_i \left(\frac{0.9e_i - \bar{e}_i}{0.2e_i}\right)^4 \quad (30)$$

This penalty could be seen as a likelihood coming from the probability distribution $p(x) = \frac{\exp^{-x^4}}{1.8128}$ defined for all values of *x*. It assumes that in the most likely case for excess mortality, 90% of unaccounted mortality should be attributed to COVID-19 deaths, but that there is significant uncertainty around this, so some 20% variation across this figure is quite plausible (70%-110% of data). However, numbers outside of this range start to impose increasingly large penalties, so that very large deviation becomes unlikely.

Combining these three components, we obtain the full likelihood function used in the analysis:

$$LL = LC + LE + \sum_{t=t_0}^{t=T} LT(t) \quad (31)$$

For each country we include the LT component from the first day they have reached 0.1% of their cumulative cases to-date, or a minimum of 50 cumulative cases. This excludes very early rates that are both unreliable and which, given very small estimated model predictions for infection, could lead to unreasonably large likelihood contributions.

Numerical Methods

The model includes a large number of parameters to be estimated: a general parameter for the impact of weather, 2 general parameters for ε_j, and 22 parameters for each country that are coupled together based on the random effects framework described above. Out of those 1 parameter (per country) is for ε_i and the other 21 are informing various features of disease transmission, testing, hospitalization, and risk perception and response. With a sample of 92 countries, this would lead to 2027 parameters to be estimated. A direct optimization approach to this problem suffers from potential risk of getting stuck in local optima, and direct use of MCMC methods to find the promising regions of parameter space suffers from the curse of dimensionality. We therefore designed the following 4-step procedure to find more reliable solutions to both problems and the synthetic data exercise in S3 provides some evidence on the effectiveness of the method.

1) We estimate the model with the full parameter vector for a smaller number of countries with larger outbreaks (3-5 countries). We use the Powell direction search method implemented in Vensim™ simulation software for this step. The method is a local search approach though it has features that allows it to escape local optima in some cases. We restart the optimization from various random points in the feasible parameter space and track the convergence of those restarts to unique local peaks. We stop this process when we are repeatedly landing on the same local peaks in the parameter space. This procedure showed that local peaks do exist, but they are not many; for example, within 100 restarts we may find 2-4 distinct peaks, with one being distinctly better than others. This quasi-global peak provides a coherent set of starting points for $\boldsymbol{\phi}$ and $\overline{\boldsymbol{\theta}}$ for next steps.
2) We go through iterations of the following two steps: A) Conduct country-specific optimizations with 50 restarts to find the vector of $\boldsymbol{\theta_i}$ given the $\boldsymbol{\phi}$ and $\overline{\boldsymbol{\theta}}$ from first optimization or from the step B. B) Conduct a global optimization, including all countries but fixing $\boldsymbol{\theta_i}$ and optimizing on $\boldsymbol{\phi}$ (and $\overline{\boldsymbol{\theta}}$; though that is simply the mean across country level parameters from

previous round). We stop when iterations offer little improvement from one round to the next (less than 0.05% improvement in log-likelihood).

3) We conduct a full optimization allowing all parameters ($\boldsymbol{\theta_i}$, $\boldsymbol{\phi}$ and $\overline{\boldsymbol{\theta}}$) to change, starting from the point found in the last iteration of step 2. This step finds the exact peak on the likelihood landscape which is the best-fitting parameter set for the model.
4) For the MCMC, theoretically one should conduct the sampling from all model parameters in the full model. However, our experiments showed that the large dimensionality of the parameter space requires an infeasible number of samples to achieve adequate mixing and ensure reliable credible regions for parameters and projections. To overcome this challenge we note that the parameters of different countries are connected to each other only through $\boldsymbol{\phi}$ and $\overline{\boldsymbol{\theta}}$, and these general parameters are rather insensitive to dynamics in each country. The insensitivity is due to the fact that a single country only contributes about 1% to the general parameters' values, and within a typical MCMC the country-level parameters often can't change more than 10% before the resulting samples become highly unlikely. Therefore, one can conduct an approximate country-level MCMC by fixing the general parameters at those from step 3, and only sampling from the $\boldsymbol{\theta_i}$ for each country. The MCMC algorithm used is one designed for exploring high dimensional parameter spaces using differential evolution and self-adaptive randomized subspace sampling (*11*). Using this method we obtain good mixing and stable outcomes (Robin-Brooks-Gelman PSFR convergence statistic remaining under 1.1) after about 600,000 samples (the burn-in period). We continue the MCMC for each country for another 400,000 samples and then randomly take a subsample of those points after the burn-in period for the next step.
5) The resulting subsamples for different countries from step 4 are assembled together to create a final sample of parameters for the full model to conduct projections and sensitivity analysis at the global scale. Uncertainties in the handful of global parameters is not identified in this procedure, but can be quantified by assessing the sensitivity of the global likelihood surface to changes in those parameters.

The process above is automated using a Python script that controls the simulation software (Vensim). We conduct the analysis using a parallel computing feature of Vensim on a Windows server with 48 cores. After compiling the simulation model into C++ code (which speeds up calculations significantly), and using a simulation time step of 0.25 days, it takes about 60 hours to complete the estimation for 91 countries, and almost two weeks to complete the full suite of sensitivity analyses reported in the paper. Full analysis code is available online at https://github.com/tseyanglim/CovidGlobal.

S3 VALIDATION OF ESTIMATION FRAMEWORK

The complexity of model and the large number of parameters involved complicates the assessment of estimation method based on theoretical considerations alone. We therefore use a synthetic data experiment to build confidence in the estimation framework. Specifically, we first simulate the model using known parameters without using historical deaths and cases to provide a 'ground-truthed' set of synthetic data. We then apply the exact estimation framework used on the actual data to infer the parameters of the model from this synthetic dataset. Finally, we assess how well the estimated parameters correspond to the "true" values and how inclusive the estimated credible intervals are of the true parameters. The ability of the estimation framework to find the true parameter values, and consistent credible intervals, would increase our confidence that parameters estimated using actual data are also not particularly biased and that the credible intervals are informative. While repeating this procedure for multiple sets of synthetic data, with various parameterizations, is desirable, the computational costs in our setting make such an approach infeasible. Nevertheless, the large number of parameters estimated in a single full calibration exercise provides ample opportunities to test the precision of the method in the range of parameter values relevant in the actual data. The three steps of the process are discussed below.

Generation of synthetic data

We used the model specified above, with the parameters estimated in the baseline analysis from actual data, to generate the synthetic data. Given the deterministic nature of the model, it would be easy for the estimation process to identify the model parameters should we use the exact outcome of the baseline simulation. To test the model in a more realistic scenario, therefore, we inject two different random noise time series into the model, effectively turning the data generation simulation model into a stochastic one with underlying noise processes not accurately captured in the estimation model (because of the autocorrelation in the driving noise). Specifically, we make the following two modifications to the model equations:

$$r_{SP} = C_I W \left(\frac{S}{N}\right) N_{PI} \tag{1b}$$

Where $\frac{dN_{PI}}{dt} = \frac{N_{PI}{}^{*} - N_{PI}}{t_{Crr}}$

$$N_{PI}{}^{*} = 1 + N_G \sigma_{NI} \sqrt{\frac{2 - \frac{d_t}{t_{Crr}}}{\frac{d_t}{t_{Crr}}}}$$

And

$$f_{(.)} = f_b \alpha_{(.)}^{s_f} s_{HF}(.) g_{Ag} N_{PD} \tag{15b}$$

Where $N_{P.}$ are the noise terms changing infection and IFR rates. N_{PD} is formulated similar to N_{PI}, with parameters t_{Crr} and σ_{ND}. N_G is a standard Gaussian random number generator producing a new independent draw every time step of the simulation (d_t) for each of the two noise streams separately and independently.

These equations specify two first order autocorrelated Normally distributed noise streams. The autocorrelation time constant, t_{Cm}, is set to 10 days for both streams of noise. The σ_{NI} and σ_{ND} parameters are set to 0.1 (i.e. leading to standard deviation of noise around infections and deaths being 10% of the model generated baselines). As in the real world, the substantial correlation time leads to significant swings in the infection and death rates beyond those explained by model mechanisms.

We also add a "measurement" noise to both daily infections and deaths in synthetic data by drawing Negative Binomial random samples from the estimated distributions for each country at any given time and using those (rather than expected values) as the data in this estimation exercise.

To best replicate the features of actual data, the model uses actual country level data for test rates (which are exogenous inputs driving simulations) and various country level statistics such as population, population density, and age structure.

We record the data generated from this simulation for confirmed cases and deaths, corresponding to the data we have available to estimate the actual model. For each country we only record the data for the days in which we have a corresponding actual data point. We also record excess mortality counts for the subset of countries and periods for which we have such data. These three data items (two time series for confirmed infections and deaths and point estimates for excess mortalities in a subset of countries) are the inputs into the estimation process.

Estimation using synthetic data

The synthetic data generated in the previous step is available on the project's GitHub repository. This data is then used, following the estimation process discussed in S2, to find the model parameters. This step requires no other assumptions and follows the exact process used in the main analysis. Note that we start the estimation with uninformed (uniform with large ranges) priors on all parameters.

Results and comparisons

Figure S5 reports the estimated parameters, their 95% credible intervals, and the true parameters across all 1932 (92 countries x 21 parameters each) country-level parameters of the model that impact outcomes. Overall, the estimation process successfully identifies the vast majority of parameters. For example the median distance between estimated and true values, as a percentage of the length of estimated 95% credible interval, is 21%. Moreover, the credible intervals envelope the true values rather consistently. Specifically, the 50% CI includes the true value in 32% of cases and this measure increases to 49%, 60%, 67%, and 75% for 80%, 90%, 95%, and 98% CIs respectively. The theoretical vs. actual intervals are showed in Figure S4.

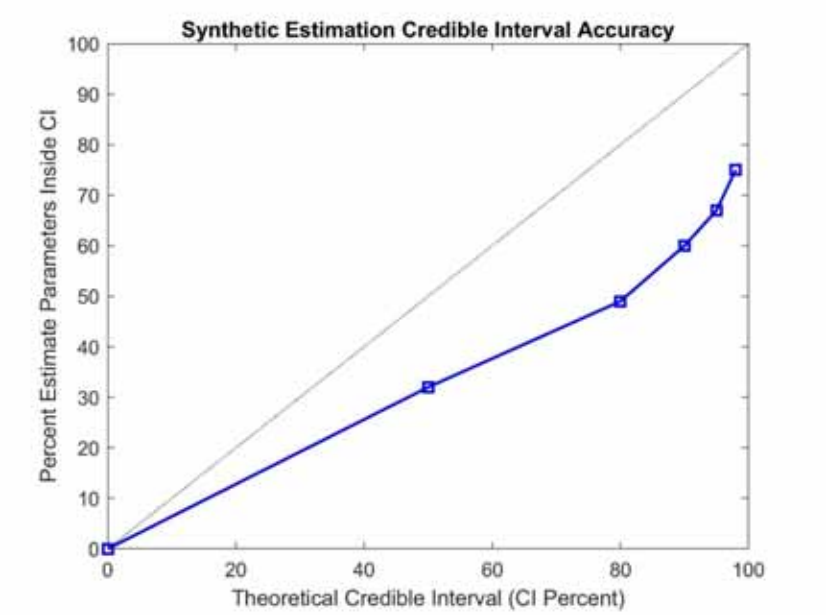
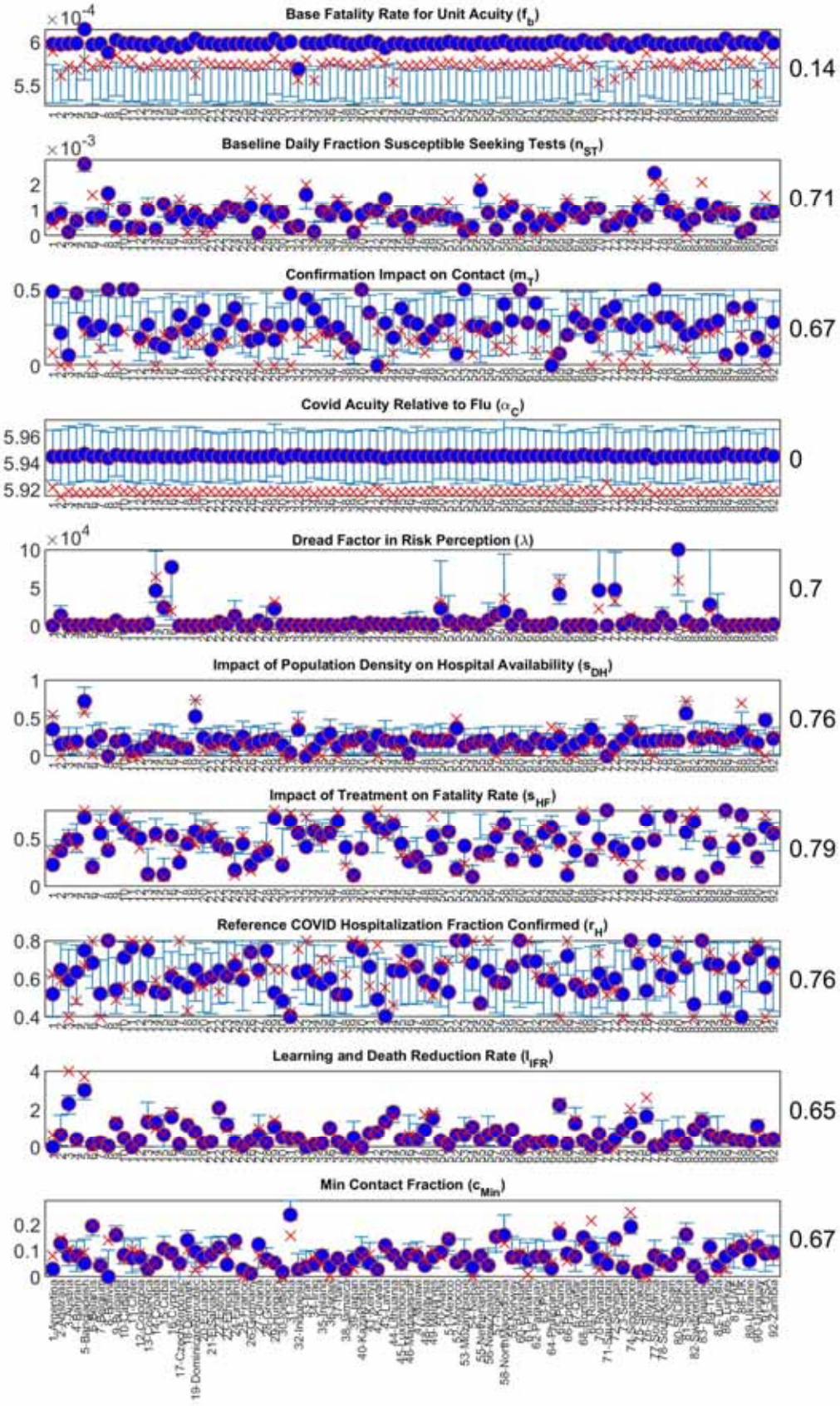


Figure S4- Theoretical vs. actual fraction of parameters enveloped by different Credible Interval percentiles.

While not identical to the expected theoretical values, these coverage levels are close, especially in the context of very large parameter spaces and complex estimation exercises where finding reliable CIs is often harder than estimating the parameters. Figure S5 also shows that some parameters are more likely to have imprecise confidence intervals than others. In fact, much of the imprecision in confidence intervals are due to two parameters, *Base Fatality Rate for Unit Acuity* and *Covid Acuity Relative to Flu* end up outside 95% confidence interval for all countries, despite estimated value being numerically very close to original value. We can't rule out the existence of a local optima in the new estimated value driving the results. Moreover, for some parameters (e.g. f_b, and β) the baseline estimated values could fall outside the 95% confidence intervals and are closer to the true values. These instances could point to asymmetric likelihood surfaces or the possibility that the MCMC chains may require larger samples for getting at true confidence intervals. Overall these results add to our confidence that the estimated credible intervals are in the right range, though some may be somewhat tighter than they should be.


Base Fatality Rate for Unit Acuity (f_b)
0.14
Baseline Daily Fraction Susceptible Seeking Tests (n_{ST})
0.71
Confirmation Impact on Contact (m_T)
0.67
Covid Acuity Relative to Flu (α_C)
0
Dread Factor in Risk Perception (λ)
0.7
Impact of Population Density on Hospital Availability (s_{DH})
0.76
Impact of Treatment on Fatality Rate (s_{HF})
0.79
Reference COVID Hospitalization Fraction Confirmed (r_H)
0.76
Learning and Death Reduction Rate (l_{IFR})
0.65
Min Contact Fraction (c_{Min})
0.67

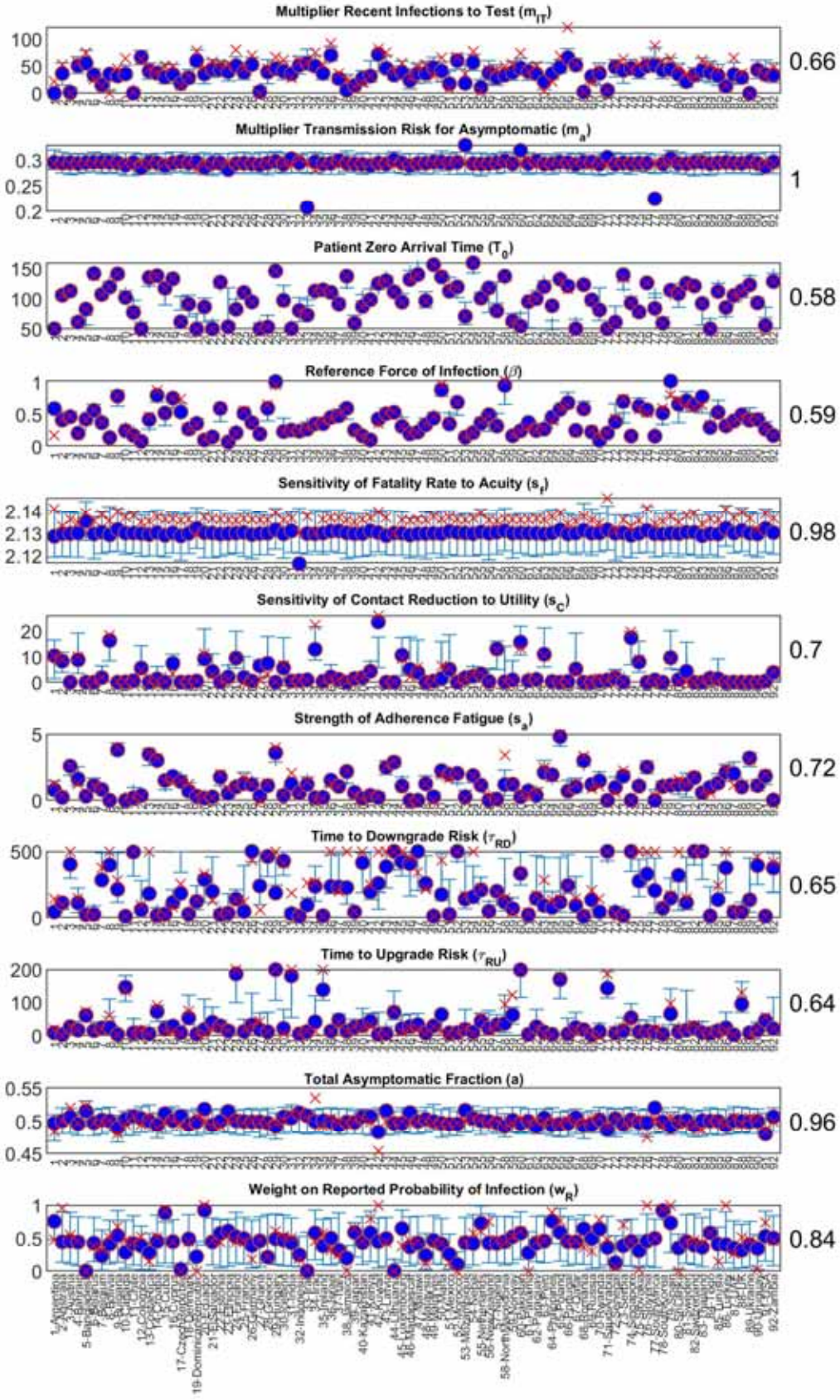

Multiplier Recent Infections to Test (m_{IT})
100
50
0
0.66
Multiplier Transmission Risk for Asymptomatic (m_a)
0.3
0.25
0.2
1
Patient Zero Arrival Time (T_0)
150
100
50
0.58
Reference Force of Infection (β)
1
0.5
0
0.59
Sensitivity of Fatality Rate to Acuity (s_f)
2.14
2.13
2.12
0.98
Sensitivity of Contact Reduction to Utility (s_C)
20
10
0
0.7
Strength of Adherence Fatigue (s_a)
5
0
0.72
Time to Downgrade Risk (τ_{RD})
500
0
0.65
Time to Upgrade Risk (τ_{RU})
200
100
0
0.64
Total Asymptomatic Fraction (a)
0.55
0.5
0.45
0.96
Weight on Reported Probability of Infection (w_R)
1
0.5
0
0.84

Figure S5-Country-level parameter estimates and 95% credible intervals from synthetic estimation exercise (blue circles and bars) compared with true values (red cross signs) across all parameters. Numbers on the right represent the fraction of true values enveloped by the 95% interval.

S4 DATA PRE-PROCESSING

Getting contemporaneous, comprehensive, national-level data on Covid-19 is a challenge. The most widely-cited data aggregators, such as the Johns Hopkins Center for Systems Science and Engineering's COVID-19 database (*12*), OurWorldInData portal (*13*), and the US-focused COVID Tracking Project (*14*), get their data from the same few official sources, such as the US Centers for Disease Control and Prevention (CDC), the European CDC (ECDC), and the World Health Organization (WHO). These official agencies in turn get their data from national and subnational public health authorities, which ultimately rely on reports from hospitals, clinics, and private and public health labs.

As a result, idiosyncrasies in the ground-level data collection processes permeate virtually all sources of aggregate data. Most notably, data collection involves time lags, which can differ from source to source. Daily death counts could reflect the date of actual death or the date a death is registered or reported; different UK government sources, for instance, use each of these metrics.[2] Daily infection or case counts could include the total new cases reported *on* a given date, or the total cases confirmed *from* that date; the latter would result in some 'backfill' whereby case counts for previous days can continue to increase for some time as delayed confirmations come in. Daily counts of tests conducted could report samples collected, samples processed, results reported, or a mix of these; the US CDC, for instance, reports a mix of testing by date of sample collection and date of sample delivery to the CDC.[3] Aside from differences in unit of measure (people vs. tests vs. samples), there may be different time lags involved as well. In addition to these idiosyncrasies, testing data in particular is also patchy for many countries, even as testing has become more widespread. The WHO does not report country-by-country testing, nor does the JHU Covid map outside the US. Furthermore, there are sometimes irregular delays in the reporting of test results, which can create occasional unexpected spikes in reported numbers of tests, infections, or both.[4]

Depending on the specifics of how daily infection and test counts are reported, there can in some cases be a disjunction between the two. Because confirmed case counts largely depend on positive test results, test and infection counts should be correlated – *ceteris paribus*, a day with a lot of samples collected for testing should see more confirmed cases attributed to it, while a day with no sample collection should see no cases. But since cases may not be reported by the date of the test, and tests may not be reported by the date of sample collection, officially reported numbers can get out of sync in either direction.

This problem is most salient when there are clear weekly cycles in daily rates. In most of the world, particularly western countries, daily test rates are far lower on weekends than during the week. As a result, infection numbers show a clear weekly cyclical component as well. But the weekly cycles in testing and infection numbers for a given country do not always line up. Our model explicitly accounts for the effect of testing on reported infections, but we do not explicitly model the country-level

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[2] https://blog.ons.gov.uk/2020/03/31/counting-deaths-involving-the-coronavirus-covid-19/

[3] https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/previous-testing-in-us.html

[4] See e.g. https://www.wcvb.com/article/massachusetts-coronavirus-reporting-delay-due-to-quest-lab-it-glitch/32288903#

idiosyncrasies of reporting and how they vary between test data and infections. Instead we account for any such lags in pre-processing of the data to align testing and case data.

The weekly cycle occurs in many countries' death rate data as well, where it presents a different problem. A weekly cycle in testing is a behaviourally realistic part of the data-generation process, as many labs, clinics, or other testing sites for instance may be closed on weekends. As testing provides the window on the state of confirmed infections, a comparable cycle in confirmed cases is to be expected as well. By linking case confirmations to testing, our model explicitly accounts for this limited visibility on the true state of the epidemic. However, a weekly cycle in death rates almost certainly reflects different limitations of the data-generation process, typically to do with hospital staffing,[5] which we do not explicitly model. As such we need to address any weekly cycle in death rates through data pre-processing as well.

To deal with these challenges, we developed a multi-step algorithm to pre-process our data before feeding it into the model for calibration. The algorithm is described below. It was implemented in Python, largely using the Pandas and NumPy packages, and the code is available in full at: https://github.com/tseyanglim/CovidGlobal.

The algorithm proceeds country-by-country, following these steps on each country.

1) Examine daily cumulative test data; if data are insufficient (6 or fewer data points), drop country from the dataset.

2) Interpolate any missing daily cumulative test data points using a piecewise cubic Hermite interpolating polynomial (PCHIP) spline. If the first reported infection is before the first reported cumulative test, also extrapolate cumulative tests back to the date of first reported infection.
    a. Extrapolation to the date of first reported infection is necessary since both in the model and, to a large extent, in reality, reported infections require testing for confirmation.
    b. PCHIP spline interpolation yields a continuous monotonic function with a continuous first derivative, thus avoiding generating any anomalous rapid change in daily test rate.
    c. We used the implementation of PCHIP interpolation from the widely used SciPy package for Python.[6]

3) Calculate daily test rate as daily cumulative tests less the preceding day's cumulative test total:

[5] It may be argued that there are weekly cycles in large-scale human behaviour that may drive some true weekly cyclicality in the true rates of infection and death, and as such it may be wrong to consider such cycles to be artefacts of the data-generation process. However, we find this unlikely for a few reasons. First, weekly cycles in human interactions, largely driven by the work and school week and weekend, will have been significantly attenuated by widespread adoption of social distancing measures around the world. Second and more importantly, variation in incubation period and time before development of symptoms means that any true cyclicality in the timing of initial infection will be further attenuated in the timing of symptom development. By the same logic, wide variability in the delay from symptom development to death means there should be minimal cyclicality, if any, in the timing of deaths, meaning any such cycles visible in the data are due to measurement and reporting lags.

[6] https://docs.scipy.org/doc/scipy/reference/generated/scipy.interpolate.PchipInterpolator.html

$$TestRate_t = CmltTest_t - CmltTest_{t-1} \quad (32)$$

4) Examine the original daily cumulative test data to estimate how much of the calculated daily test rate is based on interpolated vs. original data.
    a. Daily test rates calculated based on mostly original data should be expected to include any weekly cycles or occasional irregularities that would also be reflected in daily infection counts. Conversely, daily test rates calculated from cumulative test counts that are largely interpolated would not be expected to fully reproduce any such cycles or irregularities, since the interpolation produces a relatively smooth function.
    b. As a rule of thumb, we examine the cumulative test data for the second half of the time from the first test to the latest test. If fewer than half the days in that window have original cumulative test data, we consider the test data to be 'sparse', requiring further processing.

5) If the test data are not sparse, account for any potential lag or other reporting delay differences between daily test rate and daily infection rate using a time-shift algorithm to estimate any such lags or delays from the data and shift the test rate time series accordingly. The time-shift algorithm ensures that any weekly cycles present in the daily infection rate data are reflected in the daily test rate data and aligned as best as possible on date, thereby accounting for the fact that model-generated reported infections depends on testing but with no time lag between test and result.
    a. First, identify the weekly component of the time series of daily infection rate and daily test rate using a seasonal-trend decomposition based on LOESS (STL) procedure.[7]
        i. STL deconstructs time series data into several components, including a trend and a seasonal component over a specified period (weekly, in this case) as well as a residual. STL is an additive decomposition, and has the advantage of allowing the seasonal component to change over time (rather than being a fixed pattern repeated exactly across the whole time series).
        ii. We used the STL implementation from the Statsmodels package for Python.[8]
    b. Shift the time series over a one-week range (from -2 to +4 days of lag between test and infection reporting), calculating the cross-correlation between the weekly seasonal component of the daily infection rate data and the daily test rate data for each time shift.
    c. Identify the time shift within this range that maximizes the cross-correlation between the infection rate and test rate data, and shift the test rate data accordingly.

6) If the test data are sparse, the spline interpolation will generally cut out some of any weekly cyclicality that may be present. Visual inspection of daily test rates for countries with sparse test data also shows large, irregular spikes in reported tests are not uncommon, without necessarily having concomitant irregular spikes in reported daily infection rates. As such, rather than attempting to eliminate differences in reporting lags through the time-shift algorithm described above, we instead apply a data-smoothing algorithm to both daily test rate and daily infection rate,

[7] Cleveland R.B., Cleveland W.S., McRae J.E., Terpenning I. (1990) STL: A seasonal-trend decomposition procedure based on Loess. *J Off Stat* 6: 3-73
[8] https://www.statsmodels.org/stable/generated/statsmodels.tsa.seasonal.STL.html

in order to reduce any cyclicality and irregular spikes. This smoothing allows the calibration of the main model to focus on matching the underlying trends in the data.

7) In all cases, whether daily cumulative test data are sparse or not and whether infection and test rate data are smoothed or not, since weekly cycles in death data are reflective of reporting lags not captured in the model, daily death rate data is smoothed using the same algorithm.

8) The smoothing algorithm used is designed first to conserve the total number of reported cases (tests, infections, or deaths), and second to preserve some degree of variation in the time series, as some noise may be informative and retaining some is important to the calibration of the model.
    a. Starting from when the time series of daily rate (test or infection) exceeds a specified minimum value (5/day), calculate the rolling mean of the daily rate, using a centred moving window of 11 days.
    b. Calculate the residual between each day's data point and the rolling mean for that day, and divide by the square root of the rolling mean, to get an adjusted deviation value:

$$AdjDev_t = \frac{Value_t - RollMean_t}{\sqrt{RollMean_t}} \quad (33)$$

        i. Dividing by the square root of the rolling mean reflects a heuristic assumption that each daily rate (of infections, deaths, or tests) behaves as a Poisson process (StDev of Pois(λ) = $\lambda^{0.5}$).
        ii. The functional result of this adjustment is that both *absolute* and *relative* magnitudes of deviations from the rolling mean are given some weight – large relative deviations when absolute values are small (and data are noisier) are not ignored, but neither do they outweigh larger absolute (but smaller relative) deviations that occur when the mean is large, which is important since most of the time series data are growing significantly over the time horizon of the model.
    c. Calculate thresholds for identifying dips and peaks in the data based on the median of the adjusted deviations, ± one median absolute deviation (MAD) of the adjusted deviations:

$$Threshold = \widetilde{AdjDev} \pm Med\left(\left|AdjDev_i - \widetilde{AdjDev}\right|\right) \quad (34)$$

        i. Using the median absolute deviation to determine thresholds for peaks and dips is robust to outliers in the deviations, which do arise occasionally in the data.
        ii. A threshold width of one MAD is relatively narrow for outlier detection, but by inspection of the data, is about right for identifying most of the peaks and dips caused by weekly cycles in test, infection, and death rates, as well as larger outliers.
    d. Once thresholds are calculated, iterate through the data points in the time series first forward in time from oldest to newest, filling in any 'dips' (data points with adjusted deviations below the lower threshold), then backward in time from newest to oldest, smoothing out any 'peaks' (data points with adjusted deviations above the upper threshold) that remain. Repeat the process until all data points' adjusted deviations are within the originally calculated thresholds for the time series.

i. We infer that the underlying processes generating dips and peaks are somewhat different. Dips are generally the result of weekly cycles in the data, e.g. lower rates of testing or longer lags in death reporting that occur on weekends. Peaks arise to some extent due to the same weekly processes, e.g. some deaths that occur on weekends only being recorded at the start of the next week. However, some peaks, especially larger ones, may result from irregular random delays in reporting, such as large batches of tests being held up due to logistical issues and then getting processed all at once. As such the smoothing procedure for dips vs. peaks is slightly different.

e. The dip-filling step fills a fraction of each dip (specified as a *smoothing factor*) by redistributing data counts based on a multinomial draw from the subsequent few days following each dip.
   i. First, calculate the amount to fill based on the deviation and the smoothing factor specified, in this case 0.67:

$$FillAmt_t = SmFactor \times (RollMean_t - Value_t) \quad (35)$$

   ii. Calculate the amount redistributed from each of the following few (7) days $X_{t+1}, X_{t+2}, \dots X_{t+k}, k = 7$, based on a multinomial distribution as follows:

$$X_{t+1}, X_{t+2}, \dots X_{t+7} = Multinomial(FillAmt_t; p_{t+1}, p_{t+2}, \dots\ p_{t+7}) \quad (36)$$

Where $p_{t+1}, p_{t+2}, \dots\ p_{t+7}$ are calculated as:

$$p_{t+i} = \frac{AdjDev_{t+i} - AdjDev_t, min.0}{\sum_1^7 (AdjDev_{t+i} - AdjDev_t, min.0)} \quad (37)$$

   iii. This formulation allows some redistribution from any of the subsequent few days whose adjusted deviations exceed the focal day's adjusted deviation, but with more redistribution from days with higher adjusted deviations.

f. The peak-smoothing step similarly redistributes a fraction of each peak, specified by the smoothing factor, to the *preceding* several days based on another multinomial draw.
   i. First, calculate the amount to redistribute similarly to the dip-filling step:

$$DistAmt_t = SmFactor \times (Value_t - RollMean_t) \quad (38)$$

   ii. Calculate the amount redistributed *to* each of the preceding several (14) days $Y_{t-1}, Y_{t-2}, \dots Y_{t-k}, k = 14$, based on a multinomial distribution as follows:

$$Y_{t-1}, Y_{t-2}, \dots Y_{t-14} = Multinomial(DistAmt_t; p_{t-1}, p_{t-2}, \dots\ p_{t-14}) \quad (36)$$

Where $p_{t-1}, p_{t-2}, \dots\ p_{t-14}$ are calculated as:

$$p_{t-i} = \frac{RollMean_{t-i}}{\sum_1^{14} RollMean_{t-i}} \quad (39)$$

iii. This formulation redistributes peaks to preceding days based on the calculated rolling mean counts of those days, on the assumption that the irregular delays that generate random spikes in counts are essentially random and equally likely to affect any given unit of data over a several-day span. As such, the probability that a unit showing up in a spike due to such delays comes from a given preceding day is simply proportional to the expected count for that day, as approximated by the rolling mean.

g. By filling dips first before smoothing peaks, the combined algorithm largely addresses any peaks that are due primarily to weekly cycles during the dip-filling stage, such that remaining peaks that get smoothed tend to be the larger, irregular ones.

Overall, despite these corrections, a few countries include interpolated test data that may not be realistic and could lead to unrealistically large early outbreaks (when interpolated test rate is very small compared to number of cases). Specifically, we see such potential in estimates for Czech Republic, France, Greece, and Slovakia. Future updates to the online simulator will attempt to fix these potential inaccuracies.

S5 EXTENDED RESULTS

Quality of fit measures

Table S3 reports two quality of fit metrics for different countries and different time series. The first four columns report Mean Absolute Error Normalized by Mean (MAEN) and the last four report the R-Squared measures. Errors for cumulative infection and deaths are followed by those for the new cases and deaths (flow variables).

Table S3- Measures of fit between data and simulations for different countries. Mean Absolute Error Normalized by Mean (MAEN) and R-Squared are reported for cumulative and new cases and deaths.

	MAEN				**R-Squared**			
	Cumulative		**Flow**		**Cumulative**		**Flow**	
Country	**Infection**	**Death**	**Infection**	**Death**	**Infection**	**Death**	**Infection**	**Death**
Argentina	0.0934	0.0525	0.239	0.198	0.999	0.999	0.899	0.84
Australia	0.0277	0.288	0.483	0.65	0.998	0.97	0.691	0.72
Austria	0.239	0.335	0.576	0.59	0.991	0.962	0.852	0.943
Bahrain	0.11	0.388	0.421	0.947	0.988	0.944	0.414	0.0946
Bangladesh	0.0208	0.028	0.161	0.14	0.999	0.999	0.799	0.808
Belarus	0.109	0.123	0.182	0.494	0.996	0.972	0.918	0.466
Belgium	0.328	0.363	0.533	0.356	0.965	0.964	0.612	0.816
Bolivia	0.0515	0.0793	0.325	0.363	0.992	0.997	0.703	0.77
Bulgaria	0.0881	0.202	0.455	0.374	0.992	0.973	0.724	0.917
Canada	0.224	0.111	0.293	0.191	0.977	0.994	0.841	0.915
Chile	0.0728	0.0399	0.354	0.289	0.993	0.997	0.529	0.764
Colombia	0.0901	0.0421	0.207	0.173	0.999	0.997	0.868	0.853
CostaRica	0.057	0.064	0.464	0.332	0.999	0.996	0.372	0.717
Croatia	0.117	0.226	0.347	0.4	0.989	0.968	0.861	0.972
Cuba	0.0414	0.163	0.341	1.16	0.998	0.958	0.583	0.35
Cyprus	0.0795	0.441	0.452	1.32	0.99	0.781	0.649	0.257
CzechRepublic	0.178	0.0789	0.303	0.19	0.997	0.998	0.882	0.941
Denmark	0.0802	0.172	0.342	0.357	0.993	0.964	0.765	0.865
DominicanRepublic	0.0711	0.142	0.383	0.298	0.994	0.996	0.464	0.67
Ecuador	0.0576	0.0651	0.593	0.659	0.996	0.985	0.0681	0.153
ElSalvador	0.103	0.155	0.521	0.304	0.997	0.995	0.363	0.78
Estonia	0.0724	0.157	0.322	0.937	0.997	0.899	0.844	0.515
Ethiopia	0.0365	0.0424	0.238	0.26	0.999	0.998	0.806	0.789
Finland	0.426	0.0647	0.43	0.515	0.962	0.991	0.602	0.737
France	0.325	0.895	0.577	2.16	0.919	0.794	0.376	0.265
Germany	0.233	0.0288	0.298	0.267	0.98	0.992	0.87	0.807
Ghana	0.183	0.149	0.701	1.35	0.995	0.992	0.383	0.106
Greece	0.0696	0.0436	0.379	0.205	0.993	1	0.793	0.961
Hungary	0.0975	0.105	0.332	0.218	0.998	0.997	0.823	0.976
Iceland	0.0558	0.241	0.405	1.87	0.996	0.887	0.737	0.0427
India	0.0316	0.0141	0.147	0.116	1	1	0.915	0.929
Indonesia	0.0867	0.0358	0.225	0.176	0.999	0.998	0.813	0.829
Iran	0.0768	0.0476	0.306	0.207	0.989	0.997	0.689	0.72
Iraq	0.0897	0.118	0.233	0.314	0.994	0.984	0.855	0.572
Ireland	0.161	0.209	0.403	0.353	0.971	0.966	0.571	0.934
Israel	0.113	0.16	0.653	0.453	0.968	0.979	0.336	0.395
Italy	0.356	0.019	0.336	0.185	0.965	0.998	0.873	0.951
Jamaica	0.119	0.159	0.339	0.742	0.997	0.995	0.735	0.485
Japan	0.386	0.258	0.38	0.461	0.989	0.982	0.731	0.467
Kazakhstan	0.0458	0.109	0.578	0.468	0.996	0.996	0.157	0.676

Kenya	0.0498	0.0869	0.359	0.389	0.998	0.986	0.646	0.65
Kuwait	0.0412	0.139	0.24	0.392	0.996	0.992	0.621	0.373
Latvia	0.113	0.758	0.302	0.671	0.999	0.92	0.881	0.779
Lithuania	0.0828	0.205	0.355	0.435	0.993	0.99	0.777	0.85
Luxembourg	0.251	0.43	0.716	0.731	0.993	0.954	0.416	0.443
Madagascar	0.163	0.11	0.561	0.789	0.996	0.999	0.594	0.46
Malawi	0.332	0.132	0.802	0.649	0.998	0.988	0.421	0.687
Malaysia	0.0712	0.131	0.251	0.554	0.999	0.982	0.889	0.599
Maldives	0.0853	0.446	0.403	1.32	0.993	0.974	0.52	0.00805
Malta	0.0713	0.373	0.397	0.763	0.993	0.97	0.704	0.559
Mexico	0.127	0.041	0.378	0.189	0.999	0.997	0.353	0.689
Morocco	0.0627	0.0689	0.292	0.214	0.995	0.996	0.782	0.88
Mozambique	0.032	0.0886	0.383	0.89	0.998	0.996	0.551	0.232
Nepal	0.0732	0.236	0.335	0.378	0.993	0.972	0.685	0.639
Netherlands	0.242	0.155	0.232	0.206	0.991	0.987	0.953	0.909
NewZealand	0.338	0.216	0.72	1.87	0.851	0.688	0.71	0.178
Nigeria	0.494	0.116	0.603	0.428	0.987	0.988	0.275	0.571
NorthMacedonia	0.0823	0.0547	0.349	0.247	0.997	0.998	0.748	0.907
Norway	0.0411	0.0825	0.375	0.623	0.995	0.975	0.646	0.715
Pakistan	0.0998	0.025	0.362	0.276	0.982	0.998	0.611	0.777
Panama	0.0944	0.0882	0.387	0.386	0.981	0.982	0.528	0.245
Paraguay	0.0871	0.0511	0.229	0.177	0.999	0.998	0.863	0.925
Peru	0.319	0.0694	0.541	0.425	0.987	0.987	0.174	0.47
Philippines	0.0588	0.0305	0.28	0.274	0.995	0.999	0.682	0.704
Poland	0.126	0.129	0.303	0.223	0.991	0.997	0.867	0.928
Portugal	0.372	0.543	0.373	0.398	0.963	0.982	0.867	0.83
Qatar	0.164	0.239	0.347	0.916	0.983	0.974	0.829	0.306
Romania	0.0623	0.0489	0.355	0.204	0.993	0.998	0.675	0.845
Russia	0.0284	0.0197	0.0551	0.076	1	0.999	0.989	0.983
Rwanda	0.102	0.239	0.562	1.39	0.99	0.979	0.412	0.161
SaudiArabia	0.0669	0.0821	0.39	0.243	0.988	0.992	0.683	0.755
Senegal	0.0494	0.0601	0.353	0.664	0.995	0.991	0.545	0.333
Serbia	0.281	0.177	0.548	0.558	0.909	0.928	0.916	0.833
Singapore	0.199	2.25	0.68	3.64	0.966	0.837	0.4	0.0197
Slovakia	0.155	0.0833	0.386	0.367	0.994	0.995	0.755	0.821
Slovenia	0.289	0.582	0.423	0.617	0.994	0.931	0.818	0.83
SouthAfrica	0.196	0.117	0.282	0.21	0.99	0.998	0.842	0.909
SouthKorea	0.0722	0.136	0.346	0.599	0.987	0.969	0.849	0.409
Spain	0.22	0.167	0.418	0.344	0.986	0.985	0.672	0.733
SriLanka	0.0977	1.17	0.361	0.963	0.996	0.784	0.809	0.567
Sweden	0.377	0.121	0.808	0.397	0.546	0.967	0.00298	0.669
Switzerland	0.137	0.347	0.528	0.414	0.996	0.993	0.608	0.866
Thailand	2.92	5.44	2.19	5.7	0.881	0.994	0.151	0.621
Togo	0.13	0.163	0.561	1.54	0.991	0.985	0.176	0.0396
Tunisia	0.687	0.821	0.844	0.92	0.963	0.907	0.329	0.618
Turkey	0.212	0.0809	0.637	0.243	0.852	0.98	0.106	0.909
UAE	0.122	0.195	0.408	0.382	0.986	0.981	0.534	0.484
UK	0.292	0.282	0.383	0.283	0.976	0.966	0.767	0.839
Ukraine	0.0565	0.0664	0.237	0.19	0.996	0.996	0.84	0.896
Uruguay	0.0481	0.0878	0.276	1.08	0.993	0.988	0.952	0.366
USA	0.0716	0.0306	0.23	0.146	0.991	0.999	0.936	0.857
Zambia	0.0841	0.106	0.725	0.808	0.994	0.984	0.258	0.386

Figure S6 shows the visualization of fit between data and simulations for all the countries in our sample. These graphs include data and model outputs for reported new cases (blue; left axis in thousands per day) and deaths (red; right axis in thousands per day) starting from the beginning of the epidemic in each country until 22 December 2020.

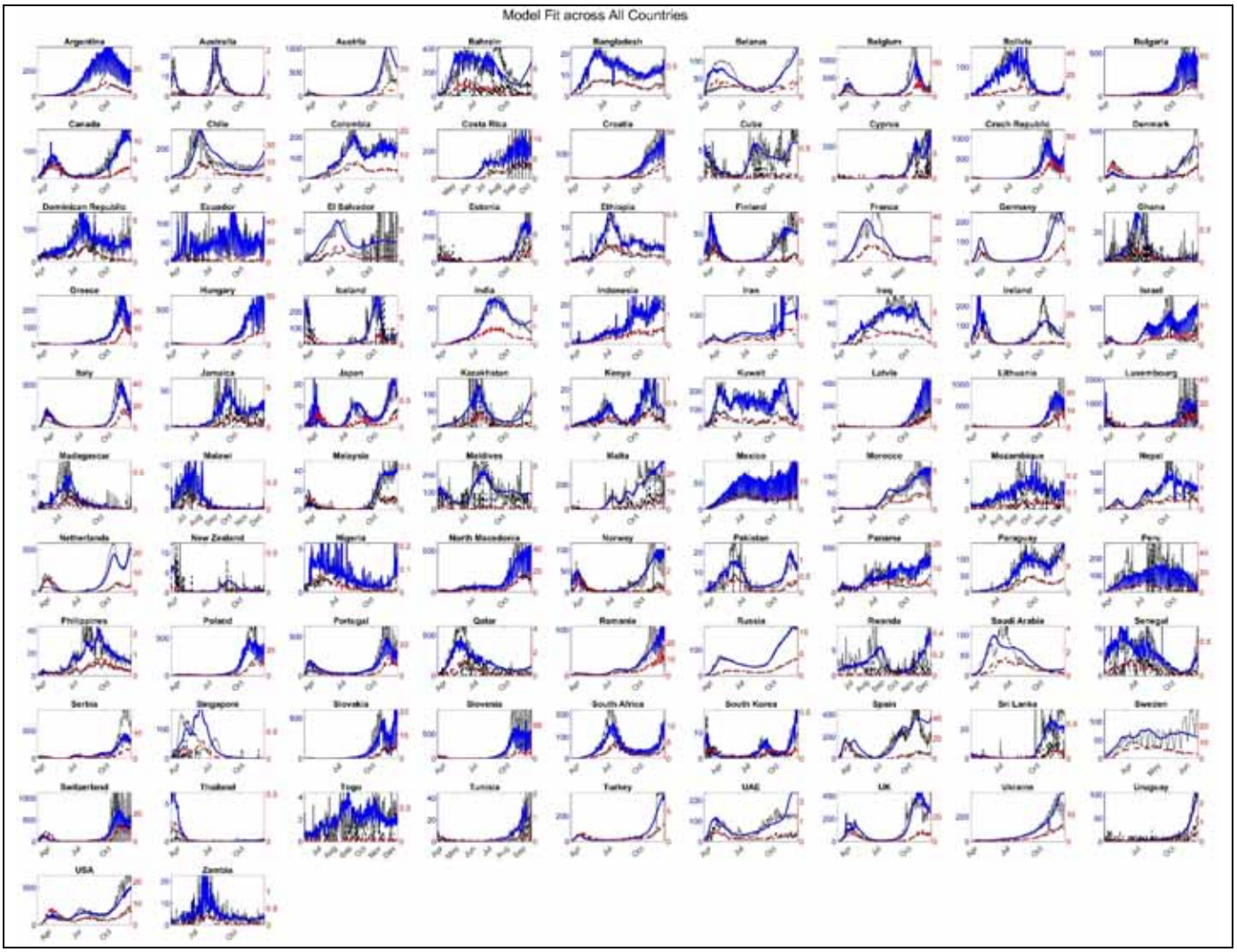


Figure S6- Comparison of data and simulation. New cases in blue (left axis, in thousands per day) and new deaths (red, right axis).

Estimates for true magnitude of epidemic

Estimates for true cumulative cases (blue; left axis in millions) and deaths (red; right axis in thousands) across different countries up to 22 December 2020 are reported in Figure S7.

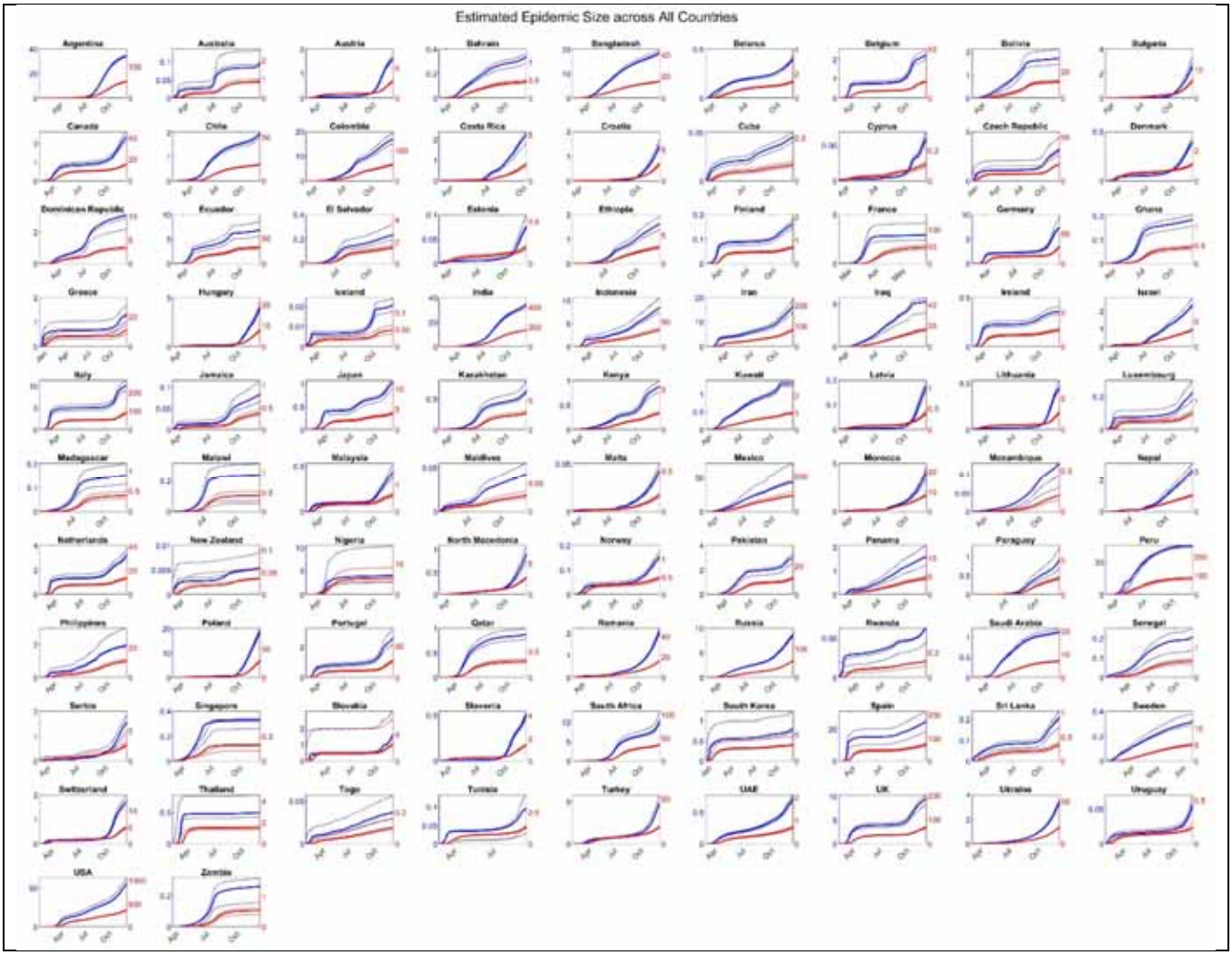


Figure S7- Estimates and 95% credible intervals for true magnitude of epidemic. Cumulative cases (blue, left axis in millions) and cumulative deaths (red, right axis, in thousands)

Excess deaths

Figure S8 shows the ratio of estimated excess deaths, i.e. COVID-19 fatalities not reported as such, to reported excess deaths, i.e. deaths over historical baseline not accounted for by reported COVID-19 deaths, for the countries for which such data are available.

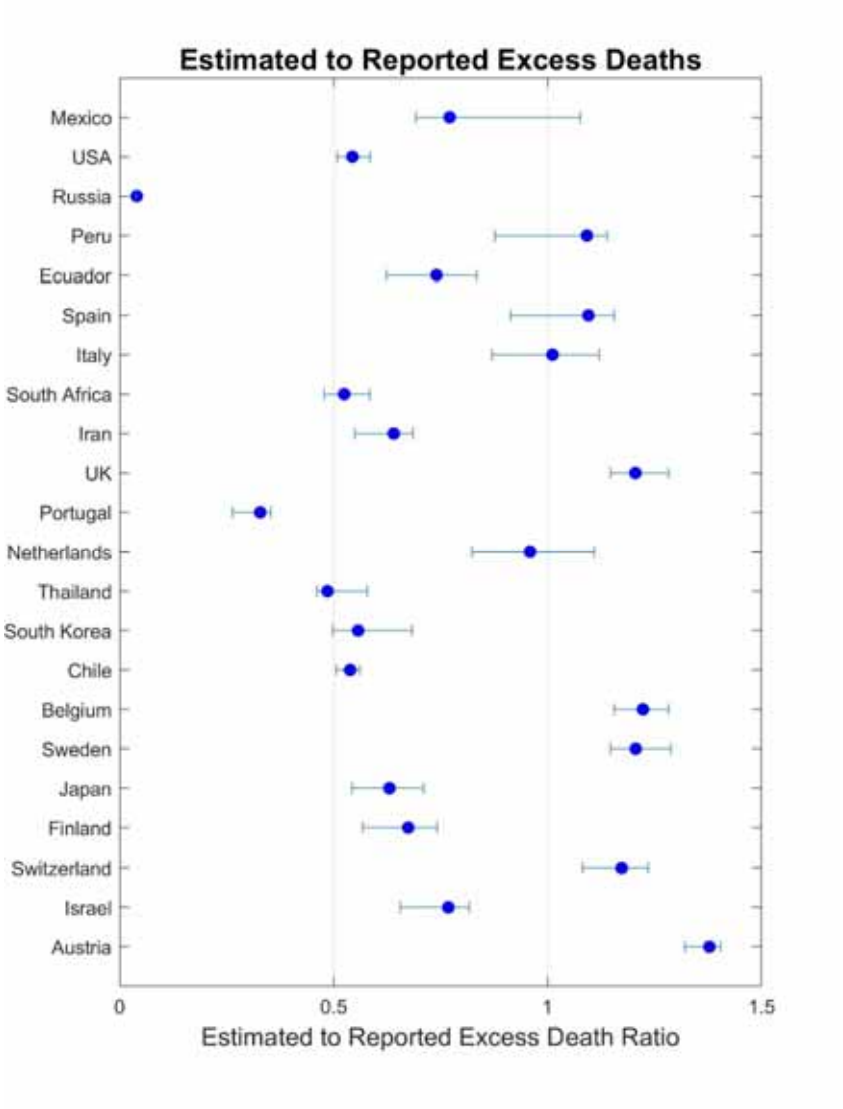


Figure S8- Ratio of estimated excess deaths to reported excess deaths for countries for which this data was available.

Maximum reproduction number

Figure S9 shows the initial reproduction number (R_E) occurring in each country. Reproduction numbers are changing dynamically and transient dynamics may lead to larger than equilibrium numbers if maximum R_E values were used. We therefore use the 90th percentile of simulated reproduction number in this graph. Also note the large credible intervals for these estimates. This range is partly driven by what exact point of the curve is represented by the 90th percentile. It is also due to the inherent uncertainty when both reproduction number and behavioral and policy responses are estimated: one can have smaller initial R_E and smaller response functions, or larger values for both, and stay consistent with the data, specially because early in the epidemic ascertainment rates are very low and data is not very informative about the true magnitude. Moreover, given the recording of R_E values at their (often initial) high values, they may reflect non-representative subpopulations or events. For example the high impact of weather conditions on transmission rates could notably alter Maximum R_E for some countries depending on weather conditions at the time of first wave.

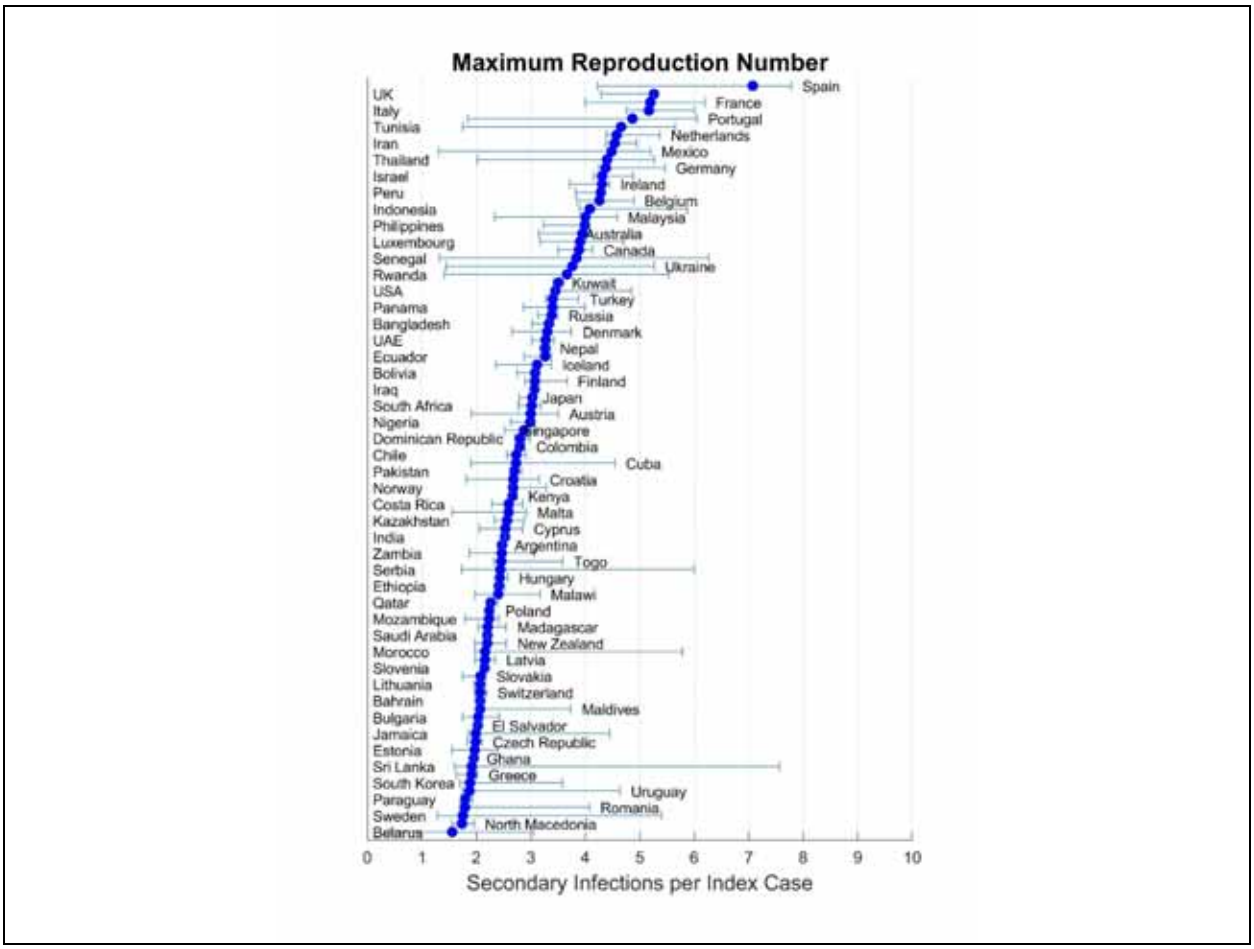


Figure S9- Maximum reproduction number R_E for each country's outbreak

Time to herd immunity

Figure S10 shows estimated time to herd immunity across nations. These estimates are based on time it takes before 60% of population has been infected by COVID-19. Depending on the basic reproduction number in each location and the heterogeneity in contacts, the 60% threshold will not be an exact value for most countries, but offers a reasonable intuition for the ranges of time involved and could be adjusted with a linear scaling to other thresholds. Two estimates are offered, one for the estimated number based on current true infection rates, and another based on the peak infection rates experienced in that country. The two may be the same if the current rates are the peak rates.

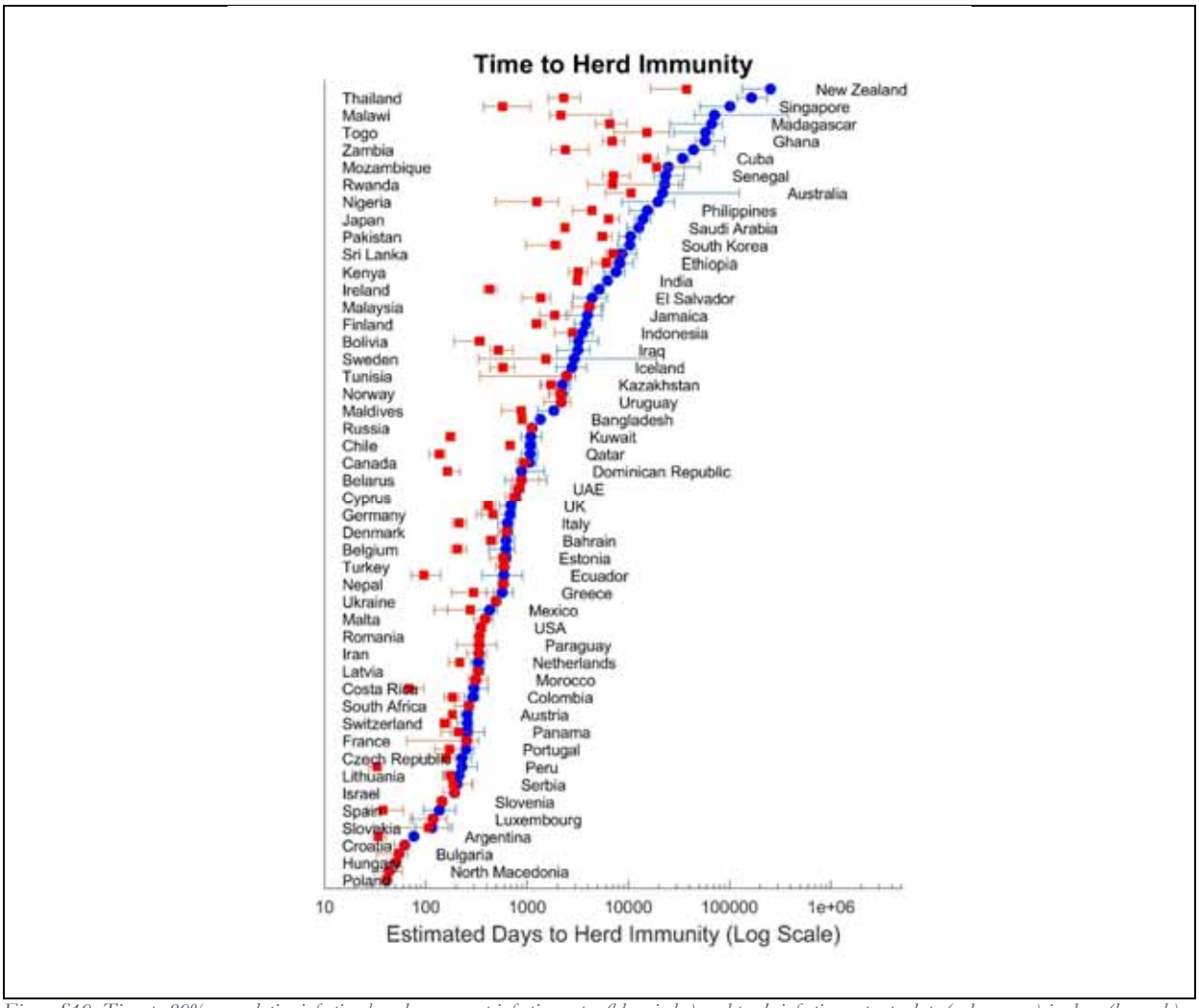
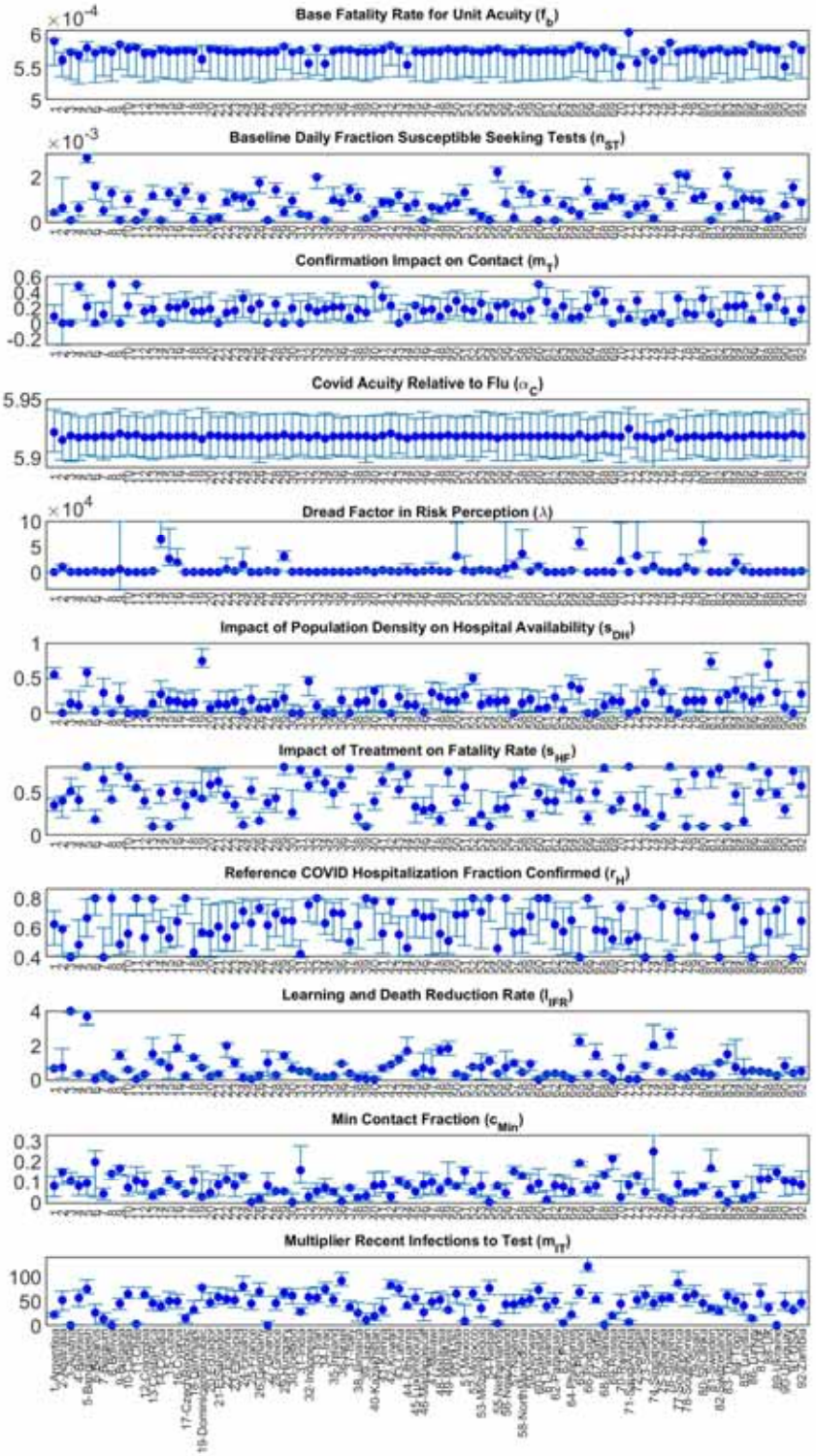


Figure S10- Time to 80% cumulative infection based on current infection rates (blue circles) and peak infection rates to-date (red squares) in days (log scale).

Parameter estimates

Figure S11 reports most likely estimates for the vector of country-specific parameters ($\boldsymbol{\theta_i}$). The figure also includes 95% credible intervals for these parameter estimates.



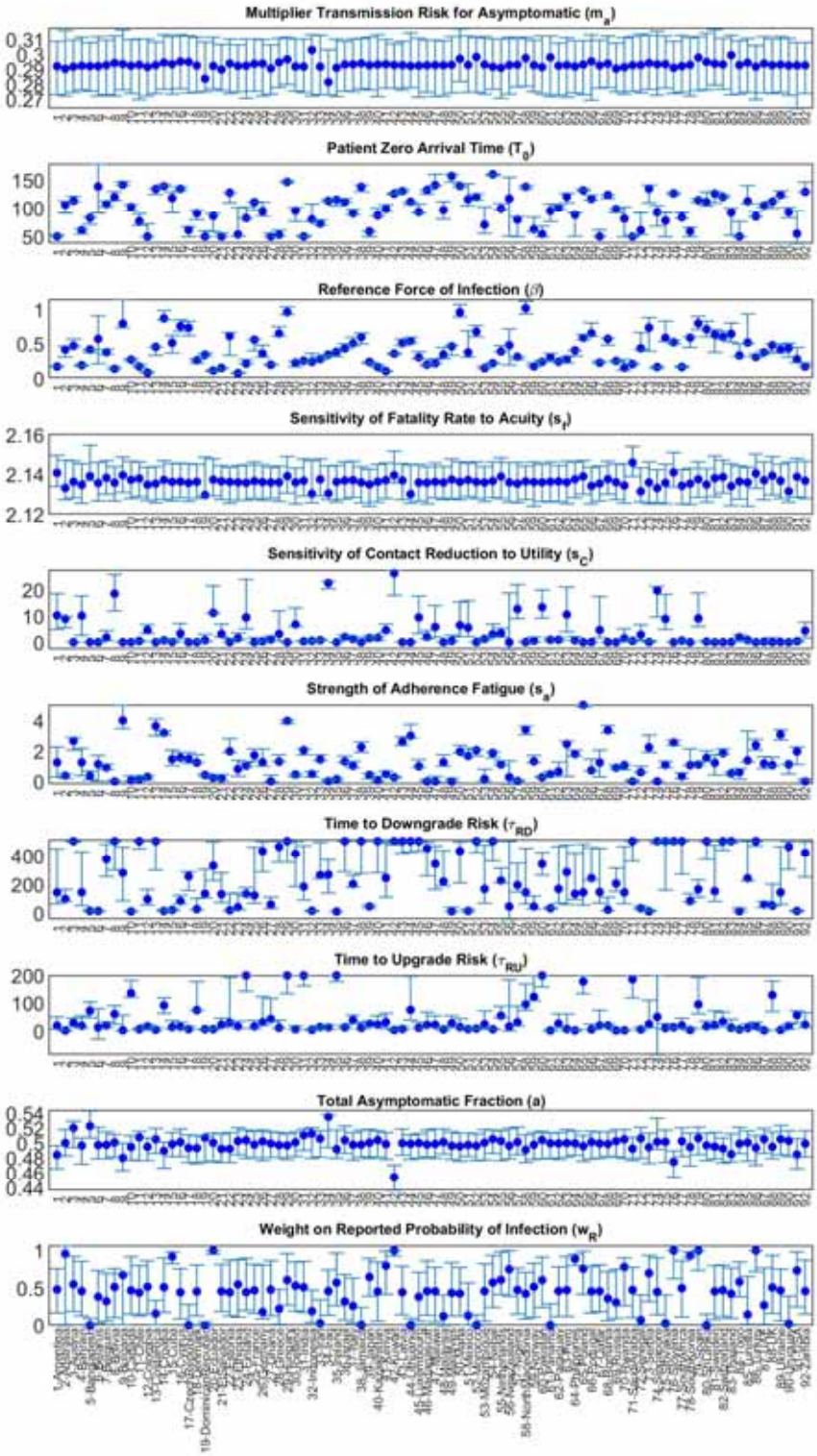


Figure S11- Parameter estimates and 95% credible regions for country-specific parameters.

Future projections

Figure S12 reports country-level projections for new cases and deaths based on the scenario I (no changes in estimated parameters; no vaccination; testing fixed at values observed for 22 December 2020; consistent with those reported in Figure 7 in the main paper).

In scenarios II and IV in the main paper (not shown here) we change responsiveness through:

- Increasing *Time to Downgrade Risk* (τ_{RD}) by 20%
- Shifting *Sensitivity of Contact Reduction to Utility* (s_C) by 20%.
- Increasing *Dread Factor in Risk Perception* (λ) by 20%.

Note that these changes primarily change contacts as a function of perceived risk, but do not necessarily entails fewer contacts overall. Vaccination scenario setups are discussed in vaccination sector (under S1).

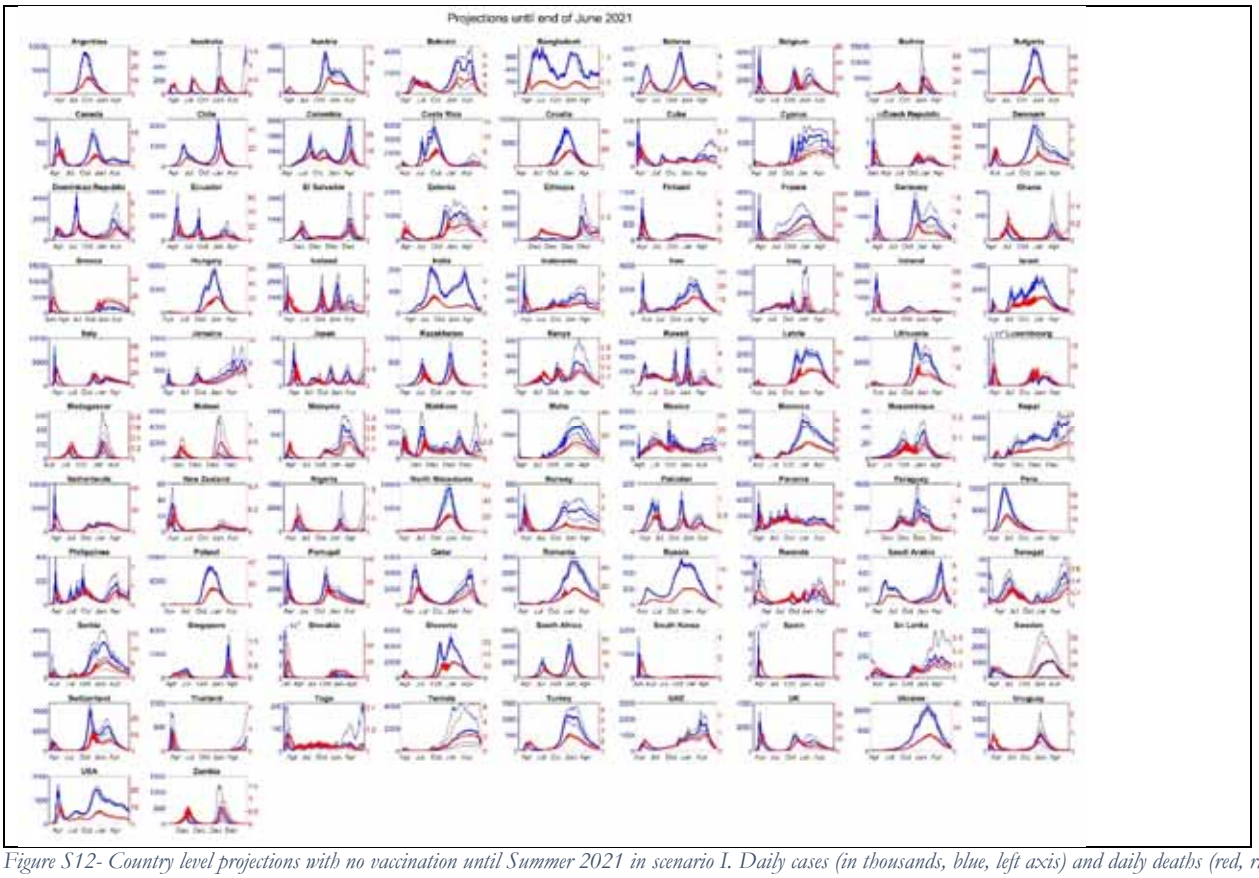


Figure S12- Country level projections with no vaccination until Summer 2021 in scenario I. Daily cases (in thousands, blue, left axis) and daily deaths (red, right axis) are graphed. For various vaccination projections see: https://exchange.iseesystems.com/public/mitsdl/covidglobal/index.html#page1

S6 OUT OF SAMPLE PREDICTION TEST

We conducted an out of sample prediction test of the model by comparing the quality of fit for model projections for future data not used in model estimation against the version of the model using that data. We calculate the quality of fit for projections of that model (the "early model") for data later released for the period 30 September 2020-22 December 2020. Those projections are reported in Figure S13 and are directly comparable with Figure S6. Note that we use the actual testing rates to drive the model for this prediction interval. Inspection of this graph points to various outcomes across countries, ranging from close fit for the prediction interval to a few with major discrepancies. For example, the model was able to predict the emergence of a second wave, before it was detectable in the infection data, for Belarus, Russia, and UK and the model predicted the third waves in Iran, Israel and USA well. On the other hand, among others, we overestimated the Fall trajectory of epidemic in India and under-estimated that in Turkey.

The discrepancies arise from both the baseline gaps between the model and data and emerging features of the epidemic in the prediction interval. The baseline gaps typically appear because our method enforces a strong coupling among countries. For instance, keeping IFR parameters similar across countries, the model cannot explain the unexpectedly low fatality rates in Qatar and Singapore (which could be due to outbreaks among younger immigrant worker communities). Moreover, the model is unable to accommodate changes in responses that are not detectable in the historical data (e.g. missing the magnitude of the "second wave" when first wave is not yet complete and thus the parameters for risk perception and response are not fully identifiable).

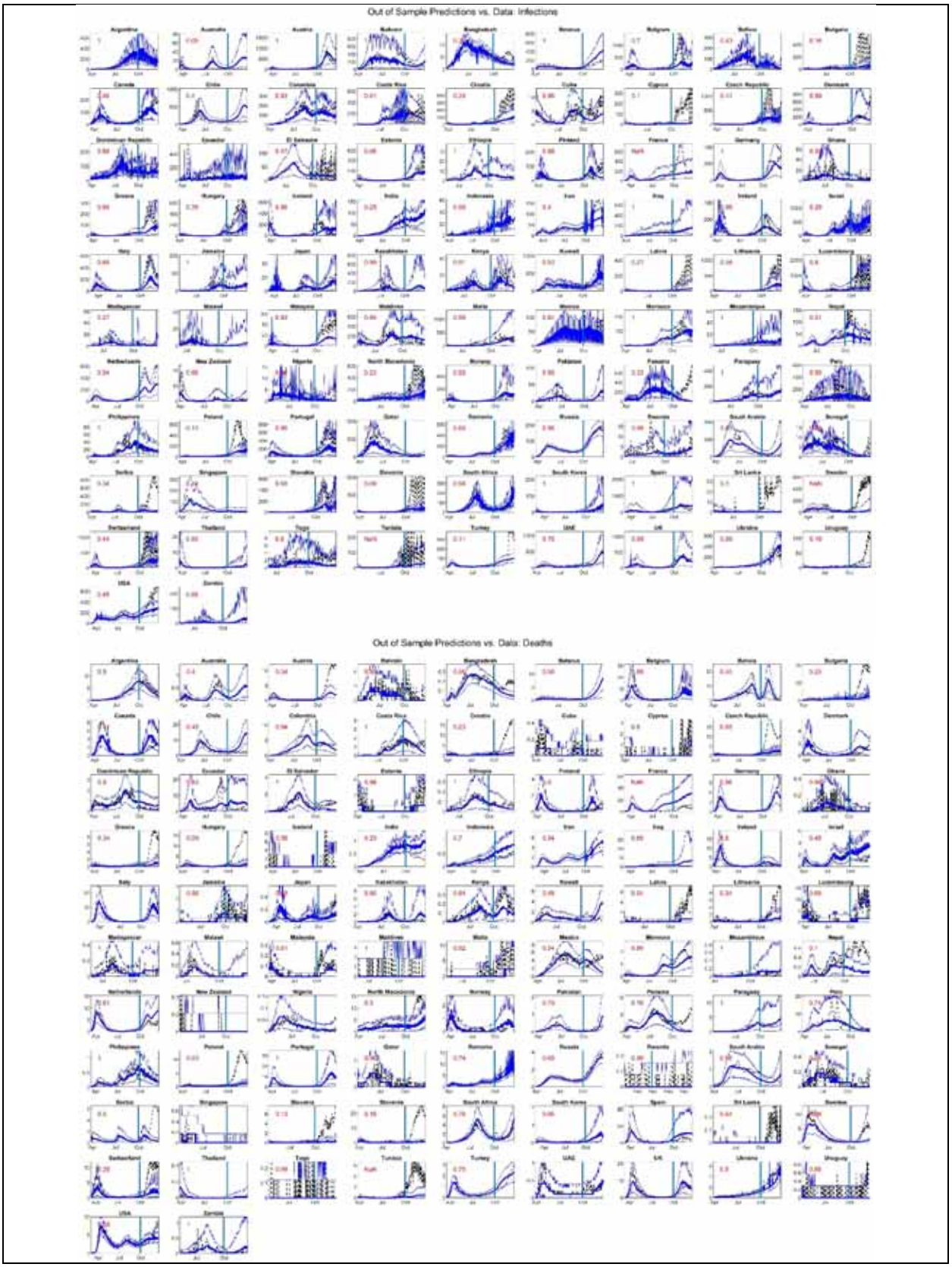


Figure S13-Predictions from the model fitted with data until 30 September 2020 for the 30 September 2020-22 December 2020 interval. The start of prediction interval is marked with a horizonal blue line. Red numbers represent the fraction of data falling within the 95% prediction intervals.

Assessing the quality of fit requires some benchmark to compare against. Defining external benchmarks in the case of current model is complicated because, to our knowledge, no other model has attempted to simultaneously match infection and fatality data across this large set of nations and offer future projections. Therefore, we focus on an internal benchmark using quality of fit for the version of the model using the data from the prediction interval for estimation. Specifically, we compare the fit measures from the early model (MAEN scores for reported infection rates and death rates) against the same fit measures coming from the model estimated until 22 December 2020. The updated version uses the data in the prediction interval and thus is likely to have a better fit than the early version of the model. The ratio of MAEN values between these two models informs the speed with which fit quality deteriorates, with values closer to one suggesting robust long-term predictions. Overall the mean fit ratio is 0.516, loosely speaking suggesting that projections lose their accuracy by about a half over 1.5 months. Table S4 reports those values across different nations.

Table S4- Quality of fit for future projections compared to when data is available. Mean Absolute Error Normalized by Mean (MAEN) for daily infection rates in the early model, current model (which uses data from prediction interval of 30 September 2020-22 December 2020), and the ratio of current model's MAEN to the early one.

Mean fit ratio: 0.516

Infection MAEN between days 352 and 431 for different countries:							
Country	**Current**	**Early**	**Ratio**	**Country**	**Current**	**Early**	**Ratio**
Argentina	0.249	0.411	0.606	Malawi	0.845	7.94	0.106
Australia	1.8	5.7	0.316	Malaysia	0.205	0.575	0.356
Austria	0.58	0.673	0.861	Maldives	0.55	2.04	0.269
Bahrain	0.523	0.708	0.739	Malta	0.346	0.686	0.504
Bangladesh	0.18	0.408	0.442	Mexico	0.42	0.594	0.707
Belarus	0.106	0.542	0.195	Morocco	0.258	0.395	0.653
Belgium	0.48	0.758	0.633	Mozambique	0.374	2.34	0.16
Bolivia	0.309	1.53	0.202	Nepal	0.34	0.524	0.649
Bulgaria	0.424	0.793	0.535	Netherlands	0.17	0.498	0.342
Canada	0.188	0.376	0.5	NewZealand	0.83	0.948	0.876
Chile	0.357	1.86	0.192	Nigeria	0.413	0.786	0.526
Colombia	0.188	0.421	0.445	NorthMacedonia	0.326	0.744	0.439
CostaRica	0.491	0.665	0.738	Norway	0.378	0.601	0.629
Croatia	0.295	0.688	0.429	Pakistan	0.304	0.841	0.361
Cuba	0.307	0.534	0.576	Panama	0.364	0.764	0.477
Cyprus	0.429	0.922	0.466	Paraguay	0.182	0.588	0.31
CzechRepublic	0.301	0.582	0.516	Peru	0.746	1.21	0.617
Denmark	0.3	0.823	0.365	Philippines	0.172	0.758	0.227
DominicanRepublic	0.369	0.475	0.776	Poland	0.271	0.508	0.534
Ecuador	0.457	0.926	0.494	Portugal	0.293	0.484	0.606
ElSalvador	0.979	0.925	1.06	Qatar	0.321	0.517	0.621

Estonia	0.292	0.622	0.471	Romania	0.363	0.364	0.998
Ethiopia	0.191	0.582	0.328	Russia	0.0383	0.133	0.289
Finland	0.322	0.597	0.54	Rwanda	0.491	0.669	0.734
France	0.614	0.689	0.891	SaudiArabia	0.631	0.839	0.752
Germany	0.233	0.501	0.466	Senegal	0.39	0.727	0.537
Ghana	0.833	1.04	0.8	Serbia	0.509	0.91	0.56
Greece	0.34	0.635	0.535	Singapore	0.554	4.04	0.137
Hungary	0.293	0.448	0.654	Slovakia	0.375	0.678	0.554
Iceland	0.401	1.08	0.373	Slovenia	0.412	0.621	0.663
India	0.147	1.02	0.145	SouthAfrica	0.227	0.347	0.655
Indonesia	0.194	0.373	0.521	SouthKorea	0.223	0.716	0.311
Iran	0.3	0.369	0.815	Spain	0.366	1.31	0.279
Iraq	0.155	1.12	0.139	SriLanka	0.313	0.968	0.323
Ireland	0.345	0.573	0.603	Sweden	0.936	0.932	1
Israel	1.23	1.54	0.798	Switzerland	0.535	0.847	0.632
Italy	0.26	0.512	0.508	Thailand	0.703	3.87	0.182
Jamaica	0.256	1.12	0.229	Togo	0.422	0.661	0.639
Japan	0.231	0.624	0.37	Tunisia	0.871	0.852	1.02
Kazakhstan	0.459	1.98	0.232	Turkey	0.729	0.89	0.819
Kenya	0.368	0.499	0.737	UAE	0.438	1.19	0.368
Kuwait	0.36	1.27	0.283	UK	0.274	0.509	0.539
Latvia	0.279	0.82	0.34	Ukraine	0.231	0.296	0.781
Lithuania	0.357	0.542	0.659	Uruguay	0.24	0.821	0.293
Luxembourg	0.687	0.798	0.86	USA	0.248	0.413	0.6
Madagascar	1.85	5.07	0.365	Zambia	0.547	6.18	0.0885

S7 SENSITIVITY ANALYSIS

Impact of Cross-country Parameter Variances

Setup- Our estimation method uses a random effects framework, which couples the parameters across different countries, specifying them as instances of some underlying distribution with a given variance. Those variance factors, explained in S2, were specified to incorporate the authors' judgement on how different each parameter may be across different countries, based on the nature of those parameters. For instance, parameters representing physiological or virological constructs should generally vary less than those representing socio-cultural and behavioral responses. In principle, one could propose other variance factors. Assuming very large variances would essentially decouple the models for different countries, while shrinking variances towards zero will force all parameters to be the same across countries. In this section we assess the sensitivity of results to changes in those variance factors. Specifically, we re-do the analysis when all variance factors are scaled by a factor of 4, or 0.25. We re-estimate the model in each case and measure how much the following 12 outcome measures (organized into 3 groups) change compared to the baseline estimates as a result:

a) Country level projections for 1) Actual to reported case ratio; 2) Actual to reported death ratio; 3) Projected infection rate at the end of Winter 2021; 4) Projected death rate at the end of winter 2021;
b) Country level MAEN values for daily infection rates and death rates;
c) Aggregate (across all countries) cumulative infections, deaths, and IFR, both on 22 December 2020 and at the end of June 2021.

The first two groups of measures are country specific, so we report them for all countries, followed by their averages, and then the aggregate outcomes.

Results- In Table S5 and Table S6 results from these two experiments are reported. As expected, increasing allowed variances enables the model to offer a better fit to data (i.e. reduces MAEN values, thus mostly negative values for fit statistics in the first experiment). Other sensitivities remain relatively small for most countries, showing few systematic changes in model's predictions as in response to changes in the cross-country parameter variances. However, trajectories for a handful of countries are sensitive to these variance factors: Australia, Bolivia, Bulgaria, Costa Rica, Croatia, El Salvador, Ghana, Hungry, Iraq, Maldives, Mozambique, New Zealand, North Macedonia, Paraguay, Poland, Portugal, Qatar, Rwanda, Singapore, Slovakia, Thailand, Togo. In these cases one would expect a separate country-specific estimation to give results that may be qualitatively different from those we find, and thus caution should be exercised.

Table S5- Impact of increasing assumed cross-country parameter variances by a factor of four. All reported outcomes measure percentage change in the given metric from baseline analysis.

Sensitivities to 4x change in variances						
Country	**Case Undercount Ratio**	**Death Undercount Ratio**	**Final Infection Rate**	**Final Death Rate**	**MAEN Infection**	**MAEN Death**
Argentina	-2.4	1.51	-27.8	-16.3	-0.598	-2.66
Australia	6.54	0.789	-50.3	-42	2.49	-1.59
Austria	2.63	0.651	-2.88	-1.32	2.45	-0.305
Bahrain	5.76	-0.985	-5.13	-10	-4.97	-0.321
Bangladesh	6.1	4.42	3.17	3.65	-1.54	-0.712
Belarus	-1.66	-3.49	-18.4	-37.2	-13	-16
Belgium	4.09	2.05	-13.9	-14.6	4.32	-6.1
Bolivia	5.57	4.14	19.1	9.16	-0.33	-0.893
Bulgaria	8.34	11.9	-66	-46.2	-3.14	-22.2
Canada	6.7	1.05	15	-4.68	-1.15	-3.25
Chile	0.313	0.54	-0.0162	0.796	1.16	0.591
Colombia	5.15	3.15	0.141	2.24	4.86	-1.09
CostaRica	-0.241	-0.176	-3.48	-4.25	0.194	-0.298
Croatia	-11.8	1.1	38.1	0.771	-7.22	-13
Cuba	7.23	6.38	87.6	-1.47	-1.66	0.218
Cyprus	-1.57	3.07	10.7	23.8	1.09	0.377
CzechRepublic	7.3	1.7	-1.66	-11.8	-4.06	-3.12
Denmark	-1.15	1.15	-7.63	-2.69	0.428	-2.93
DominicanRepublic	3.83	2.53	-3.73	-3.39	-3.87	1.22
Ecuador	-2.44	-0.457	0.773	6.77	-1.21	-0.779
ElSalvador	13.7	3.6	382	113	-3.69	-5.77
Estonia	-1.18	4.28	8.43	3.91	0.817	-0.0563
Ethiopia	18.4	8.4	19.4	34.8	-0.683	-4.19
Finland	2.53	-0.747	13.9	8.82	-9.07	-2.22
France	8.58	0.654	-21.3	-25.6	-3.83	-2.8
Germany	13	4.94	8.23	-1.72	-1.53	-6.32
Ghana	0.0961	-2.99	883	111	-1.21	-1.51
Greece	10.6	6.14	-6.19	-9.94	2.45	-4.32
Hungary	7.05	8.15	-15.8	-11.7	-6.2	-17.9
Iceland	2.05	0.375	-22.8	-9.36	-1.8	0.348
India	-1.16	0.507	-5.71	-2.22	-0.93	-1.02
Indonesia	10	1.42	33.7	1.88	-0.47	-3.17
Iran	6.56	1.76	-7.62	-13.2	-0.223	0.033
Iraq	-0.25	-0.115	-78.7	20	-0.507	-0.305
Ireland	7	6.63	89.5	43.8	2.51	-11.6
Israel	9.8	3.51	-26.9	-26.5	-7.7	-0.895
Italy	5.97	-0.44	-1.51	-8.66	-6.67	-8.15
Jamaica	3.13	0.218	-21.5	-14.6	-6.78	-0.978
Japan	-0.977	-1.84	8.04	-5.16	2.87	-0.776
Kazakhstan	-0.859	0.344	15.9	4.75	-0.22	-3.47
Kenya	-3.65	-0.158	-20.8	-5.16	-0.158	-2.52
Kuwait	2.05	3.51	-48.2	-45.2	-3.62	-0.351
Latvia	5.58	4.18	-7.61	-14.6	-4.86	-3.08
Lithuania	1.5	0.727	-3.58	2.33	0.646	-2.17
Luxembourg	5.02	3.85	7.44	-7.68	-1.84	-3.58
Madagascar	-9.76	-11.6	17.9	28.1	1.94	-0.36
Malawi	-4.34	-2.08	40.9	-14.7	-2.95	-9.22
Malaysia	10.3	-1.89	-1.39	0.931	-3.8	-3.55
Maldives	-2.84	5.95	6.46	18	-2.01	1.42
Malta	8.72	-0.132	-3.44	0.666	-8.25	-3.44
Mexico	8.31	-2.17	1.96	-15	-0.358	-1.11
Morocco	5.98	2.1	-5.88	-6.73	-0.46	-1.18
Mozambique	-20.1	-10.1	-65.2	-39.3	-3.78	-0.717

Nepal	5.87	4.08	4.76	-7.05	-2.08	-3.19
Netherlands	-0.153	3.17	-4.7	-15.2	-17.4	-3.14
NewZealand	2.52	-13.6	-24.4	-29.2	-5.02	-7.2
Nigeria	2.96	1.02	-27.6	-28.2	0.401	0.138
NorthMacedonia	2.42	3.39	-14.6	-3.5	-3.11	-3.8
Norway	1.6	1.58	-11	-9.97	0.0685	-2.2
Pakistan	14.8	3.45	18.9	-0.586	0.482	-5.33
Panama	1.36	0.608	8.6	5.81	-1.02	-2.92
Paraguay	28.4	3.56	-45.4	-63.6	1.4	-2.88
Peru	-0.539	-1.06	27.7	30	0.736	0.308
Philippines	-1.03	-0.0881	24.5	30	-0.0283	-1.88
Poland	3.48	9.08	-20.9	-21.4	3.81	-15.6
Portugal	24.3	-0.662	-49.4	-66.7	2	-29.3
Qatar	0.149	3.89	-50.7	-32.9	-9.35	3.78
Romania	0.458	0.485	5.1	3.72	1.87	-2.34
Russia	-0.149	0.186	-7.83	-6.79	-3.05	-0.208
Rwanda	4.32	-0.00907	-34.6	-29.5	-0.834	-0.494
SaudiArabia	-6.25	4.24	-4.14	4.87	-3.88	2.26
Senegal	2.66	1.03	5.4	2.5	-1.32	-0.238
Serbia	17.9	7.21	-29	-20.5	2.59	-4.21
Singapore	13.1	6.47	344	167	-39.2	-8.7
Slovakia	9.65	0.864	-44.2	-50.3	-0.368	-3.87
Slovenia	1.57	8.69	-4.1	7.36	-3.13	-4.98
SouthAfrica	11.9	3	-14.8	-11.3	1.34	-6.72
SouthKorea	25.2	3.89	-12.8	-13.9	-2.6	-5.92
Spain	3.52	0.503	-9.22	1.67	-4.95	-2.09
SriLanka	8.71	9.87	21	18.5	-2.96	-1.03
Sweden	-5.71	0.964	12.3	12.9	1.56	2.37
Switzerland	-4.17	2.43	-0.919	5.64	0.00177	-3.64
Thailand	17.8	-2.4	100	131	-30.5	-40.4
Togo	-8.88	-4.63	189	-32.9	-3.3	-0.166
Tunisia	40.9	21.2	72.7	18.8	-3	-1.88
Turkey	3.9	-5.47	-6.91	-42.2	0.335	-5.23
UAE	3.35	0.36	-25.6	-31.4	-17.4	-10
UK	-0.541	2.77	4.79	-1.36	-4.06	-14.8
Ukraine	1.53	0.371	-3.97	-19	-1.38	-1.23
Uruguay	0.629	0.0577	-10.4	-1.42	0.927	-0.185
USA	-1.65	1.15	-2.69	0.315	-6.02	-0.526
Average	**4.31**	**1.78**	**16.9**	**-1.49**	**-2.7**	**-3.98**
Global Percentage Changes and Elasticities						
	Cases Early	**Deaths Early**	**IFR Early**	**Cases Proj.**	**Deaths Proj.**	**IFR Proj.**
Global	3.31	0.892	-2.14	3.55	-0.917	-4.41

Table S6- Impact of decreasing assumed cross-country parameter variances by a factor of four. All reported outcomes measure percentage change in the given metric from baseline analysis.

Sensitivities to 0.25x change in variances						
Country	**Case Undercount Ratio**	**Death Undercount Ratio**	**Final Infection Rate**	**Final Death Rate**	**MAEN Infection**	**MAEN Death**
Argentina	0.0032	-1.36	81	72.6	0.919	-0.0141
Australia	3.01	-2.07	62	40.5	-0.812	1.58
Austria	-4.18	-4.18	17.4	4.89	-2.17	4.15
Bahrain	-4.72	-1.82	7.7	9.64	3.71	-0.432
Bangladesh	-8.91	-3.49	-4.02	-4.68	19.4	12.1

Belarus	0.182	5.85	14.4	13.5	0.671	15.2
Belgium	-2.66	-5.38	13.8	5.09	-5.81	7.07
Bolivia	-5.01	-1.56	-52	-26	-1.35	7.59
Bulgaria	-7.48	-12.2	404	73.1	4.82	32.5
Canada	-8.34	-2.11	-5.7	15.1	-0.343	19.7
Chile	0.638	-1.1	-3	-2.84	-0.304	-0.582
Colombia	-7.24	-3.38	-1.81	-4.02	-6.18	0.364
CostaRica	-8.21	-5.22	54.9	208	-0.475	-3.69
Croatia	2.38	-2.77	-65.2	-55.4	4.45	14
Cuba	-9.97	2.21	11.2	29.2	5.01	5.26
Cyprus	3.52	-3.83	7.45	-4.84	-1.31	-0.502
CzechRepublic	-2.58	1.85	-2.27	8.77	12.3	3.07
Denmark	1.45	-1.47	6.75	4.58	0.531	7.28
DominicanRepublic	2.59	2.72	-5.52	-7.23	10.3	5.39
Ecuador	5.13	2.67	-32.5	-31.4	1.85	1.56
ElSalvador	4.71	-0.495	26.8	12.6	8.22	4.38
Estonia	4.31	-5.45	19.2	-0.147	0.186	1.23
Ethiopia	-10.6	-3.01	-23.4	-23	1.95	7.59
Finland	-2.05	5	6.41	14.1	14.4	7.5
France	-12.6	-13.3	28	23.1	-2.97	-18.3
Germany	-7.69	-4.65	-5.2	-0.402	-0.297	3.5
Ghana	47.1	35.7	-58.8	-39.9	-7.31	13.7
Greece	-6.14	-1.51	4.37	9.37	-4	9.83
Hungary	-12.8	-14.1	145	54.5	6.25	48.9
Iceland	-2.75	5.01	55.8	43.6	1.76	2.24
India	2.68	-0.794	-0.0667	0.299	5.87	1.84
Indonesia	9.53	10.9	-12.6	0.469	3.93	4.27
Iran	-12.2	-1.77	18.2	40.9	4.42	2.03
Iraq	-1.54	0.124	1280	220	0.0163	1.18
Ireland	-8.19	-4.05	-14.3	-8.38	-1.83	9.61
Israel	-2.57	-2.86	17.4	14.6	11.2	1.71
Italy	-5.05	0.128	0.804	6.79	4.64	7.65
Jamaica	-7.29	-3.05	26.5	-25.2	14.1	5.11
Japan	2.06	5.34	27.5	11.5	-7.99	1.91
Kazakhstan	2.14	1.06	-43.5	-36.2	1.14	7.05
Kenya	-2.51	-4.49	24	9.31	0.0898	3.43
Kuwait	-3	-7.44	-51.5	-43.3	10.6	3.69
Latvia	-2.96	-6.57	29.7	7.88	17.5	5.12
Lithuania	-1.68	-4.73	8.72	-6.46	-1.22	8.81
Luxembourg	-2.47	-1.47	2.31	13.5	1.9	5.21
Madagascar	1.74	15.6	-55.9	-37.2	2.21	6.21
Malawi	-4.68	3.35	-19.4	3.6	-1.32	6.77
Malaysia	-6.36	8.01	-31.9	-28.8	6.76	6.84
Maldives	12.5	-5.48	191	-2.97	8.62	-0.978
Malta	-0.808	-2.83	0.0203	-18	15.9	4.25
Mexico	4.45	12	3.91	17.3	-2.08	6.14
Morocco	-15.1	1.06	12	5.07	0.934	5.96
Mozambique	0.515	13.9	103	117	0.995	6.68
Nepal	-6.76	-0.677	-0.023	-1.49	5.02	11.9
Netherlands	-2.32	-2.01	-3.84	-1.02	7	8.4
NewZealand	-7.31	24.3	269	73.5	7.28	13.6
Nigeria	4.01	0.931	-1.94	33.3	-0.171	-1.5
NorthMacedonia	-18.1	-3.59	241	162	4.72	6.86
Norway	-3.18	-2.46	9.2	19.1	-0.327	2.96
Pakistan	-7.15	-4.5	-19	-2.03	9.23	9.83
Panama	2.54	5.11	-8.52	-6.08	4.57	12
Paraguay	-7.1	-0.318	21.3	38	-1.29	2.99
Peru	0.943	2.62	-40.2	-38.6	0.246	2.4
Philippines	13.4	2.05	70.1	54.9	4.43	6.87
Poland	-13.9	-12.8	212	138	2.88	32.8

Portugal	-15	-2.65	19.5	49.1	-9.08	11.8
Qatar	-8.86	-7.39	-13.9	-18	1.52	-2.18
Romania	-2.37	-0.667	-13.2	-1.71	-3.38	6.69
Russia	0.622	-0.501	16.1	15.4	14.3	1.72
Rwanda	-11.1	0.649	144	111	9.8	2.37
SaudiArabia	2.87	-2.52	-26	-8.98	-5.29	5.63
Senegal	-4.36	-3.47	-4.1	-6.93	0.538	0.731
Serbia	-8.06	-4.08	8.66	18.4	1.51	6.16
Singapore	12	24.9	-91.6	-72.7	24.4	24.5
Slovakia	-12.2	2.86	84.1	129	0.854	7.3
Slovenia	-7.98	-9.61	43.6	13.8	0.709	6.76
SouthAfrica	-13.6	-2.55	-6.48	2.99	-3.25	17.9
SouthKorea	-20	-5.71	9.12	27.1	4.94	9.99
Spain	11.4	1.46	-38.8	-47.9	18.8	9.43
SriLanka	-11.5	0.297	-10.1	-29.5	2.93	5.82
Sweden	9.33	-8.45	-21.5	-33	-2.01	3.42
Switzerland	1.58	-6.69	3.85	-16.2	0.784	11.8
Thailand	10.6	9.39	-1.08	71.8	49.9	38.5
Togo	-11.3	-9	463	-28.9	6.87	-0.477
Tunisia	-12.2	6.43	58.7	-2.13	0.903	-0.345
Turkey	-1.71	-1.53	-4.86	-2.57	1.65	6.99
UAE	5.22	1.05	16.4	12.7	18.1	-1.96
UK	-10.6	-4.67	10.4	24.9	-11.3	23.7
Ukraine	-0.855	-0.811	-1.31	11.8	1.05	1.14
Uruguay	-0.885	0.233	2.91	7.16	-0.93	-0.215
USA	1.52	-0.786	-4.56	-3.82	9.35	2.71
Average	**-2.54**	**-0.301**	**39.1**	**15.1**	**3.69**	**6.87**
Global Percentage Changes and Elasticities						
	Cases Early	**Deaths Early**	**IFR Early**	**Cases Proj.**	**Deaths Proj.**	**IFR Proj.**
Global	-1.83	-1.02	0.318	-1.57	0.275	2.07

Sensitivity to Parametric Assumptions

Setup- We conducted sensitivity analysis changing all the major pre-specified (i.e. not estimated) model parameters to assess 1) How sensitive key results are to those parametric assumptions. 2) How overall model fit to data changes with changing those general parameters. In this analysis we changed each parameter by +/- 5%, and calculated the elasticities of the 12 outcome measures discussed in the previous section with respect to each parameter. Those elasticities are calculated as fractional change in the outcome measure divided by fractional change in the input parameter. As such, they are dimensionless, with values below one indicating minor to modest sensitivities.

Table S7 reports the parameters over which we conducted the sensitivity analysis, their base values, and an overview of the results where averages over country-level outcomes and fit measures are reported (first row) along with aggregate outcomes (second row; for a total of 12 outcomes per parameter in two rows). We report full country-level sensitivity results for the reported outcomes online, in the GitHub repository for the research. All reported numbers are elasticity values.

Results- Overall elasticities remain modest (Table S7) but also include more notable cases where results for a specific country are rather sensitive to one parameter or the other. Note that the mechanisms generating these elasticities are complex, as they emerge from new calibration of the

model and thus incorporate various compensatory mechanisms and feedback effects. Thus we do not attempt to explain detailed country-level elasticities (reported on GitHub). With that caveat in mind, we provide an overview of the results here and tables on GitHub provide more in-depth outcomes.

The average residence time in hospitals has an impact on death rates and IFR, as increasing the residence time reduces available beds and exacerbates hospital shortages but also increased disease period in hosptial allows for more infection inside hospitals (note that in the sensitivity analysis the change in hospital residence time is not coupled with changing the disease duration outside of hospital). Increasing incubation period may modestly increase death under-count ratio and projected death rates, but slightly reduce projected infection rates; results for infection and death numbers are sensitive for a few countries due to shifts in overall parameters as a result of changing incubation period. Impact of Onset-to-detection delay is somewhat similar. Post-detection resolution time slightly increases cases and deaths as people spend more time in infectious states. Relative risk of transmission by presymptomatics would increase undercounts, infections and deaths, with a stronger impact on case under-count (thus reducing IFR). Increasing this parameter would also slightly increase the gap between the model and case data (MAEN). Finally, increasing the sensitivity of COVID test would reduce undercounts in cases and deaths and thus bring down total cases and deaths by stronger behavioral responses.

Table S7- Overview of parametric sensitivity results, reported as ***elasticities (fractional change in outcome divided by fractional change in input parameter)****. Each parameter is followed by its base value, and two rows of outcomes identified on the top. First row includes averages of elasticities for 4 outcomes and 2 fit measures across 92 countries. Second row includes elasticity measures calculated over all simulated populations on 22 December 2020 and 30 June 2021.*

Parameter	**Ave Case Undercount Ratio**	**Ave Death Undercount Ratio**	**Ave 6/30/21 Infection Rate**	**Ave 6/30/21 Death Rate**	**Ave MAEN Infection Rate**	**Ave MAEN Death Rate**
	Dec 22 Cml. Cases	**Dec 22 Cml. Deaths**	**Historical IFR**	**6/30/21 Cml. Cases**	**6/30/21 Cml. Deaths**	**6/30/21 Cml. IFR**
Hospitalized Resolution Time (20 days)	-0.00889	0.0105	0.355	0.501	-0.00379	0.0116
	0.0173	-0.0227	-0.0456	-0.0574	-0.0684	-0.0163
Incubation Period (5 days)	0.142	0.00899	0.0789	0.192	0.0117	-0.0163
	0.231	0.105	-0.104	0.207	0.141	-0.0688
Onset to Detection Delay (5 days)	0.12	0.0298	0.135	0.219	0.00522	-0.0257
	0.169	0.0254	-0.117	0.182	0.0836	-0.1
Post-Detection Phase Resolution Time (10 days)	0.000354	-0.0037	0.00163	0.0044	-0.0002	0.00281
	-0.0069	-0.00299	0.00388	-0.00112	0.00556	0.00741
Relative Risk of Transmission by Presymptomatic (1)	0.259	-0.00558	-0.398	-0.558	0.0125	0.0334
	0.19	0.0162	-0.189	0.12	-0.043	-0.175
Sensitivity of COVID Test (0.7)	-0.421	-0.509	-0.183	-0.398	0.0395	-0.0364
	-0.287	-0.51	-0.241	-0.316	-0.488	-0.159

Country level outcome elasticities for model parameters

See the online Github repository at https://github.com/tseyanglim/CovidGlobal for country-level outcome tables.

Sensitivity of results to exclusion of major countries

We repeated the analysis in three additional setups, excluding the top five countries by population (India, USA, Indonesia, Pakistan, Nigeria), by true infections to date (USA, Mexico, Iran, Peru, Indonesia), and by reported infections to date (USA, Russia, India, UK, Spain) from the estimation and analysis. These analyses inform the sensitivity of overall findings to data from specific countries.

In each case we report the *percentage* of change in the country level and aggregate outcome measures (those defined and discussed above). Table S*8* summarizes the results; full country-level outcome tables are available on the online Github repository at https://github.com/tseyanglim/CovidGlobal.

Results- Overall, the impact of excluding the top countries from analysis on historical fit and outcome measures is modest: fit quality does not change by more than 1.2% in 95% of country-outcome combinations. Moreover, the historical under-reporting ratios remain largely unchanged (changing by no more than 1.3% overall for 95% of country-outcome combinations). Cases and deaths summed up over the sample naturally change when excluding the larger countries or those with more infections (the bottom rows for each analysis). Long-term country level projections (items 3 and 4 in odd rows) change little (less than 2%) for most countries, however, a few show notable variations, suggesting high sensitivity to their response functions such that minor changes in parameters (which change due to the coupling with other nations) could significantly alter future projected outcomes. Those

countries with significant sensitivity include: Australia, Cuba, El Salvador, Iceland, Kuwait, New Zealand, and Togo.

Table S8-Sensitivity of outcomes (in percentage change from baseline) to exclusion of top five countries by true infection, population, and reported infection. Each analysis is specified by the removed countries and followed by two rows of outcomes identified on the top. First row includes averages of 4 outcomes and 2 fit measures across 92 countries. Second row includes measures calculated over all simulated populations on 22 December 2020 and 30 June 2021.

Removed Countries	**Ave Case Undercount Ratio**	**Ave Death Undercount Ratio**	**Ave 6/30/21 Infection Rate**	**Ave 6/30/21 Death Rate**	**Ave MAEN Infection Rate**	**Ave MAEN Death Rate**
	Dec 22 Cml. Cases	**Dec 22 Cml. Deaths**	**Historical IFR**	**6/30/21 Cml. Cases**	**6/30/21 Cml. Deaths**	**6/30/21 Cml. IFR**
Top True Infections: USA, Mexico, Iran, Peru, Indonesia	-0.011	0.0164	0.0743	-0.117	-0.0969	0.0701
	-33.5	-38.2	-5.94	-32.4	-35.2	-4.43
Top Populations: India, USA, Indonesia, Pakistan, Nigeria	-0.0178	0.00581	0.0606	0.0535	-0.0374	0.0373
	-22.8	-27.9	-6.95	-24.8	-25.9	-1.96
Top Reported Infections: USA, Russia, India, UK, Spain	0.183	0.0948	0.19	0.0557	0.0315	-0.176
	-28.4	-34.9	-9.4	-27.5	-32	-5.91

S8 ONLINE SIMULATOR

We have developed an online simulator that uses the model documented in this paper and provides users the option to project the burden of the disease in the coming months under various scenarios. This simulator can be found at:

https://exchange.iseesystems.com/public/mitsdl/covidglobal/index.html#page1

The underlying model is the same as the one in this paper. Moreover, we regularly attempt to update the simulator by calibrating the model to new data across the globe, including incoming vaccination data, so that the projections are based on best available data to-date. Various versions of the model used in the online simulator, as well as any structural changes in the model should some occur in future, will be documented at: https://github.com/tseyanglim/CovidGlobal.

S9 COMPLETE MODEL DOCUMENTATION

Below we provide complete model equations and units. The model, in the .mdl format, which can be opened using the Vensim simulation software, or the free Vensim model reader) is available with this appendix as well, and online at https://github.com/tseyanglim/CovidGlobal. Most of the equations are self-explanatory. The "[…]" notation is used to subscript variables over a set of members. For example, the subscript "Rgn" is used to identify different countries. Therefore [Rgn] indicates that a variable is defined separately for each member of the set "Rgn". Other subscript ranges used in the equations are:

expnt: Used for numerically solving the probability of missing symptoms equation.

pdim: Used for setting policy levels for a few variables.

Priors: Used for implementing the random effects estimation components. Each estimated parameter is mapped into an element of this subscript to simplify vector-based calculations.

Series: The data series (Infection, Death, Recovery).

TstSts: The test status including those confirmed ('Tested') and those unconfirmed ('Notest').

Variables units are provided for most equations. Those missing units are ones subscripted over different variable types or using equations that (utilizing power or log functions) cannot have consistent units.

Complete equations and units

1) a[Rgn] = XIDZ (Potential Test Demand from Susceptible Population[Rgn] , Positive Candidates Interested in Testing Poisson Subset Adj[Rgn] , 1) Units: dmnl
2) AbsPrcErr[Rgn,Series] = if then else (DataIncluded[Rgn] = 0, :NA:, ZIDZ (abs (FlowResiduals[Rgn,Series]) , DataFlowOverTime[Rgn,Series])) Units: dmnl
3) AbsStd[Priors] = 0.2, 0.3, 0.1, 0.2, 0.0002, 0.2, 10, 0.03, 6, 0.1, 0.1, 0.1, 0.8, 0.1, 1e-05, 10, 0.01, 0.005, 0.01, 10, 10, 10, 0.01, 0.5, 0.5 Units: **undefined**
4) Active Test Rate[Rgn] = if then else (Time < New Testing Time , DataTestRate[Rgn] , External Test Rate[Rgn]) Units: Person/Day
5) ActiveAve[PriorEndoAve] = INITIAL(InputAve[PriorEndoAve] * (1 - SW EndoAve) + SW EndoAve * CalcAve[PriorEndoAve])
6) ActiveAve[PMT] = InputAve[PMT] Units: **undefined**
7) Activities Allowed by Government[Rgn] = 1 Units: dmnl [0,1,0.01]
8) Additional Asymptomatic Fraction Init[Rgn] = Additional Asymptomatic Relative to Symptomatic Init[Rgn] / (1 + Additional Asymptomatic Relative to Symptomatic Init[Rgn]) Units: dmnl
9) Additional Asymptomatic Post Detection[Rgn] = Weighted Infected Post Detection Gate[Rgn] * Additional Asymptomatic Relative to Symptomatic[Rgn] / (1 + Additional Asymptomatic Relative to Symptomatic[Rgn]) Units: Person
10) Additional Asymptomatic Relative to Symptomatic[Rgn] = ZIDZ (Total Asymptomatic Fraction Net[Rgn] - exp (- Covid Acuity[Rgn]) , 1 - Total Asymptomatic Fraction Net[Rgn]) Units: dmnl
11) Additional Asymptomatic Relative to Symptomatic Init[Rgn] = INITIAL(ZIDZ (Total Asymptomatic Fraction Init Net[Rgn] - exp (- Covid Acuity Relative to Flu Init Net[Rgn] * Flu Acuity) , 1 - Total Asymptomatic Fraction Init Net[Rgn])) Units: dmnl
12) Adherence Fatigue Time = 100 Units: Day
13) AdvCntrs[Rgn] = 1 Units: dmnl
14) All Recovery[Rgn] = Recovery of Confirmed[Rgn] + Recovery of Untested[Rgn] + sum (Hospital Discharges[Rgn,TstSts!]) Units: Person/Day

15) Allocated Fraction COVID Hospitalized[Rgn] = min (1, (- Expected Positive Poisson Covid Patients[Rgn] + Sqrt (Expected Positive Poisson Covid Patients[Rgn] ^ 2 + 4 * Effective Hospital Capacity[Rgn] * Effective Hospital Capacity[Rgn])) / (2 * Effective Hospital Capacity[Rgn])) Units: dmnl
16) Allocated Fration NonCOVID Hospitalized[Rgn] = SMOOTHI (Allocated Fraction COVID Hospitalized[Rgn] ^ 2, Hospital Adj T , 1) Units: dmnl
17) alp[Rgn,Infection] = min (maxAlp , ialp * alpR[Rgn])
18) alp[Rgn,Death] = min (1, dalp * alpR[Rgn])
19) alp[Rgn,Test] = min (1, talp * alpR[Rgn]) Units: dmnl
20) alpR[Rgn] = 1 Units: dmnl
21) AntiVaxxerFrac[Rgn] = 0 Units: dmnl
22) Area of Region[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 5) Units: Km*Km
23) Average Acuity Hospitalized[Rgn,Tested] = Average Acuity of Positively Tested[Rgn] * XIDZ ((1 - Probability of Missing Acuity Signal at Hospitals[Rgn,Tested] * Fraction Poisson not Hospitalized[Rgn,Tested] ^ 2) , 1 - Fraction Poisson not Hospitalized[Rgn,Tested] , 2 * Probability of Missing Acuity Signal at Hospitals[Rgn,Tested])
24) Average Acuity Hospitalized[Rgn,Notest] = ZIDZ (Average Acuity of Untested Poisson Subset[Rgn] * (1 - Probability of Missing Acuity Signal at Hospitals[Rgn,Notest] * Fraction Poisson not Hospitalized[Rgn,Notest] ^ 2) , 1 - Fraction Poisson not Hospitalized[Rgn,Notest]) Units: dmnl
25) Average Acuity in Susceptible[Rgn] = ZIDZ (Sympthoms in Susceptible[Rgn] , Susceptible[Rgn]) Units: dmnl
26) Average Acuity Not Hospitalized[Rgn,Notest] = ZIDZ (Average Acuity Not Hospitalized Poisson[Rgn,Notest] * Infectious not Tested or in Hospitals Poisson[Rgn] , "Infected Unconfirmed Post-Detection"[Rgn])
27) Average Acuity Not Hospitalized[Rgn,Tested] = Average Acuity Not Hospitalized Poisson[Rgn,Tested] Units: dmnl
28) Average Acuity Not Hospitalized Poisson[Rgn,Tested] = Max (0, Probability of Missing Acuity Signal at Hospitals[Rgn,Tested] * Average Acuity of Positively Tested[Rgn] * Fraction Poisson not Hospitalized[Rgn,Tested])
29) Average Acuity Not Hospitalized Poisson[Rgn,Notest] = Max (0, Probability of Missing Acuity Signal at Hospitals[Rgn,Notest] * Average Acuity of Untested Poisson Subset[Rgn] * Fraction Poisson not Hospitalized[Rgn,Notest]) Units: dmnl
30) Average Acuity of Positively Tested[Rgn] = Covid Acuity[Rgn] * XIDZ ((1 - Prob Missing Symptom[Rgn] * Fraction Interested not Tested[Rgn] ^ 2) , 1 - Fraction Interested not Tested[Rgn] , 2 * Prob Missing Symptom[Rgn]) Units: dmnl
31) Average Acuity of Untested Poisson Subset[Rgn] = ZIDZ (Poisson Subset Reaching Test Gate[Rgn] * Covid Acuity[Rgn] - Positive Tests of Infected[Rgn] * Average Acuity of Positively Tested[Rgn] , Poisson Subset Not Tested Passing Gate[Rgn]) Units: dmnl
32) b[Rgn] = ZIDZ (Testing on Living[Rgn] - Positive Candidates Interested in Testing Poisson Subset Adj[Rgn] - Potential Test Demand from Susceptible Population[Rgn] , Positive Candidates Interested in Testing Poisson Subset Adj[Rgn]) Units: dmnl
33) Base Fatality Rate for Unit Acuity[Rgn] = 0.0006 Units: dmnl
34) Base Fatality Rate for Unit Acuity Net[Rgn] = INITIAL(Base Fatality Rate for Unit Acuity[Rgn] * (1 - SW Gen[BsFtRt]) + SW Gen[BsFtRt] * InputAve[BsFtRt]) Units: dmnl [0,0.01]
35) BaseError = 5 Units: Person
36) Baseline Cumulative Cases for Learning = 0.005 Units: dmnl
37) Baseline Daily Fraction Susceptible Seeking Tests[Rgn] = 0.001 Units: 1/Day
38) Baseline Fatality Multiplier[Rgn] = INITIAL(Demographic Impact on Fatality Relative to China[Rgn] * Base Fatality Rate for Unit Acuity Net[Rgn] * Liver Disease Impact on Fatality[Rgn] * Obesity Impact on Fatality[Rgn] * Chronic Impact on Fatality[Rgn]) Units: dmnl [0,0.1]
39) Baseline Risk of Transmission by Asymptomatic[Rgn] = INITIAL(Baseline Transmission Multiplier for Untested Symptomatic * Multiplier Transmission Risk for Asymptomatic Net[Rgn]) Units: dmnl
40) Baseline Transmission Multiplier for Untested Symptomatic = 1 Units: dmnl
41) Bed per Square Kilometer[Rgn] = INITIAL(Nominal Hospital Capacity[Rgn] / Area of Region[Rgn]) Units: Person/(Km*Km)

42) Beds per Thousand Population[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 11) Units: dmnl
43) CalcAve[Priors] = INITIAL(sum (RegionalInputs[Priors,Rgn!]) / ELMCOUNT(Rgn)) Units: **undefined**
44) cft[Rgn,p2] = lnymix[Rgn,p2]
45) cft[Rgn,p3] = lnymix[Rgn,p3] - lnymix[Rgn,p2]
46) cft[Rgn,p4] = (ln (min (100, Max (1e-06, ZIDZ (lnymix[Rgn,p4] - lnymix[Rgn,p2] , lnymix[Rgn,p3] - lnymix[Rgn,p2]) / ln (2))))) Units: dmnl
47) Chng Cml Dth Untst Untrt[Rgn] = Deaths of Symptomatic Untested[Rgn] - Post Mortem Test Rate[Rgn] * Frac Post Mortem from Untreated[Rgn] Units: Person/Day
48) Chronic Death Rate[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 17) Units: dmnl
49) Chronic Impact on Fatality[Rgn] = INITIAL((Chronic Death Rate[Rgn] / MeanChronic) ^ Sens Chronic Impact Net[Rgn]) Units: dmnl
50) Cml Death Frac In Hosp[Rgn] = XIDZ (Cumulative Deaths at Hospital[Rgn,Tested] + Cumulative Deaths at Hospital[Rgn,Notest] , Cumulative Deaths[Rgn] , 1) Units: dmnl
51) Cml Death fraction in hospitals large enough = sum (if then else (Cml Death Frac In Hosp[Rgn!] < MinHspDTresh , 1, 0)) Units: dmnl
52) Cml Death Hsp Inc[Rgn,Tested] = Hospitalized Infectious Deaths[Rgn,Tested] + PostMortemCorrection[Rgn]
53) Cml Death Hsp Inc[Rgn,Notest] = Hospitalized Infectious Deaths[Rgn,Notest] - PostMortemCorrection[Rgn] Units: Person/Day
54) Cml Known Death Frac Hosp[Rgn] = XIDZ (Cumulative Deaths at Hospital[Rgn,Tested] , Cumulative Deaths[Rgn] , 1) Units: dmnl
55) CmltErrPW = 2 Units: dmnl
56) CmltPenaltyScl = 0 Units: dmnl
57) CmltToInclude[Series] = 0, 0, 0 Units: dmnl
58) Confirmation Impact on Contact[Rgn] = 0.002 Units: dmnl
59) Confirmed Recovered[Rgn] = INTEG(Recovery of Confirmed[Rgn] , 0) Units: Person
60) Constant Data File :IS: 'CovidModelInputs - ConstantData.vdf'
61) Contacts Relative to Normal[Rgn] = min (Voluntary Reduction in Contacts[Rgn] , Activities Allowed by Government[Rgn]) Units: dmnl
62) Continue without Testing[Rgn] = Reaching Testing Gate[Rgn] - Symptomatic Infected to Testing[Rgn] - Untested symptomatic Infected to Hospital[Rgn] Units: Person/Day
63) Count Missed Death[Rgn] = if then else (Excess Death Start Count[Rgn] = :NA:, 0, if then else (Time >= Excess Death Start Count[Rgn] :AND: Time <= Excess Death End Count[Rgn] , Cml Death Hsp Inc[Rgn,Notest] + Chng Cml Dth Untst Untrt[Rgn] , 0)) Units: Person/Day
64) Covid Acuity[Rgn] = Flu Acuity * Covid Acuity Relative to Flu Net[Rgn] Units: dmnl
65) Covid Acuity Relative to Flu[Rgn] = 6 Units: dmnl
66) Covid Acuity Relative to Flu Init Net[Rgn] = INITIAL(Covid Acuity Relative to Flu[Rgn] * (1 - SW Gen[Acty]) + SW Gen[Acty] * InputAve[Acty]) Units: dmnl
67) Covid Acuity Relative to Flu Net[Rgn] = Average Acuity in Susceptible[Rgn] / (1 - Additional Asymptomatic Fraction Init[Rgn]) Units: dmnl
68) Covid Poisson Fraction in Hospital[Rgn] = ZIDZ (Total Covid Hospitalized[Rgn] , Infectious not Tested or in Hospitals Poisson[Rgn] + Infectious Confirmed Not Hospitalized[Rgn] + Total Covid Hospitalized[Rgn]) Units: dmnl
69) CRW[Rgn] Units: dmnl
70) Cumulative Cases[Rgn] = INTEG(New Cases[Rgn] , 0) Units: Person
71) Cumulative Confirmed Cases[Rgn] = INTEG(SimFlowOverTime[Rgn,Infection] , 0) Units: Person
72) Cumulative Confirmed Recovered[Rgn] = Confirmed Recovered[Rgn] + Cumulative Recovered at Hospitals[Rgn,Tested] Units: Person
73) Cumulative Death Fraction[Rgn] = ZIDZ (Cumulative Deaths[Rgn] , Cumulative Deaths[Rgn] + Cumulative Recoveries[Rgn]) Units: dmnl
74) Cumulative Deaths[Rgn] = INTEG(Death Rate[Rgn] , 0) Units: Person

75) Cumulative Deaths at Hospital[Rgn,TstSts] = INTEG(Cml Death Hsp Inc[Rgn,TstSts] , 0) Units: Person
76) Cumulative Deaths of Confirmed[Rgn] = INTEG(SimFlowOverTime[Rgn,Death] , 0) Units: Person
77) Cumulative Deaths of Confirmed Untreated[Rgn] = INTEG(Deaths of Confirmed[Rgn] + Post Mortem Test Untreated[Rgn] , 0) Units: Person
78) Cumulative Deaths Untested Untreated[Rgn] = INTEG(Chng Cml Dth Untst Untrt[Rgn] , 0) Units: Person
79) Cumulative Fraction Total Cases Hospitalized[Rgn] = ZIDZ (sum (Cumulative Deaths at Hospital[Rgn,TstSts!] + Cumulative Recovered at Hospitals[Rgn,TstSts!] + Hospitalized Infectious[Rgn,TstSts!]) , Cumulative Cases[Rgn]) Units: dmnl
80) Cumulative Missed Death[Rgn] = INTEG(Count Missed Death[Rgn] , 0) Units: Person
81) Cumulative Negative Tests[Rgn] = INTEG(Negative Test Results[Rgn] , 0) Units: Person
82) Cumulative Recovered at Hospitals[Rgn,TstSts] = INTEG(Hospital Discharges[Rgn,TstSts] , 0) Units: Person
83) Cumulative Recoveries[Rgn] = INTEG(All Recovery[Rgn] , 0) Units: Person
84) Cumulative Tests Conducted[Rgn] = INTEG(SimTestRate[Rgn] , 0) Units: Person
85) Cumulative Tests Data[Rgn] = INTEG(TstInc[Rgn] , 0) Units: Person
86) Current Test Rate per Capita[Rgn] = INITIAL(if then else (DataLastTestRate[Rgn] = :NA:, 0, DataLastTestRate[Rgn] / Population[Rgn])) Units: 1/Day
87) dalp = 0.1 Units: dmnl
88) Data Excess Deaths[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 15) Units: Person
89) DataAttentionTime[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 9) Units: Day
90) DataCmltDeath[Rgn] Units: Person
91) DataCmltInfection[Rgn] Units: Person
92) DataCmltOverTime[Rgn,Infection] :RAW: := DataCmltInfection[Rgn]
93) DataCmltOverTime[Rgn,Death] :RAW: := DataCmltDeath[Rgn]
94) DataCmltOverTime[Rgn,Test] = DataCmltTest[Rgn] Units: Person
95) DataCmltTest[Rgn] Units: Person
96) DataFlowDeath[Rgn] Units: Person/Day
97) DataFlowInfection[Rgn] Units: Person/Day
98) DataFlowOverTime[Rgn,Infection] :RAW: := DataFlowInfection[Rgn]
99) DataFlowOverTime[Rgn,Death] :RAW: := DataFlowDeath[Rgn]
100) DataFlowOverTime[Rgn,Test] :RAW: := DataTestRate[Rgn] Units: Person/Day
101) DataFlowRecovery[Rgn] :RAW: Units: Person/Day
102) DataIncluded[Rgn] = if then else (Max (Cumulative Deaths[Rgn] , Max (Cumulative Confirmed Cases[Rgn] , DataCmltOverTime[Rgn,Infection])) > ThrsInc[Rgn] , 1, 0) * DataLimitFromTime[Rgn] Units: dmnl
103) DataLastTestRate[Rgn] = INITIAL(GET DATA AT TIME (DataTestRate[Rgn] , min (LastTestDate[Rgn] , New Testing Time))) Units: Person/Day
104) DataLimitFromTime[Rgn] = if then else (Time > StopDataUseTime[Rgn] , 0, 1) Units: dmnl
105) DataTestCapacity[Rgn] Units: Person/Day
106) DataTestRate[Rgn] Units: Person/Day
107) Day of First Case Report in JHU Database = 99 Units: Day
108) Days per Year = 365 Units: Day/Year
109) Death Rate[Rgn] = Deaths of Confirmed[Rgn] + Deaths of Symptomatic Untested[Rgn] + sum (Hospitalized Infectious Deaths[Rgn,TstSts!]) Units: Person/Day
110) DeathFractionCounted[Rgn] = if then else (DataCmltOverTime[Rgn,Death] = :NA:, 0, ZIDZ (DataCmltOverTime[Rgn,Death] , Cumulative Deaths[Rgn])) Units: dmnl
111) Deaths of Confirmed[Rgn] = Tested Untreated Resolution[Rgn] * Fatality Rate Untreated[Rgn,Tested] Units: Person/Day
112) Deaths of Symptomatic Untested[Rgn] = Infectious not Tested or in Hospitals Poisson[Rgn] / "Post-Detection Phase Resolution Time" * Fatality Rate Untreated[Rgn,Notest] Units: Person/Day
113) Delay Order = 1 Units: dmnl
114) Demographic Impact on Fatality Relative to China[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 12) Units: dmnl

115) Di[Rgn,Series] = DataFlowOverTime[Rgn,Series] Units: Person/Day
116) Different Infectious Counted[Rgn] = "Pre-Symptomatic Infected"[Rgn] + Infected pre Detection[Rgn] + (Additional Asymptomatic Post Detection[Rgn] + "Poisson Not-tested Asymptomatic"[Rgn]) + (Infectious not Tested or in Hospitals Poisson[Rgn] - "Poisson Not-tested Asymptomatic"[Rgn]) + Infectious Confirmed Not Hospitalized[Rgn] + sum (Hospitalized Infectious[Rgn,TstSts!]) Units: Person
117) Discount Rate Annual = 0.03 Units: 1/Year [1e-05,0.2]
118) Discount Rate per Day = INITIAL(Discount Rate Annual / Days per Year) Units: 1/Day
119) Dread Factor in Risk Perception[Rgn] = 25 Units: dmnl [0,10000]
120) Dread Factor in Risk Perception Net[Rgn] = if then else (Response Policy Time On < Time , (1 + Response Policy Weight) * Dread Factor in Risk Perception[Rgn] , Dread Factor in Risk Perception[Rgn]) * Impact of Adherence Fatigue[Rgn] Units: dmnl
121) Dread Factor Policy = 3000 Units: dmnl
122) Effective Hospital Capacity[Rgn] = Nominal Hospital Capacity[Rgn] * Normalized Hospital density[Rgn] ^ Impact of Population Density on Hospital Availability[Rgn] Units: Person
123) eps = 0.001 Units: Person/Day
124) Excess Death End Count[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 14) Units: Day
125) Excess Death Mean Frac = 0.9 Units: dmnl
126) Excess Death Range Frac = 0.2 Units: dmnl
127) Excess Death Rate Error[Rgn] = if then else (Data Excess Deaths[Rgn] < 50, 0, ZIDZ (Cumulative Missed Death[Rgn] - Excess Death Mean Frac * Data Excess Deaths[Rgn] , Excess Death Range Frac * Data Excess Deaths[Rgn]) ^ 4) Units: dmnl
128) Excess Death Start Count[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 13) Units: Day
129) Expected Positive Poisson Covid Patients[Rgn] = sum (Potential Hospital Demand[Rgn,TstSts!]) * "Post-Detection Phase Resolution Time" Units: Person
130) expnt : (p2-p4)
131) External Test Rate[Rgn] = Population[Rgn] * Policy Test Rate[Rgn] Units: Person/Day
132) Extrapolated Estimator[Rgn] = if then else (Covid Acuity Relative to Flu Net[Rgn] > 1, cft[Rgn,p2] + cft[Rgn,p3] * (Covid Acuity Relative to Flu Net[Rgn] - 1) ^ cft[Rgn,p4] , lnymix[Rgn,p2]) Units: dmnl
133) Fatality Rate Treated[Rgn,TstSts] = min (1, Baseline Fatality Multiplier[Rgn] * TimeVar Impact of Treatment on Fatality[Rgn] * Average Acuity Hospitalized[Rgn,TstSts] ^ Sensitivity of Fatality Rate to Acuity Net[Rgn]) Units: dmnl
134) Fatality Rate Untreated[Rgn,TstSts] = min (1, Baseline Fatality Multiplier[Rgn] * Average Acuity Not Hospitalized Poisson[Rgn,TstSts] ^ Sensitivity of Fatality Rate to Acuity Net[Rgn] * Time variant change in fatality[Rgn]) Units: dmnl
135) Final Test Rate Per Capita[Rgn] = INITIAL(Current Test Rate per Capita[Rgn] + Weight Max in Test Goal * Max (0, (Max Test Rate per Capita - Current Test Rate per Capita[Rgn]))) Units: 1/Day
136) FINAL TIME = 444 Units: Day [50,182,1]
137) FlowResiduals[Rgn,Series] = if then else (DataFlowOverTime[Rgn,Series] = :NA:, :NA:, DataFlowOverTime[Rgn,Series] - MeanFlowOverTime[Rgn,Series]) Units: Person/Day
138) FlowToInclude[Series] = 1, 1, 0 Units: dmnl
139) Flu Acuity = 1 Units: dmnl
140) Flu Acuity Relative to Covid[Rgn] = Flu Acuity / Covid Acuity[Rgn] Units: dmnl
141) Frac Post Mortem from Untreated[Rgn] = SMOOTHI (ZIDZ (Deaths of Symptomatic Untested[Rgn] , Deaths of Symptomatic Untested[Rgn] + Hospitalized Infectious Deaths[Rgn,Notest]) , Post Mortem Test Delay , 1) Units: dmnl
142) frac rampup = 0.5 Units: dmnl
143) FracNotVaccinated Susceptible[Rgn] = Susceptible[Rgn] / (Initial Population[Rgn] - Vaccinated[Rgn]) Units: dmnl
144) FracThresh = 0.001 Units: dmnl
145) Fraction Covid Death In Hospitals Previously Tested[Rgn] = ZIDZ (Hospitalized Infectious Deaths[Rgn,Tested] , sum (Hospitalized Infectious Deaths[Rgn,TstSts!])) Units: dmnl

146) Fraction Covid Hospitalized Positively Tested[Rgn] = ZIDZ (Hospitalized Infectious[Rgn,Tested] , Total Covid Hospitalized[Rgn]) Units: dmnl
147) Fraction Infected[Rgn] = Cumulative Cases[Rgn] / Initial Population[Rgn] Units: dmnl
148) Fraction Interested not Tested[Rgn] = 1 - ZIDZ (Total Test on Covid Patients[Rgn] , Positive Candidates Interested in Testing Poisson Subset[Rgn]) Units: dmnl
149) Fraction Interseted not Correctly Tested[Rgn] = 1 - (1 - Fraction Interested not Tested[Rgn]) * Sensitivity of COVID Test Units: dmnl
150) Fraction of Additional Symptomatic[Rgn] = Additional Asymptomatic Relative to Symptomatic[Rgn] / (1 + Additional Asymptomatic Relative to Symptomatic[Rgn]) Units: dmnl
151) Fraction of Fatalities Screened Post Mortem[Rgn] = Indicated Fraction Post Mortem Testing[Rgn] * Switch for Government Response[Rgn] Units: dmnl
152) Fraction of Population Hospitalized for Covid[Rgn] = Total Covid Hospitalized[Rgn] / Population[Rgn] Units: dmnl
153) Fraction Poisson not Hospitalized[Rgn,Tested] = exp (- Average Acuity of Positively Tested[Rgn] * (1 - Probability of Missing Acuity Signal at Hospitals[Rgn,Tested]))
154) Fraction Poisson not Hospitalized[Rgn,Notest] = exp (- Average Acuity of Untested Poisson Subset[Rgn] * (1 - Probability of Missing Acuity Signal at Hospitals[Rgn,Notest])) Units: dmnl
155) Fraction Seeking Test[Rgn] = 1 Units: dmnl
156) Fraction Tests Positive[Rgn] = ZIDZ (Positive Tests of Infected[Rgn] , Testing on Living[Rgn]) Units: dmnl
157) Fraction Tests Positive Data[Rgn] = min (1, ZIDZ (DataFlowInfection[Rgn] , Active Test Rate[Rgn])) Units: dmnl
158) Global Cases = sum (Cumulative Cases[Rgn!]) Units: Person
159) Global Deaths = sum (Cumulative Deaths[Rgn!]) Units: Person
160) Global IFR = ZIDZ (Global Deaths , Global Cases - sum (Different Infectious Counted[Rgn!])) Units: dmnl
161) Government Response Start Time[Rgn] = INITIAL(DataAttentionTime[Rgn] + Day of First Case Report in JHU Database) Units: Day
162) Herd Immunity Fraction = 0.6 Units: dmnl
163) Hospital Adj T = 1 Units: Day
164) Hospital Admission Infectious[Rgn,TstSts] = Hospital Admits All[Rgn,TstSts] Units: Person/Day
165) Hospital Admit Ratio[Rgn,TstSts] = XIDZ (Hospital Admits All[Rgn,TstSts] , Potential Hospital Demand[Rgn,TstSts] , 1) Units: dmnl
166) Hospital Admits All[Rgn,Tested] = Hospital Demand from Tested[Rgn] * Allocated Fraction COVID Hospitalized[Rgn]
167) Hospital Admits All[Rgn,Notest] = Hospital Demand from Not Tested[Rgn] * Allocated Fraction COVID Hospitalized[Rgn] Units: Person/Day
168) Hospital Demand from Not Tested[Rgn] = Poisson Subset Not Tested Passing Gate[Rgn] * (1 - exp (- Average Acuity of Untested Poisson Subset[Rgn] * (1 - PMAS Unconfirmed for Hospital Demand[Rgn]))) Units: Person/Day
169) Hospital Demand from Tested[Rgn] = Positive Tests of Infected[Rgn] * (1 - exp (- Average Acuity of Positively Tested[Rgn] * (1 - PMAS Confirmed for Hospital Demand[Rgn]))) Units: Person/Day
170) Hospital Discharges[Rgn,TstSts] = (1 - Fatality Rate Treated[Rgn,TstSts]) * Hospital Outflow Covid Positive[Rgn,TstSts] Units: Person/Day
171) Hospital Outflow Covid Positive[Rgn,TstSts] = Hospitalized Infectious[Rgn,TstSts] / Hospitalized Resolution Time Units: Person/Day
172) Hospitalized CFR Cumulative[Rgn,TstSts] = ZIDZ (Cumulative Deaths at Hospital[Rgn,TstSts] , Cumulative Deaths at Hospital[Rgn,TstSts] + Cumulative Recovered at Hospitals[Rgn,TstSts]) Units: dmnl
173) Hospitalized Infectious[Rgn,TstSts] = INTEG(Hospital Admission Infectious[Rgn,TstSts] - Hospitalized Infectious Deaths[Rgn,TstSts] - Hospital Discharges[Rgn,TstSts] , 0) Units: Person
174) Hospitalized Infectious Deaths[Rgn,TstSts] = Fatality Rate Treated[Rgn,TstSts] * Hospital Outflow Covid Positive[Rgn,TstSts] Units: Person/Day
175) Hospitalized Resolution Time = 20 Units: Day

176) Hospitalized True CFR[Rgn] = ZIDZ (sum (Hospitalized Infectious Deaths[Rgn,TstSts!]) , sum (Hospital Outflow Covid Positive[Rgn,TstSts!])) Units: dmnl
177) Hospitalized True CFR Cumulative[Rgn] = ZIDZ (sum (Cumulative Deaths at Hospital[Rgn,TstSts!]) , sum (Cumulative Deaths at Hospital[Rgn,TstSts!] + Cumulative Recovered at Hospitals[Rgn,TstSts!])) Units: dmnl
178) ialp = 0.1 Units: dmnl
179) Impact of Adherence Fatigue[Rgn] = Recent Relative Contacts[Rgn] ^ (Strength of Adherence Fatigue[Rgn] * if then else (Time to Stop Adherence Fatigue > Time , 1, SWadhFtg)) Units: dmnl
180) Impact of Population Density on Hospital Availability[Rgn] = 0.72 Units: dmnl
181) Impact of Treatment on Fatality Rate[Rgn] = 0.32 Units: dmnl
182) Incubation Period = 5.6 Units: Day
183) Indicated fraction negative demand tested[Rgn] = 1 - exp (Flu Acuity * (Prob Missing Symptom[Rgn] - 1)) Units: dmnl
184) Indicated fraction positive demand tested[Rgn] = 1 - exp (Covid Acuity[Rgn] * (Prob Missing Symptom[Rgn] - 1)) Units: dmnl
185) Indicated Fraction Post Mortem Testing[Rgn] = Fraction Covid Death In Hospitals Previously Tested[Rgn] ^ Sensitivity Post Mortem Testing to Capacity[Rgn] Units: dmnl
186) Indicated Risk of Life Loss[Rgn] = Perceived Hazard of Death[Rgn] / Discount Rate per Day Units: dmnl
187) Infected pre Detection[Rgn] = INTEG(Onset of Symptoms[Rgn] - Continue without Testing[Rgn] - Symptomatic Infected to Testing[Rgn] - Untested symptomatic Infected to Hospital[Rgn] , 0) Units: Person
188) "Infected Unconfirmed Post-Detection"[Rgn] = INTEG(Continue without Testing[Rgn] - Deaths of Symptomatic Untested[Rgn] - Recovery of Untested[Rgn] , 0) Units: Person
189) Infection Rate[Rgn] = Infectious Contacts[Rgn] * (Susceptible[Rgn] / Population[Rgn]) * Weather Effect on Transmission[Rgn] Units: Person/Day
190) InfectionUFractionCounted[Rgn] = if then else (DataCmltOverTime[Rgn,Infection] = :NA:, 0, ZIDZ (DataCmltOverTime[Rgn,Infection] , Cumulative Cases[Rgn])) Units: dmnl
191) Infectious Confirmed Not Hospitalized[Rgn] = INTEG(Positive Testing of Infected Untreated[Rgn] - Deaths of Confirmed[Rgn] - Recovery of Confirmed[Rgn] , 0) Units: Person
192) Infectious Contacts[Rgn] = ("Pre-Symptomatic Infected"[Rgn] * Transmission Multiplier Presymptomatic[Rgn] + Infected pre Detection[Rgn] * Transmission Multiplier Pre Detection[Rgn] + (Additional Asymptomatic Post Detection[Rgn] + "Poisson Not-tested Asymptomatic"[Rgn]) * Baseline Risk of Transmission by Asymptomatic[Rgn] + (Infectious not Tested or in Hospitals Poisson[Rgn] - "Poisson Not-tested Asymptomatic"[Rgn]) * Baseline Transmission Multiplier for Untested Symptomatic + Infectious Confirmed Not Hospitalized[Rgn] * Transmission Multiplier for Confirmed[Rgn] + sum (Hospitalized Infectious[Rgn,TstSts!] * Transmission Multiplier for Hospitalized[Rgn,TstSts!])) * Reference Force of Infection[Rgn] * Contacts Relative to Normal[Rgn] Units: Person/Day
193) Infectious not Tested or in Hospitals Poisson[Rgn] = "Infected Unconfirmed Post-Detection"[Rgn] - Additional Asymptomatic Post Detection[Rgn] Units: Person
194) Initial Population[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 1) Units: Person
195) INITIAL TIME = 30 Units: Day
196) InpAveErr = INITIAL(sum (InpAveErrCmp[PriorEndoAve!] * PriorCounts[PriorEndoAve!])) Units: **undefined**
197) InpAveErrCmp[PriorEndoAve] = INITIAL((abs (CalcAve[PriorEndoAve] - InputAve[PriorEndoAve]) / Max (1e-06, CalcAve[PriorEndoAve]) * SW EndoAve)) Units: **undefined**
198) InputAve[Priors] = 1, 1.8, 0.47, 1, 0.0009, 0.81, 58, 0.017, 6.2, 0.1, 0.24, 0.4, 2.27, 0.52, 0.00055, 0.76, 5.9, 2.07, 0.55, 1e-06, 1e-06, 1e-06, 0.28, 0, 0 Units: **undefined**
199) IrD : Travel,InformalDeath
200) Known death fraction in hospitals large enough = sum (if then else (Cml Known Death Frac Hosp[Rgn!] < MinHspDTreshAdv , 1, 0) * AdvCntrs[Rgn!]) Units: dmnl
201) lastTestData[Rgn] = INITIAL(GET DATA Last TIME (DataTestRate[Rgn])) Units: Day
202) LastTestDate[Rgn] = INITIAL(GET DATA Last TIME (DataTestRate[Rgn])) Units: Day
203) Learning and Death Reduction Rate[Rgn1] = 0 Units: dmnl

204) Liver Disease Impact on Fatality[Rgn] = INITIAL((Liver Disease Rate[Rgn] / MeanLiver) ^ Sens Liver Impact Net[Rgn]) Units: dmnl
205) Liver Disease Rate[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 18) Units: dmnl
206) lnymix[Rgn,expnt] = - ln (Max (1e-06, 1 - Ymix[Rgn,expnt])) Units: dmnl
207) lnymix 0[Rgn,expnt] = - ln (Max (1e-06, 1 - Ymix[Rgn,expnt])) Units: dmnl
208) Max Test Rate per Capita = 0.001 Units: 1/Day
209) Max Time Data Used = 550 Units: Day
210) maxAlp = 1 Units: dmnl
211) MaxData[Rgn] = INITIAL(GET DATA MAX (DataCmltOverTime[Rgn,Infection] , 0, 500)) Units: Person
212) MaxRTresh = 8 Units: dmnl
213) MaxVacRate[Rgn] = INITIAL(if then else (Vaccination Period < 10, 0, Initial Population[Rgn] * (1 - AntiVaxxerFrac[Rgn]) / (Vaccination Period - frac rampup * Vaccination Period / 2))) Units: Person/Day
214) MeanChronic = GET VDF CONSTANTS(Constant Data File , 'MeanChronic', 1) Units: dmnl
215) MeanFlowOverTime[Rgn,Infection] = Post Mortem Test Rate[Rgn] + Positive Tests of Infected[Rgn]
216) MeanFlowOverTime[Rgn,Death] = Recorded Deaths[Rgn]
217) MeanFlowOverTime[Rgn,Test] = Total Simulated Tests[Rgn] Units: Person/Day
218) MeanLiver = GET VDF CONSTANTS(Constant Data File , 'MeanLiver', 1) Units: dmnl
219) MeanObesity = GET VDF CONSTANTS(Constant Data File , 'MeanObesity', 1) Units: dmnl
220) Min Contact Fraction[Rgn] = 0.04 Units: dmnl
221) Min Excess Death Attributable to COVID = 0.5 Units: dmnl
222) Min Fatality Multiplier = 0.1 Units: dmnl
223) Min Vaccination Time = 10 Units: Day
224) MinAdjT = 1 Units: Day
225) MinHspDTresh = 0.2 Units: dmnl
226) MinHspDTreshAdv = 0.8 Units: dmnl
227) MinSuscTresh = 0.7 Units: dmnl
228) MinTimeDwngRisk = 5 Units: Day
229) Mu[Rgn,Series] = Max (eps , MeanFlowOverTime[Rgn,Series]) Units: Person/Day
230) Multiplier Recent Infections to Test[Rgn] = 45 Units: dmnl
231) Multiplier Transmission Risk for Asymptomatic[Rgn] = 0.3 Units: dmnl
232) Multiplier Transmission Risk for Asymptomatic Net[Rgn] = INITIAL(Multiplier Transmission Risk for Asymptomatic[Rgn] * (1 - SW Gen[MTrAsym]) + SW Gen[MTrAsym] * InputAve[MTrAsym]) Units: dmnl
233) NBL1[Rgn,Series] = if then else (DataFlowOverTime[Rgn,Series] = 0, - ln (1 + alp[Rgn,Series] * Mu[Rgn,Series]) / alp[Rgn,Series] , 0) Units: dmnl
234) NBL2[Rgn,Series] = if then else (DataFlowOverTime[Rgn,Series] > 0, GAMMA LN (Di[Rgn,Series] + 1 / alp[Rgn,Series]) - GAMMA LN (1 / alp[Rgn,Series]) - GAMMA LN (Di[Rgn,Series] + 1) - (Di[Rgn,Series] + 1 / alp[Rgn,Series]) * ln (1 + alp[Rgn,Series] * Mu[Rgn,Series]) + Di[Rgn,Series] * (ln (alp[Rgn,Series]) + ln (Mu[Rgn,Series])) , 0) Units: dmnl
235) NBL3[Rgn,Series] = if then else (Di[Rgn,Series] > 0, - GAMMA LN (Di[Rgn,Series] + 1) - (Di[Rgn,Series] + 1 / alp[Rgn,Series]) * ln (1 + alp[Rgn,Series] * Mu[Rgn,Series]) + Di[Rgn,Series] * (ln (alp[Rgn,Series]) + ln (Mu[Rgn,Series])) , 0) Units: dmnl
236) NBLLFlow[Rgn,Series] = (NBL1[Rgn,Series] + NBL2[Rgn,Series]) * FlowToInclude[Series] * DataIncluded[Rgn] Units: dmnl
237) Negative Test Results[Rgn] = Testing on Living[Rgn] - Positive Tests of Infected[Rgn] Units: Person/Day
238) New Cases[Rgn] = Infection Rate[Rgn] + Patient Zero Arrival[Rgn] Units: Person/Day
239) New Testing Time = 1000 Units: Day
240) Nominal Hospital Capacity[Rgn] = INITIAL(Initial Population[Rgn] * Beds per Thousand Population[Rgn] / 1000) Units: Person
241) Normalized Hospital density[Rgn] = INITIAL(Bed per Square Kilometer[Rgn] / Reference Hospital Density) Units: dmnl
242) Not too few susceptibles = sum (if then else (SuscFrac[Rgn!] < MinSuscTresh , 1, 0)) Units: dmnl

243) NSeed = 1 Units: dmnl
244) numTrial[Rgn,UsedSeries] = INITIAL(Max (1.01, 1 / alp[Rgn,UsedSeries])) Units: dmnl
245) Obesity Impact on Fatality[Rgn] = INITIAL((Obesity Rates[Rgn] / MeanObesity) ^ Sens Obesity Impact Net[Rgn]) Units: dmnl
246) Obesity Rates[Rgn] = GET VDF CONSTANTS(Constant Data File , 'DataConstants[Rgn]', 16) Units: dmnl
247) Onset of Symptoms[Rgn] = DELAY N (Infection Rate[Rgn] , Incubation Period ,0, Delay Order) Units: Person/Day
248) Onset to Detection Delay = 5 Units: Day
249) OtherVaccination[Rgn] = Vaccination On[Rgn] * min (Total Vaccination Rate[Rgn] * (1 - FracNotVaccinated Susceptible[Rgn]) , RemainingFractionForVaccine[Rgn] * (Initial Population[Rgn] - Vaccinated[Rgn] - Susceptible[Rgn]) / Min Vaccination Time) Units: Person/Day
250) Overall Death Fraction[Rgn] = ZIDZ (Death Rate[Rgn] , All Recovery[Rgn]) Units: dmnl
251) Patient Zero Arrival[Rgn] = if then else (Time < Patient Zero Arrival Time[Rgn] :AND: Time + TIME STEP >= Patient Zero Arrival Time[Rgn] , PatientZero / TIME STEP , 0) Units: Person/Day
252) Patient Zero Arrival Time[Rgn] = 1 Units: Day [0,200]
253) PatientZero = 1 Units: Person
254) payoff = 0 Units: dmnl
255) pdim : tstP,dfcP,dgtP,scuP
256) Perceived Hazard of Death[Rgn] = (Weight on Reported Probability of Infection[Rgn] * Reported Hazard of Death[Rgn] + (1 - Weight on Reported Probability of Infection[Rgn]) * True Hazard of death[Rgn]) Units: 1/Day
257) Perceived Risk of Life Loss[Rgn] = INTEG((Indicated Risk of Life Loss[Rgn] - Perceived Risk of Life Loss[Rgn]) / if then else (Indicated Risk of Life Loss[Rgn] > Perceived Risk of Life Loss[Rgn] , Time to Upgrade Risk[Rgn] , Time to Downgrade Risk With Vaccine[Rgn]) , 0) Units: dmnl
258) PG1 : PG
259) PMAS Confirmed for Hospital Demand[Rgn] = (1 - Reference COVID Hospitalization Fraction Confirmed[Rgn]) ^ (1 / Average Acuity of Positively Tested[Rgn]) Units: dmnl
260) PMAS Unconfirmed for Hospital Demand[Rgn] = PMAS Confirmed for Hospital Demand[Rgn] + (1 - PMAS Confirmed for Hospital Demand[Rgn]) * Untested PMAS Gap with Tested[Rgn] Units: dmnl
261) "Poisson Not-tested Asymptomatic"[Rgn] = Infectious not Tested or in Hospitals Poisson[Rgn] * exp (- Average Acuity Not Hospitalized Poisson[Rgn,Notest]) Units: Person
262) Poisson Subset Not Tested Passing Gate[Rgn] = Poisson Subset Reaching Test Gate[Rgn] - Positive Tests of Infected[Rgn] Units: Person/Day
263) Poisson Subset Reaching Test Gate[Rgn] = Reaching Testing Gate[Rgn] / (1 + Additional Asymptomatic Relative to Symptomatic[Rgn]) Units: Person/Day
264) Policy Test Rate[Rgn] = if then else (Time < New Testing Time , Current Test Rate per Capita[Rgn] , Final Test Rate Per Capita[Rgn]) Units: 1/Day
265) Population[Rgn] = Infected pre Detection[Rgn] + "Infected Unconfirmed Post-Detection"[Rgn] + Susceptible[Rgn] + Recovered Unconfirmed[Rgn] + Confirmed Recovered[Rgn] + Infectious Confirmed Not Hospitalized[Rgn] + "Pre-Symptomatic Infected"[Rgn] + sum (Hospitalized Infectious[Rgn,TstSts!]) + sum (Cumulative Recovered at Hospitals[Rgn,TstSts!]) Units: Person
266) PopulationCheck[Rgn] = Recovered Unconfirmed[Rgn] + Confirmed Recovered[Rgn] + sum (Cumulative Recovered at Hospitals[Rgn,TstSts!]) + Different Infectious Counted[Rgn] + Susceptible[Rgn] Units: Person
267) Positive Candidates Interested in Testing Poisson Subset[Rgn] = Poisson Subset Reaching Test Gate[Rgn] * Fraction Seeking Test[Rgn] Units: Person/Day
268) Positive Candidates Interested in Testing Poisson Subset Adj[Rgn] = Max (0.001 * Potential Test Demand from Susceptible Population[Rgn] , Positive Candidates Interested in Testing Poisson Subset[Rgn]) Units: Person/Day
269) Positive Testing of Infected Untreated[Rgn] = Positive Tests of Infected[Rgn] * Fraction Poisson not Hospitalized[Rgn,Tested] Units: Person/Day
270) Positive Tests of Infected[Rgn] = Positive Candidates Interested in Testing Poisson Subset[Rgn] * (1 - Fraction Interseted not Correctly Tested[Rgn]) Units: Person/Day
271) Post Mortem Test Delay = 1 Units: Day

272) Post Mortem Test Rate[Rgn] = Post Mortem Tests Total[Rgn] * Sensitivity of COVID Test Units: Person/Day
273) Post Mortem Test Untreated[Rgn] = Post Mortem Test Rate[Rgn] * Frac Post Mortem from Untreated[Rgn] Units: Person/Day
274) Post Mortem Testing Need[Rgn] = SMOOTHI ((Deaths of Symptomatic Untested[Rgn] + Hospitalized Infectious Deaths[Rgn,Notest]) * Fraction of Fatalities Screened Post Mortem[Rgn] , Post Mortem Test Delay , 0) Units: Person/Day
275) Post Mortem Tests Total[Rgn] = min (Post Mortem Testing Need[Rgn] , Active Test Rate[Rgn]) Units: Person/Day
276) "Post-Detection Phase Resolution Time" = 10 Units: Day
277) PostMortemCorrection[Rgn] = min (Hospitalized Infectious[Rgn,Notest] / MinAdjT , Post Mortem Test Rate[Rgn] * (1 - Frac Post Mortem from Untreated[Rgn])) Units: Person/Day
278) Potential Hospital Demand[Rgn,Notest] = Hospital Demand from Not Tested[Rgn]
279) Potential Hospital Demand[Rgn,Tested] = Hospital Demand from Tested[Rgn] Units: Person/Day
280) Potential Test Demand from Susceptible Population[Rgn] = (Susceptible[Rgn] + Recovered Unconfirmed[Rgn] + Cumulative Recovered at Hospitals[Rgn,Notest]) * (Baseline Daily Fraction Susceptible Seeking Tests[Rgn] * Fraction Seeking Test[Rgn] + Multiplier Recent Infections to Test[Rgn] / Population[Rgn] * Recent Detected Infections[Rgn]) Units: Person/Day
281) "Pre-Symptomatic Infected"[Rgn] = INTEG(Infection Rate[Rgn] + Patient Zero Arrival[Rgn] - Onset of Symptoms[Rgn] , 0) Units: Person
282) PriorCounts[PriorEndoAve] = INITIAL(if then else (PriorEndoAve < 26, 1, 0)) Units: dmnl
283) PriorEndoAve : UpAdj,DwnAdj,RFI,RfSkTs,WRpPIn,MInfTs,MnCnFrc,SnCnRdUt,CfImCn,ImPDnHs,ImTrFt,DrdFac,MxHsFr,BsFtRt,SnsWth,Acty,SnFtAc,TtAsyFr,ObsImp,ChrImp,LivImp,MTrAsym,HspLrng,AdhrFtg
284) PriorErrs[Rgn,Priors] = INITIAL(ZIDZ (ActiveAve[Priors] - RegionalInputs[Priors,Rgn] , (AbsStd[Priors] * StdScale)) ^ 2 / 2) Units: **undefined**
285) PriorGen : BsFtRt,SnsWth,Acty,SnFtAc,TtAsyFr,ObsImp,ChrImp,LivImp,MTrAsym
286) Priors : UpAdj,DwnAdj,RFI,PMT,RfSkTs,WRpPIn,MInfTs,MnCnFrc,SnCnRdUt,CfImCn,ImPDnHs,ImTrFt,DrdFac,MxHsFr,BsFtRt,SnsWth,Acty,SnFtAc,TtAsyFr,ObsImp,ChrImp,LivImp,MTrAsym,HspLrng,AdhrFtg
287) Prob Missing Symptom[Rgn] = Max (0, ln (Y[Rgn]) / Flu Acuity + 1) Units: dmnl
288) Probability of Missing Acuity Signal at Hospitals[Rgn,Tested] = ZIDZ (ln (Max (1e-06, 1 - ZIDZ (Hospital Admits All[Rgn,Tested] , Positive Tests of Infected[Rgn]))) , Average Acuity of Positively Tested[Rgn]) + 1
289) Probability of Missing Acuity Signal at Hospitals[Rgn,Notest] = ZIDZ (ln (Max (1e-06, 1 - ZIDZ (Hospital Admits All[Rgn,Notest] , Poisson Subset Not Tested Passing Gate[Rgn]))) , Average Acuity of Untested Poisson Subset[Rgn]) + 1 Units: dmnl
290) PseudoCFR Units: dmnl
291) R Effective Reproduction Rate[Rgn] = ZIDZ (Infection Rate[Rgn] , Total Weighted Infected Population[Rgn]) * Total Disease Duration Units: dmnl
292) RandFlowTime = 1000 Units: Day
293) Reaching Testing Gate[Rgn] = Infected pre Detection[Rgn] / Onset to Detection Delay Units: Person/Day
294) Realistic R0 = sum (if then else (R Effective Reproduction Rate[Rgn!] > MaxRTresh , 1, 0)) Units: dmnl
295) Recent Detected Infections[Rgn] = SMOOTHI (Positive Tests of Infected[Rgn] , Time to Respond with Tests , 0) Units: Person/Day
296) Recent Relative Contacts[Rgn] = SMOOTHI (Contacts Relative to Normal[Rgn] , Adherence Fatigue Time , 1) Units: dmnl
297) Recorded Deaths[Rgn] = Post Mortem Test Rate[Rgn] + Deaths of Confirmed[Rgn] + Hospitalized Infectious Deaths[Rgn,Tested] Units: Person/Day
298) Recovered Unconfirmed[Rgn] = INTEG(Recovery of Untested[Rgn] , 0) Units: Person
299) Recovery of Confirmed[Rgn] = Tested Untreated Resolution[Rgn] * (1 - Fatality Rate Untreated[Rgn,Tested]) Units: Person/Day

300) Recovery of Untested[Rgn] = ("Infected Unconfirmed Post-Detection"[Rgn] / "Post-Detection Phase Resolution Time") - Deaths of Symptomatic Untested[Rgn] Units: Person/Day
301) Reference COVID Hospitalization Fraction Confirmed[Rgn] = 0.7 Units: dmnl
302) Reference Force of Infection[Rgn] = 0.6 Units: 1/Day [0,2]
303) Reference Hospital Density = 6.06 Units: Person/(Km*Km)
304) RegionalInputs[UpAdj,Rgn] = INITIAL(Log (Time to Upgrade Risk[Rgn] , 10))
305) RegionalInputs[DwnAdj,Rgn] = Log (Time to Downgrade Risk[Rgn] , 10)
306) RegionalInputs[RFI,Rgn] = Reference Force of Infection[Rgn]
307) RegionalInputs[PMT,Rgn] = Sensitivity Post Mortem Testing to Capacity[Rgn]
308) RegionalInputs[RfSkTs,Rgn] = Baseline Daily Fraction Susceptible Seeking Tests[Rgn]
309) RegionalInputs[WRpPIn,Rgn] = Weight on Reported Probability of Infection[Rgn]
310) RegionalInputs[MInfTs,Rgn] = Multiplier Recent Infections to Test[Rgn]
311) RegionalInputs[MnCnFrc,Rgn] = Min Contact Fraction[Rgn]
312) RegionalInputs[SnCnRdUt,Rgn] = Sensitivity of Contact Reduction to Utility[Rgn]
313) RegionalInputs[CfImCn,Rgn] = Confirmation Impact on Contact[Rgn]
314) RegionalInputs[ImPDnHs,Rgn] = Impact of Population Density on Hospital Availability[Rgn]
315) RegionalInputs[ImTrFt,Rgn] = Impact of Treatment on Fatality Rate[Rgn]
316) RegionalInputs[DrdFac,Rgn] = Log (Dread Factor in Risk Perception[Rgn] , 10)
317) RegionalInputs[MxHsFr,Rgn] = Reference COVID Hospitalization Fraction Confirmed[Rgn]
318) RegionalInputs[BsFtRt,Rgn] = Base Fatality Rate for Unit Acuity Net[Rgn]
319) RegionalInputs[SnsWth,Rgn] = Sensitivity to Weather Net[Rgn]
320) RegionalInputs[Acty,Rgn] = Covid Acuity Relative to Flu Init Net[Rgn]
321) RegionalInputs[SnFtAc,Rgn] = Sensitivity of Fatality Rate to Acuity Net[Rgn]
322) RegionalInputs[TtAsyFr,Rgn] = Total Asymptomatic Fraction Init Net[Rgn]
323) RegionalInputs[ObsImp,Rgn] = Sens Obesity Impact Net[Rgn]
324) RegionalInputs[ChrImp,Rgn] = Sens Chronic Impact Net[Rgn]
325) RegionalInputs[LivImp,Rgn] = Sens Liver Impact Net[Rgn]
326) RegionalInputs[MTrAsym,Rgn] = Multiplier Transmission Risk for Asymptomatic Net[Rgn]
327) RegionalInputs[HspLrng,Rgn] = Learning and Death Reduction Rate[Rgn]
328) RegionalInputs[AdhrFtg,Rgn] = Strength of Adherence Fatigue[Rgn] Units: **undefined**
329) Relative Risk of Transmission by Hospitalized = 1 Units: dmnl
330) Relative Risk of Transmission by Presymptomatic = 1 Units: dmnl
331) RemainingFractionForVaccine[Rgn] = (1 - AntiVaxxerFrac[Rgn]) - Vaccinated Fraction[Rgn] Units: dmnl
332) Reported Hazard of Death[Rgn] = SimFlowOverTime[Rgn,Death] / Population[Rgn] Units: 1/Day
333) Response Policy Time On = 1000 Units: Day
334) Response Policy Weight = 0 Units: dmnl
335) Rgn :
Argentina,Australia,Austria,Bahrain,Bangladesh,Belarus,Belgium,Bolivia,Bulgaria,Canada,Chile,Colombia,CostaRica,Croatia,Cuba,Cyprus,CzechRepublic,Denmark,DominicanRepublic,Ecuador,ElSalvador,Estonia,Ethiopia,Finland,France,Germany,Ghana,Greece,Hungary,Iceland,India,Indonesia,Iran,Iraq,Ireland,Israel,Italy,Jamaica,Japan,Kazakhstan,Kenya,Kuwait,Latvia,Lithuania,Luxembourg,Madagascar,Malawi,Malaysia,Maldives,Malta,Mexico,Morocco,Mozambique,Nepal,Netherlands,NewZealand,Nigeria,NorthMacedonia,Norway,Pakistan,Panama,Paraguay,Peru,Philippines,Poland,Portugal,Qatar,Romania,Russia,Rwanda,SaudiArabia,Senegal,Serbia,Singapore,Slovakia,Slovenia,SouthAfrica,SouthKorea,Spain,SriLanka,Sweden,Switzerland,Thailand,Togo,Tunisia,Turkey,UAE,UK,Ukraine,Uruguay,USA,Zambia
336) Rgn1 : Rgn
337) Risk threshold for response[Rgn] = if then else (Response Policy Time On < Time , (1 - Response Policy Weight) * Sensitivity of Contact Reduction to Utility[Rgn] , Sensitivity of Contact Reduction to Utility[Rgn]) / Impact of Adherence Fatigue[Rgn] Units: dmnl
338) SAVEPER = 1 Units: Day [0,?]
339) Sens Chronic Impact = 1e-06 Units: dmnl
340) Sens Chronic Impact Net[Rgn] = INITIAL(Sens Chronic Impact * (1 - SW Gen[ChrImp]) + SW Gen[ChrImp] * InputAve[ChrImp]) Units: dmnl

341) Sens Liver Impact = 1e-06 Units: dmnl
342) Sens Liver Impact Net[Rgn] = INITIAL(Sens Liver Impact * (1 - SW Gen[LivImp]) + SW Gen[LivImp] * InputAve[LivImp]) Units: dmnl
343) Sens Obesity Impact = 1e-06 Units: dmnl
344) Sens Obesity Impact Net[Rgn] = INITIAL(Sens Obesity Impact * (1 - SW Gen[ObsImp]) + SW Gen[ObsImp] * InputAve[ObsImp]) Units: dmnl
345) SensCovidUntestedAdmission = 1 Units: dmnl
346) Sensitivity of Contact Reduction to Utility[Rgn] = 15 Units: dmnl
347) Sensitivity of Contact Reduction to Utility Policy = 10 Units: dmnl
348) Sensitivity of COVID Test = 0.7 Units: dmnl
349) Sensitivity of Fatality Rate to Acuity[Rgn] = 2 Units: dmnl
350) Sensitivity of Fatality Rate to Acuity Net[Rgn] = INITIAL(Sensitivity of Fatality Rate to Acuity[Rgn] * (1 - SW Gen[SnFtAc]) + SW Gen[SnFtAc] * InputAve[SnFtAc]) Units: dmnl [0,3]
351) Sensitivity Post Mortem Testing to Capacity[Rgn] = 1 Units: dmnl
352) Sensitivity to Weather = 0.76 Units: dmnl
353) Sensitivity to Weather Net[Rgn] = INITIAL(Sensitivity to Weather * (1 - SW Gen[SnsWth]) + SW Gen[SnsWth] * InputAve[SnsWth]) Units: dmnl
354) Series : Infection,Death,Test
355) SeriesErrorTerm[Rgn,Series] = if then else (DataCmltOverTime[Rgn,Series] = :NA:, 0, (abs (DataCmltOverTime[Rgn,Series] - SimCmltOverTime[Rgn,Series])) ^ CmltErrPW) / (BaseError + DataCmltOverTime[Rgn,Series]) * CmltPenaltyScl * CmltToInclude[Series] * DataIncluded[Rgn] Units: dmnl
356) Sim Pseudo Case Fatality[Rgn] = ZIDZ (Cumulative Deaths of Confirmed[Rgn] , Cumulative Confirmed Cases[Rgn]) Units: dmnl
357) SimCmltOverTime[Rgn,Infection] = Cumulative Confirmed Cases[Rgn]
358) SimCmltOverTime[Rgn,Death] = Cumulative Deaths of Confirmed[Rgn]
359) SimCmltOverTime[Rgn,Test] = Cumulative Tests Conducted[Rgn] Units: Person
360) SimFlowOverTime[Rgn,UsedSeries] = if then else (SwitchRandFlowTime < Time , RANDOM NEGATIVE BINOMIAL (-1, 1e+06, successP[Rgn,UsedSeries] , numTrial[Rgn,UsedSeries] , 0, 1, NSeed) , Mu[Rgn,UsedSeries]) Units: Person/Day
361) SimTestRate[Rgn] = Total Simulated Tests[Rgn] Units: Person/Day
362) SqrdErr[Rgn,Series] = if then else (FlowResiduals[Rgn,Series] = :NA:, :NA:, FlowResiduals[Rgn,Series] ^ 2) Units: Person*Person/(Day*Day)
363) StdScale = 1 Units: dmnl
364) StopDataUseTime[Rgn] = INITIAL(min (lastTestData[Rgn] , Max Time Data Used)) Units: Day
365) Strength of Adherence Fatigue[Rgn] = 0 Units: dmnl
366) successP[Rgn,UsedSeries] = 1 / (1 + alp[Rgn,UsedSeries] * Mu[Rgn,UsedSeries]) Units: dmnl
367) Susceptible[Rgn] = INTEG(- Infection Rate[Rgn] - Susceptible Vaccination[Rgn] , Initial Population[Rgn]) Units: Person
368) Susceptible Vaccination[Rgn] = Vaccination On[Rgn] * min (Total Vaccination Rate[Rgn] * FracNotVaccinated Susceptible[Rgn] , RemainingFractionForVaccine[Rgn] * Susceptible[Rgn] / Min Vaccination Time) Units: Person/Day
369) SuscFrac[Rgn] = Susceptible[Rgn] / Population[Rgn] Units: dmnl
370) SW EndoAve = INITIAL(if then else (ELMCOUNT(Rgn) > 1, 1, 0)) Units: dmnl
371) SW Gen[PriorGen] = 0 Units: dmnl
372) SWadhFtg = 0 Units: dmnl
373) Switch for Government Response[Rgn] = if then else (Time > Government Response Start Time[Rgn] , 1, 0) Units: dmnl
374) SwitchRandFlow = 0 Units: dmnl
375) SwitchRandFlowTime = if then else (SwitchRandFlow = 1, min (Max Time Data Used , RandFlowTime) , 1000) Units: Day
376) Sympthom Reduction by Infectioun[Rgn] = Average Acuity in Susceptible[Rgn] * Infection Rate[Rgn] Units: Person/Day

377) Sympthom Reduction by Vaccination[Rgn] = Susceptible Vaccination[Rgn] * Average Acuity in Susceptible[Rgn] * Vaccination Priority Multiplier Units: Person/Day
378) Sympthoms in Susceptible[Rgn] = INTEG(- Sympthom Reduction by Infectioun[Rgn] - Sympthom Reduction by Vaccination[Rgn] , Susceptible[Rgn] * (1 - Additional Asymptomatic Fraction Init[Rgn]) * Covid Acuity Relative to Flu Init Net[Rgn]) Units: Person
379) Symptomatic Fraction in Poisson[Rgn] = INITIAL(1 - exp (- Covid Acuity[Rgn])) Units: dmnl
380) Symptomatic Fraction Negative[Rgn] = INITIAL(1 - exp (- Flu Acuity)) Units: dmnl
381) Symptomatic Infected to Testing[Rgn] = Positive Testing of Infected Untreated[Rgn] + Hospital Admission Infectious[Rgn,Tested] Units: Person/Day
382) t3[Rgn] = (-9 * b[Rgn] + 1.7321 * Sqrt (4 * a[Rgn] ^ 3 + 27 * b[Rgn] ^ 2)) ^ (1 / 3) Units: dmnl
383) talp = 5 Units: dmnl
384) Tested Untreated Resolution[Rgn] = Infectious Confirmed Not Hospitalized[Rgn] / "Post-Detection Phase Resolution Time" Units: Person/Day
385) TestErrorFrac = 0.0001 Units: dmnl
386) TestFlowErr[Rgn] = ((DataFlowOverTime[Rgn,Test] - MeanFlowOverTime[Rgn,Test]) * WTestFlowErr[Rgn]) ^ 2 Units: dmnl
387) Testing Capacity Net of Post Mortem Tests[Rgn] = Active Test Rate[Rgn] - Post Mortem Tests Total[Rgn]
  Units: Person/Day
388) Testing Demand[Rgn] = Positive Candidates Interested in Testing Poisson Subset[Rgn] * Symptomatic Fraction in Poisson[Rgn] + Potential Test Demand from Susceptible Population[Rgn] * Symptomatic Fraction Negative[Rgn]
  Units: Person/Day
389) Testing on Living[Rgn] = min (Testing Capacity Net of Post Mortem Tests[Rgn] , Testing Demand[Rgn])
  Units: Person/Day
390) Tests on Negative Patients[Rgn] = Testing on Living[Rgn] * ZIDZ (Indicated fraction negative demand tested[Rgn] * Potential Test Demand from Susceptible Population[Rgn] , Indicated fraction negative demand tested[Rgn] * Potential Test Demand from Susceptible Population[Rgn] + Indicated fraction positive demand tested[Rgn] * Positive Candidates Interested in Testing Poisson Subset[Rgn]) Units: Person/Day
391) Tests Per Million[Rgn] = Cumulative Tests Data[Rgn] / Initial Population[Rgn] * 1e+06Units: dmnl
392) ThrsInc[Rgn] = Max (FracThresh * MaxData[Rgn] , 50) Units: Person
393) TIME STEP = 0.25 Units: Day [0,?]
394) Time to Adjust Testing = 30 Units: Day
395) Time to Downgrade Risk[Rgn] = 60 Units: Day
396) Time to Downgrade Risk Net[Rgn] = if then else (Response Policy Time On < Time , (1 + Response Policy Weight) * Time to Downgrade Risk[Rgn] , Time to Downgrade Risk[Rgn]) Units: Day
397) Time to Downgrade Risk Policy = 300 Units: Day
398) Time to Downgrade Risk With Vaccine[Rgn] = Time to Downgrade Risk Net[Rgn] * (1 - (1 - SuscFrac[Rgn]) * Vaccination On[Rgn]) + (1 - SuscFrac[Rgn]) * Vaccination On[Rgn] * MinTimeDwngRisk Units: Day
399) Time to Herd Immunity[Rgn] = XIDZ (Herd Immunity Fraction * Susceptible[Rgn] , Total Weighted Infected Population[Rgn] / Total Disease Duration , 0) Units: Day
400) Time to Respond with Tests = 5 Units: Day
401) Time to Stop Adherence Fatigue = 1000 Units: Day
402) Time to Upgrade Risk[Rgn] = 10 Units: Day
403) Time variant change in fatality[Rgn] = Max (Min Fatality Multiplier , (Max (Baseline Cumulative Cases for Learning , Cumulative Cases[Rgn] / Initial Population[Rgn]) / Baseline Cumulative Cases for Learning) ^ (- Learning and Death Reduction Rate[Rgn])) Units: dmnl
404) TimeVar Impact of Treatment on Fatality[Rgn] = Impact of Treatment on Fatality Rate[Rgn] * Time variant change in fatality[Rgn] Units: dmnl
405) Total Asymptomatic Fraction[Rgn] = 0.5 Units: dmnl
406) Total Asymptomatic Fraction Init Net[Rgn] = INITIAL(Total Asymptomatic Fraction[Rgn] * (1 - SW Gen[TtAsyFr]) + SW Gen[TtAsyFr] * InputAve[TtAsyFr]) Units: dmnl
407) Total Asymptomatic Fraction Net[Rgn] = Additional Asymptomatic Fraction Init[Rgn] + exp (- Covid Acuity[Rgn]) * (1 - Additional Asymptomatic Fraction Init[Rgn]) Units: dmnl
408) Total Covid Hospitalized[Rgn] = sum (Hospitalized Infectious[Rgn,TstSts!]) Units: Person

409) Total Disease Duration = Onset to Detection Delay + "Post-Detection Phase Resolution Time" + Incubation Period Units: Day
410) Total Simulated Tests[Rgn] = Post Mortem Tests Total[Rgn] + Testing on Living[Rgn] Units: Person/Day
411) Total Test on Covid Patients[Rgn] = Max (0, min (Positive Candidates Interested in Testing Poisson Subset[Rgn] , Testing on Living[Rgn] - Tests on Negative Patients[Rgn])) Units: Person/Day
412) Total to Official Cases Simulated[Rgn] = ZIDZ (Cumulative Cases[Rgn] , SimCmltOverTime[Rgn,Infection]) Units: dmnl
413) Total Vaccination Rate[Rgn] = if then else (Vaccination Period < 10, 0, MaxVacRate[Rgn] * (1 - min (1, Max (0, (frac rampup * Vaccination Period - (Time - Vaccine Start Time)) / (Vaccination Period * frac rampup))))) Units: Person/Day
414) Total Weighted Infected Population[Rgn] = Infected pre Detection[Rgn] + "Pre-Symptomatic Infected"[Rgn] + Weighted Infected Post Detection Gate[Rgn] Units: Person
415) Transmission Multiplier for Confirmed[Rgn] = INITIAL(Baseline Transmission Multiplier for Untested Symptomatic * Confirmation Impact on Contact[Rgn]) Units: dmnl
416) Transmission Multiplier for Hospitalized[Rgn,TstSts] = INITIAL(Baseline Transmission Multiplier for Untested Symptomatic * Relative Risk of Transmission by Hospitalized * if then else (TstSts = 1, Confirmation Impact on Contact[Rgn] , 1)) Units: dmnl
417) Transmission Multiplier Pre Detection[Rgn] = INITIAL(Baseline Transmission Multiplier for Untested Symptomatic * (1 - Total Asymptomatic Fraction Net[Rgn]) + Total Asymptomatic Fraction Net[Rgn] * Baseline Risk of Transmission by Asymptomatic[Rgn]) Units: dmnl
418) Transmission Multiplier Presymptomatic[Rgn] = INITIAL((Baseline Transmission Multiplier for Untested Symptomatic * Relative Risk of Transmission by Presymptomatic) * (1 - Total Asymptomatic Fraction Net[Rgn]) + Total Asymptomatic Fraction Net[Rgn] * Baseline Risk of Transmission by Asymptomatic[Rgn] * Relative Risk of Transmission by Presymptomatic) Units: dmnl
419) True Hazard of death[Rgn] = Death Rate[Rgn] / Population[Rgn] Units: 1/Day
420) TstInc[Rgn] = Active Test Rate[Rgn] Units: Person/Day
421) TstSts : Tested,Notest
422) Untested PMAS Gap with Tested[Rgn] = (1 - Allocated Fration NonCOVID Hospitalized[Rgn]) ^ SensCovidUntestedAdmission Units: dmnl
423) Untested symptomatic Infected to Hospital[Rgn] = Hospital Admission Infectious[Rgn,Notest] Units: Person/Day
424) UsedSeries : Infection,Death
425) Vaccinated[Rgn] = INTEG(OtherVaccination[Rgn] + Susceptible Vaccination[Rgn] , 0) Units: Person
426) Vaccinated Fraction[Rgn] = Vaccinated[Rgn] / Initial Population[Rgn] Units: dmnl
427) Vaccination On[Rgn] = if then else (Time < Vaccine Start Time , 0, 1) Units: dmnl
428) Vaccination Period = 150 Units: Day
429) Vaccination Priority Multiplier = 1.5 Units: dmnl
430) Vaccine Start Time = 800 Units: Day
431) VacWinStart[Rgn] = if then else (Vaccination Period > 1, if then else (Time > Vaccine Start Time , 2, -1) , -1) Units: dmnl
432) Voluntary Reduction in Contacts[Rgn] = exp (- Max (0, Dread Factor in Risk Perception Net[Rgn] * Perceived Risk of Life Loss[Rgn] - Risk threshold for response[Rgn])) * (1 - Min Contact Fraction[Rgn]) + Min Contact Fraction[Rgn] Units: dmnl
433) W Ave Acuity Hospitalized[Rgn] = ZIDZ (sum (Average Acuity Hospitalized[Rgn,TstSts!] * Hospitalized Infectious[Rgn,TstSts!]) , sum (Hospitalized Infectious[Rgn,TstSts!])) Units: dmnl
434) Weather Effect on Transmission[Rgn] = CRW[Rgn] ^ Sensitivity to Weather Net[Rgn] Units: dmnl
435) Weight Max in Test Goal = 0 Units: dmnl
436) Weight on Reported Probability of Infection[Rgn] = 0.78 Units: dmnl [0,1,0.01]
437) Weighted Infected Post Detection Gate[Rgn] = "Infected Unconfirmed Post-Detection"[Rgn] + Infectious Confirmed Not Hospitalized[Rgn] + sum (Hospitalized Infectious[Rgn,TstSts!]) * "Post-Detection Phase Resolution Time" / Hospitalized Resolution Time Units: Person
438) WTestFlowErr[Rgn] = if then else (DataFlowOverTime[Rgn,Test] = :NA:, 0, 1 / Max (10, DataFlowOverTime[Rgn,Test] * TestErrorFrac)) Units: Day/Person

439) Y[Rgn] = min (1, Max (1e-06, 1 - exp (- Extrapolated Estimator[Rgn]))) Units: dmnl
440) Ymix[Rgn,p2] = - b[Rgn] / (1 + a[Rgn])
441) Ymix[Rgn,p3] = (Sqrt (a[Rgn] ^ 2 - 4 * b[Rgn]) - a[Rgn]) / 2
442) Ymix[Rgn,p4] = (-0.87358 * a[Rgn]) / t3[Rgn] + 0.38157 * t3[Rgn] Units: dmnl

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