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Dynamical regulations on mobility and vaccinations to control Covid19 spread

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Abstract

Using a system of time-dynamical equations, we investigate how daily mobility indices, such as homestay above the pre-Covid normal ($H\%$; or H -forcing), and cumulative vaccinations ($V_c\%$; or V -forcing) impact the net reproductive rate (R_0) of COVID19 in ten island nations as a prototype, and then, extending it to 124 countries Worldwide. Our H - and V -forcing model of R_0 could explain the new trends in 106 countries. The disease transmission can be controlled by forcing down $R_0(H, V_c) < 1$ with enforcement of continuous $H > 40\%$ in 91% of countries with 0% vaccinated plus recovered, V_p . The required critical $H\%$ decreases with increasing $V_p\%$, dropping it down to 20% with 25% V_p , and further down to 8% with 50% V_p .

However, the regulations on $H\%$ are context-dependent and country-specific. Our model is useful in forecasting and controlling the disease spread when the effectiveness of the vaccines is a concern due to new variants, and/or delays in vaccination rollout programs.

Introduction

When a novel virus emerges, the community mitigation strategies, especially those concerning population mobility, are the most readily available intervention to slow down the transmission¹. Most countries implemented strict population mobility policies to suppress transmission of SARS-CoV-2 (Covid19), and in some countries, a convincing reduction in case incidence was observed, at least temporarily^{2,3}. Even though many vaccination programs are rolled out World-wide, the current rate of the spread of Covid19 as a new infection wave with Delta and other variants concerns whether the vaccines may not be effective against the new variants. The reproductive rate, R_0 , of the Delta variant is far higher (5.08) compared to the ancestral virus (2.79)^{4,5}. Due to the high R_0 associated with higher transmissibility, low vaccine coverage rates, and lower vaccine effectiveness, the social measures will need to be strengthened to combat the ever emerging variants. A high R_0 also means much higher vaccine coverage rates need to be achieved compared to the ancestral variant⁵.

Understanding the extent of population mobility and the ongoing vaccination programs of a nation is essential for tracking the trajectory of the national epidemic and assessing the effectiveness of continuing control measures. Many studies have analyzed the efforts in controlling people's mobility to reduce the spread of the disease^{6,7,8,9}. Those work include studies of correlations of R_0 with the mobility metrics developed by Google¹⁰. Those metrics are based on Google logins by people and location identifiers and computed as proxies for people's spatial density movement as a percentage change from the pre-Covid scenarios. Nouvellet et al.⁹ have shown that a drop in R_0 below the critical $R_0 = 1$ requiring for disease extinction, correlates

with the homestay $H\%$. Further studies also show similar findings^{6,7,8}. However, the combined effect of people's mobility restraints with nations' vaccination percentages has not yet been understood enough through dynamical process modeling on Covid19 disease transmission.

Here we designed a simple study to predict the degree of population mobility restrictions needed to bring the R_0 below one, for countries with varying levels of cumulative vaccinations. We used a system of time-dynamical equations incorporating the effect of homestay percentage ($H\%$) and the cumulative vaccinations ($V_c\%$), fitting to the data of new cases and deaths obtained from the University of Oxford Covid19 database¹¹, to compute the net reproductive rate R_0 in 124 nations. We used data from ten island nations as a prototype to select the best alternative model-hypothesis among three nested that we tested: (1) Model 1: M_H : incorporating the homestay $H\%$ effect, (2) Model 2: M_V : incorporating the effect of vaccinations, and (3) Model 3: M_{HV} : the effect of the combination of the both, the $H\%$ and the $V_c\%$, on the disease dynamics.

Results

The global picture

Among the three alternative models fitted to the data of New cases and Deaths from ten island nations as a prototype, Model 3 (M_{HV}) that combined the effects of both the homestay ($H\%$) and the vaccination ($V_c\%$), fitted the best, in general, as per the Akaike information criterion (AIC) (Table 1). In nations that had homestay regulations as the primary method of controlling the spread, the M_H Model fitted equally well or slightly better than the M_{HV} model, explaining the variations and the trends in the new case and the death data. Similarly, in nations that had vaccination as the primary method of controlling the spread, the M_V model fitted to the data equally well or better than the M_{HV} model. This suggested that the M_{HV}

model represents the effect of both the homestay and the vaccinations controlled via nations' respective regulations on Covid19 disease spread as a general all-inclusive hypothesis in understanding the $R0$ dynamics.

We extended the M_{HV} model-fitting and the analyses to the World data of 124 countries (see the Appendix). The model M_{HV} could explain the variations and the trends in the data in 106 countries well w.r.t. the trends in their respective residuals. Ninety five out of the 106 countries showed a calibratable functional relationship between the $R0$ and the $H\%$ (Fig. 1), given their respective percentages of the people vaccinated plus the number recovered, denoted by $V_p\%$. Note that $V_p\% \geq$ the percentage vaccinated, $V_c\%$. The eleven out of the 106 countries that did not show a marked variation in the $R0$ with respect to an increase in the $H\%$ was because the variation in the $H\%$ data was not sufficient to capture such changes in the functional response of $R0$. That is, for those nations, the functional response of $R0$ with respect to $H\%$ was non-calibratable, other than the values of $R0$ for their given $V_p\%$.

When the $H\%$ is increased, the $R0$ decreased for nations at different percentages of vaccinations plus recovered, V_p : 0%, 25%, and 50%, in the said 106 countries (Fig. 1). The model M_{HV} indicated that 91% of the nations, with both mobility regulations and effective vaccination programs, out of the 106, requires a minimum of 40% homestay above the pre-Covid normal to bring the $R0 < 1$ from the status quo (Fig. 1). This threshold of $H\%$ at $R0 = 1$ lowers with the increasing percentage of the cumulative vaccinations. For example, with $> 25\%$ more vaccinated ($V_c\%$) plus the recovered, the $H\%$ at $R0 = 1$ lowers down to 20% in 97% of the 106 countries. For countries with $> 50\%V_p$, the $H\%$ requiring for $R0 < 1$ turns out to be about 8 for about 99% of the 106 nations (Fig. 1). Figure. 2. shows how $H\%$ at $R = 1$ decreases with the increasing $V_p\%$, vaccination plus recovered percentage. Overall, the $R0$, averaged over the last seven days, is negatively correlated with the percentage-vaccinated in the nations, with $R^2 = 0.41$ and $p < 0.01$ (Fig. 65 in the Appendix). It indicates that $> 80\%$ vaccinated in a nation has not fully guaranteed a $R0 < 1$, with upper 95% confidence interval

crossing $R0 = 1$ at 70% vaccinated. The detailed countrywide plots are given in the Appendix.

Model-selection based on the island data -the prototype

The four nations presented in Figure 3 and 4, among the ten island nations in the prototype analysis: Australia, Taiwan, Sri Lanka, and the UK represent contrasting levels of $H\%$ vs $V_c\%$. Three of them, namely, Taiwan, Sri Lanka, and the UK showed a significant reduction in $R0$, but not Australia. In Taiwan, the decline was due to an increased mobility restriction forcing a hike in $H\%$, but not due to vaccinations, while in the UK, it was due to escalating vaccinations but not by marked mobility restrictions (Fig. 3). In Sri Lanka, the control was driven by both the vaccinations and the mobility restrictions. The $R0$, in almost all islands in the analysis except for Australia, was less than 1, indicating that their disease spread is under control. There was not enough variation in $H\%$ in the Australia to calibrate how $R0$ functionally responds to the change in $H\%$. All four islands showed a concave-up relationship with respect to the increase in $H\%$. Sri Lanka shows the lowest sensitivity of $R0$ to the change of H , thus, needing a significant $H\%$ in reducing a unit of $R0$ compared to any other nation. The estimated parameter values and AICs of the three alternative models M_H , M_V and M_{HV} for ten island nations are given in Table.1 (and also in Table 1. in the Appendix). The graphs of the model M_{HV} , fitted to new cases and deaths, plus other functional relationship of $R0$ vs. $H\%$ and $V_c\%$ are given in the Appendix for all nations, with estimated parameter values given in a respective Table in the same.

The simulation results of island nations in Figure 4 show the level of $H\%$ needed for $R0 < 1$, indicating that the disease can be forced to go extinct, i.e., $R0(H) < 1$, from the status quo (i.e., with the already administered $V_c\%$ of the respective countries plus recovered), with an enforcement of a continuous homestay of $H\% > 20$, from the pre-Covid normal. This is the same case for many other in the 106 nations given in the Appendix. The $R0$ vs. $H\%$ panels in Figure 4 show that the percentage of vaccination, $V_c\%$, brings the required critical $H\%$ to

130 meet the $R_0(H) = 1$ threshold further lower, yielding a complementary effect on the reduction
131 in the R_0 forced by $H\%$. The analyses of the World nations in the Appendix also show similar
132 trends as those we discussed here regarding the island nations.

133

134 Discussion

135 There is escalating uncertainty regarding the complexity behind the building up of the new
136 infection wave of COVID19, both among the vaccinated and the non-vaccinated nations, in
137 the presence of the ever-evolving new variants. Studies are inconclusive as to how the recom-
138 mended, and approved vaccinations, respond to the new variants. Hence, it is imperative that
139 we explore it in depth using models as to how the disease transmission responds to regulations
140 on mobility along with the on-going vaccination efforts.

141

142 We show how the net reproductive rate, R_0 , functionally relates to the effect of Home-stay
143 ($H\%$) and the percentage of vaccinations (V_C). The regulations on people's mobility, confining
144 them to stay at homes $> 20\%$ more than the pre-Covid scenario (except for $> 40\%$ for three
145 countries), has a grip on flattening the infection curve, and controlling the spread markedly
146 at about 75% of the people remaining susceptible, and $> 8\%$ when 50% of the population
147 remaining susceptible. Here, the susceptibility is a function of the number vaccinated, infected
148 and died as at present. Nouvellet et al ⁴ indicate that 73% more mobility restrictions from the
149 pre-Covid normal baseline is required to reduce the R_0 less than 1, based on a model which
150 has not regarded the effect of vaccinations, analyzing the data for 52 countries. We show how
151 V -forcing initiatives complement the H -forcing initiatives, flattening the infection curve further
152 down lowering the R_0 when the effect of vaccinations are taken into consideration. Studying,
153 which policies and regulations of mobility restrictions that correlate with the Google mobility
154 indices will be country-specific, and will need ground-truthing. It will be more informative to
155 model the same in spatially explicitly in countries such as Japan and other, where the regional

data on new cases, deaths, and mobility are available.

Eighteen countries out of 124, showing miss-fits to the model, may indicate either the vaccinations do not respond to the disease spread as expected due to new variants, or the data are not representative enough of the true situations. There are a dearth of complaints regarding the miss-appropriate handling of the data by authorities in countries for political gains. Hence, the data can be biased and sparsed as well, not consistently reported, being unsuitable to model the reality.

The effect of restrictions on quantitative and quality H are country specific, depending on the nature of people's responses against the nature of regulations, such as semi vs. full lockdowns in local vs. country-wide scenarios, together with other provisions -these need to be further studied specific to the given countries and localities. However, our study shows how the net reproductive rate responds to H -forcing and V -forcing, giving concave-up vs concave-down functional responses, along with V -forcing, beginning to turn $R_0 < 1$ in many nations. The apparent in-elasticity in R_0 w.r.t. H in Sri Lanka may suggest that there may be mixed-effects in people's adhering to regulations. In contrast, countries such as Taiwan are more elastic, thus showing the firmness and the strength in controlling the wave drastically. What regulations attribute to the elasticity in the degree of $H\%$ needs a country-specific analyses.

Our findings may be useful as a tool for decision-support in controlling the disease spread and deaths in nations, when the effect of vaccines on forcing down the transmission is either weak, given the new variants, or not administered, or less affordable to nations.

Models and Methods

We obtained Covid19 related daily new cases $C(t)$, deaths $D(t)$ and vaccinations $V(t)$ data of 127 countries from Oxford University Covid19 database¹¹ (Note: t is time). Taking Sri Lanka as a reference, we modeled the data from April 15, 2021 as a starting point of a new infection wave, as its new surge of deaths began around such time. We obtained Home-stay ($H\%$) proxy metrics from Google¹⁰ as a surrogate for the percentage increase in people's homestay as per the mobility restrictions with respect to their pre-Covid normal. The $H\%$ data, which the Google had, were for the same 127 countries. We used a system of discrete time-dynamical equations to model the disease transmission processes over time, incorporating the effects of $H(t)\%$ on decreasing the infection rate β , and $V(t)$ on decreasing the number of susceptible $S(t)$ in the population over time. This allowed us to compute the net reproductive rate R_0 of the disease in each country, and to analyze how it responds to various levels of $H\%$ and cumulative vaccinations $V_c\%$ to support in management decision making.

Firstly, we took ten island nations greater than 25000 to 8.0E6 km² in land area, ranging from Haiti to Australia, with countries' populations ranging from 10 to 270 million, to test our prototype disease dynamical models that we developed. We tested three alternative nested model hypotheses: (1) M_H incorporating only the effect of $H\%$, (2) M_V incorporating only the effect of $V_c\%$, and (3) M_{HV} incorporating the effect of both the $H\%$ and the $V\%$. We used the all-representative best-fitted model for the general analyses of the disease dynamics across all 127 nations.

Modeling R_0 as a function of $H(t)$ and $V_c(t)$

We take $S(t)$ as the number of susceptible individuals to the disease in a total population of, N , and $I(t)$ as the number of newly infected individuals on day t . Per the mass-action law, we write the number of daily new infections as a linear function of $S(t)$, normalized with

207 respect to N , with a time-integral of $I(t)$ of the infected individuals during the past period
 208 from $t = (t - t_{Is})$ to $t = (t - t_{Ie})$ days through which the infection is transferable to others after
 209 staying an incubation period of t_{Ie} days by each. Thus, we write the number of new infections
 210 on day t as $\beta(S(t)/N)I_r(t)$, where β is the infection rate per day, and $I_r(t)$ is an integral given
 211 by $I_r = \int_{t=t-t_{Ie}}^{t=t-t_{Is}} I(t)$ normalized dividing by the infection period $(t_{Ie} - t_{Is})$. A meta-analysis
 212 by Elias et al.¹² has indicated that the mean incubation period for Covid19 was 6.38 days on
 213 average. In a review on epidemic models of Covid19, Xiang et al.¹³ have suggested that the in-
 214 fectionous period persists for 2.3–10 days on average. Thus, we take the range of infectious period
 215 to be a conservative 5 to 13 days backwards in time from day t , of the individuals belong in the
 216 above integral that are infectious as at day t . We assume that the recovered individuals never
 217 get re-infected during the modeling time, which is 144 days since the beginning of the new Covid
 218 wave. Thus, at the beginning of the process, we write $S(t = 0) = N - \int_{-\inf}^{t=0-t_{Ie}} I(t) - \int_{-\inf}^{t=0} D(t)$
 219 for the non-vaccinated scenario, where $D(t)$ are the number of daily deaths.

220
 221 For the vaccinated scenario, we deduct the $S(t = 0)$ by the cumulative number vaccinated,
 222 V_c , up to t_v days backwards from day $t = 0$, assuming that it takes about $t_v = 14$ days for an
 223 individual to be fully immune after receiving the full vaccination as per the recommendation
 224 by health experts, thus, writing the the likelihood of those vaccinated being non-reinfecting, or
 225 removed from the susceptible as, $\nu V(t - t_v)$, with ν being the vaccine efficacy, s.t., $0 < \nu < 1$.
 226 Shapiro et al.¹⁴ have indicated that the efficacy of Covid19 vaccines against the known variants
 227 was at 84% on average, and while those vaccinated get infected, their likelihood of transmission
 228 of the disease to others estimated at 54%. However, we assume ν to be between a conservative
 229 fixed 0.8 in initial model parameterization of the ten nations, and between 0.4 to 0.9 later in
 230 parameterising the models for all nations. This wide range allows lowering the efficacy of the
 231 vaccine in scenarios such as in the emergent of new variants.

232
 233 We consider the observed, or the identified new cases, $C(t)$, are immediately self-quarantined
 234 or hospitalized in the case of Covid19, such that, they are isolated from being able to infect

other individuals in the community, that is, being removed from the $I_r(t)$, not being considered for the mass-action effect in contributing to further disease spread. We take the probability of identification of the infected from the currently infectious as ϵ , allowing its range to be between a conservative, 0.15 to 0.6, in the parameter estimations. It is known that symptomatic percentage was 13 – 18%¹⁵ in Covid19. Thus, we further allowed a provision for being some identified in random checking.

We assume daily deaths $D(t)$ are a fraction of those identified and quarantined, or hospitalized cases, $C(t)$, accumulated between the t_{Ds} and t_{De} time window into the past, such that, the daily deaths are give by μC_r , s.t., $C_r = \int_{t=t_{De}}^{t=t_{Ds}} C(t)$ averaged over the interval $(t_{De} - t_{Ds})$, s.t., $0 < \mu < 1$. Contou et al.¹⁶ have reported that the median survival time, of 73 out of 153 patients admitted to ICU's being critically ill due to refractory respiratory failure, shock with multiorgan failure, cardiac death, and neurological death, was 14 days. Geetha et al.¹⁷ have shown that the average time to peak the severity of symptoms, since the symptoms began, was 7 days on average. Hence, we take a conservative 7 to 14 day window for t_{De} and t_{Ds} from the day of showing up symptoms for individuals, identified as new cases, C , to be subjected to death. Since the deaths are considered from those quarantined $C(t)$, removed from $I(t)$, $D(t)$ also has already been taken off from the $I(t)$ similar to $C(t)$, out of the mass-action effect.

Thus, a discrete time-dynamical community Covid19 infection model can be written as

$$S(t + \Delta t) = S(t) - \beta(S(t)/N)I_r(t)\Delta t - \nu V(t - t_v)\Delta t \quad (1)$$

$$I(t + \Delta t) = \beta(S(t)/N)I_r(t)\Delta t - \epsilon I_r(t)\Delta t \quad (2)$$

$$C(t + \Delta t) = \epsilon I_r(t)\Delta t \quad (3)$$

$$D(t + \Delta t) = \mu C_r(t), \quad (4)$$

where, $\Delta t = 1$ is one day in our study.

To model the effect of Home-stay $H(t)\%$ percentage on reducing the infection rate β , we take β as, $\beta = \gamma(1 - \theta(H(t)/100)^k)$. Note that this functional formulation allows β to decrease as a concave-up or -down function with increasing $H\%$, capturing the effectiveness of mobility regulations on $H\%$ reflecting on the rate of infection. We assume that countries having firm restriction on people's mobility may produce a concave-down relationships, vice versa. Furthermore, $k = 1$ yields the linearity in the relationship, and $\theta = 0$ yields the Null model, in which the $H\%$ has no impact on the dynamics yielding $\beta = \gamma$.

Thus, the three alternative model-hypotheses we considered are give as below:

Model 1 (M_H) : Given by setting $\nu = 0$.

Model 2 (M_V) : Given by setting $\theta = 0$.

Model 3 (M_{HV}) : The Full model.

From the above system of equations, we can write the number gets newly infected at day $t + \Delta t$ as $I(t + \Delta t) = \beta(S(t)/N)I_r(t) - \epsilon I_r(t)$. Hence, it yields the proportion $I(t + \Delta t)/I_r(t) = (\beta\Psi(t) - \epsilon)$, where $\Psi(t) = S(f(V_c(t - t_v)))/N$ between 0 and 1, s.t., $V_c = \int_{t=-inf}^{t=t-t_v} V(t)$, i.e., the cumulative number of vaccinations at time point $(t - t_v)$. Note that when the $\int I(t + \Delta t)/\int I_r(t) > 1$ over an infectious window, the number infected in the community inclines, whereas, when it is < 1 , the number infected in the community declines. Incorporating the H -forcing, s.t., $\beta = \gamma(1 - \theta(H(t)/100)^k)$, thus, we can write,

$$R0(H(t)) = \gamma\Psi(t)(1 - \theta(H(t)/100)^k) - \epsilon. \quad (5)$$

This is a metric of net reproductive rate $R0$ of the infection written as function of H - and V -forcing over time.

Fitting alternative model-hypotheses to the data and running simulations

We fitted the discrete system of time-dynamical equations to daily $C(t)$ and $D(t)$ data using the Matlab non-linear least-squares optimization function *lsqcurvefit* to estimate the model parameters. We used the *nlparci* function to derive the confidence intervals of the estimations from the resulting residuals, together with the Jacobian. Furthermore, we computed the Arkaike information criteria (AIC), of which the smallest value suggests the best among the competing alternative model hypotheses, after penalizing for the degrees of freedom of the models in explaining the variations in the dynamical data. Using the model that best explained the data, we computed the net reproductive rate $R_0(H(t), V(t))$ and $\beta(H(t))$ and their functional relationships with H - and V - forcing for further analyses. In fitting the data to models, we did not smooth data, but let the models capture the moving averages by themselves.

We simulated forecast of the model dynamics based on the general M_{HV} model for the following different scenario: $H(t)\% = [0, 10, 20]$, and $V(t) = [0, 5E+5]$ per day. It also allowed comparing the threshold values of $H(R_0 = 1)$ which the mathematical theory suggested.

Analysis of the World data from 124 countries

We fitted the generalized model M_{HV} to the data from 124 countries (listed in the Appendix). We also (1) tracked $R_0(t)$ and $\beta(t)$ over time t with their confidence intervals, (2) computed the functional responses of R_0 and β w.r.t. $H\%$, (3) change of R_0 w.r.t. vaccinated percentage $V_c\%$, and (4) R_0 w.r.t. $H\%$ and $V_c\%$ simultaneously, for each individual nation. We summarize the functional relationships between the (1) current R_0 (averaged over the last 7 days) and the percentage vaccinations $V_c\%$ for all nations, (2) $H(R_0 = 1)$ vs. $V_p\%$, the proportion non-susceptible, and (3) R_0 vs. $H\%$ for all nations. Here, the functional relationships used for the above were: $R_0 = \gamma\Psi(1 - \theta(H/100)^k) - \epsilon$, where Ψ is the susceptible population proportion which is a function of $V_c\%$, and $H(R_0 = 1) = [(1/\theta)(1 - (1/(\gamma\Psi))(1 + \epsilon))]^{1/k}$.

Data availability

The copies of the Covid19 new cases, deaths and vaccination data obtained from the Oxford University¹¹ and the community mobility reports for the same from Google¹⁰, of the 127 nations, plus the Matlab program coding developed for model fitting and data analyses needing to reproduce the results of all graphs and tables and estimations, will be made available to the reviewers upon request, and will be published online for public access.

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Author Contributions:

RR developed the concept and the focus of the research. HR contributed to developing mathematical and statistical model formulations. MR fitted the data to models with improvisations to models and produced the results. All authors contributed to writing.

Figures and Tables

Figure 1: The World data: The net reproductive rate R_0 vs. the percentages of Home-stay $H\%$ at different percentages of the population vaccinated plus recovered, $V_p\%$

The R_0 decreases with the increasing $H\%$ at (a) $V_p = 0\%$, that is 0% is vaccinated plus recovered from the susceptible, (b) $V_p = 25\%$, and (c) $V_p = 50\%$. Here, we plotted the 106 out of the 124 nations based on the estimated M_{HV} model that explained the variation in the nations' respective data. The 95 nations out of the 106 allowed enough variation in the degree of $H\%$ above the pre-Covid normal to make it possible to calibrate the R_0 vs. $H\%$ functional relationship based on the model. (Note that $V_p \geq V_c$, where V_c is the vaccinated population percentage). The functional relationship: $R_0 = \gamma \Psi (1 - \theta (H/100)^k) - \epsilon$, where Ψ is the susceptible population proportion, that is, the proportion of the total population N minus the effective number out of the vaccinated, νV_c , minus the number recovered, assuming ν as the likelihood that a vaccinated individuals is not re-infected, or as a proxy for the average efficacy of the vaccines. The $R_0 < 1$ indicates the threshold below which there is a tendency for the disease to go extinct. (see Appendix for country-specific graphs).

Figure 2: **The World data: Homestay $H\%$ percentages vs. the vaccinated plus recovered population percentages**

The homestay $H\%$, required at $R0 = 1$, given by the estimated M_{HV} model, declines with the increase in the percentage $V_p\%$, that is, the vaccinated plus the recovered in the populations. The functional relationship: $H(R0 = 1) = [(1/\theta)(1 - (1/(\gamma\Psi))(1 + \epsilon))]^{(1/k)}$, where $\Psi = (1 - V_p\%/100)$. The graph is drawn based on the M_{HV} model that explained the variations in data in 106 out of the 124 nations.

Figure 3: **Example: The M_{HV} model hypothesis, incorporating forcing by Homestay $H\%$ and cumulative Vaccinations $V_c\%$ on disease spread dynamics, fitted to the data in four regulatory-wise contrasting island nations.**

The top panel: Daily homestay $H(t)\%$ and the cumulative vaccinations $V_c(t)\%$ over time: Australia: No major V -forcing nor H -forcing; Taiwan: No major V -forcing but high H -forcing, Sri Lanka: Major increase in both V -forcing and H -forcing, United Kingdom: Major increase in V -forcing and no H -forcing. The bottom panels: The model M_{HV} fitted to new Cases, $C(t)$, and Death, $D(t)$, data, and the resulting net reproductive rate, $R_0(H(t), V_c(t))$, and the infection rate, $\beta(H(t))$, over time. The $R_0 < 1$ indicates a tendency towards disease-extinction. The estimated parameter values and model selection criterion AIC are given in Table.1 and also the Table.1 in the Appendix. The model fitted to 124 countries are given in the Appendix.

Figure 4: **Example: Functional responses of R_0 vs. $H\%$ and $V_c\%$ for management forecasting:**

Top: The Home-stay percentage $H(t)\%$ and the cumulative vaccinations $V_c(t)\%$ in four contrasting island nations: Australia: showing No major V -forcing nor H -forcing; Taiwan: No major V -forcing but high H -forcing, Sri Lanka: Major increase in both V -forcing and H -forcing, United Kingdom: Major increase in V -forcing and no H -forcing. Bottom: Functional relationships between the infection rate β vs. $H\%$, and net reproductive rate R_0 vs. $H\%$. The concave-up or-down relation is determined by the parameter k , depending on if $k < > 1$ in the H -forcing function, which is $\beta = \gamma(1 - \theta(H/100)^k)$. The $k = 1$ yields the linear relationship. The curve may turn up or down depending on the quality and the strictness of the mobility controls. The $V_c\%$ pulls the $R_0(H)\%$ curve down forcing it towards $R_0 = 1$ or lower. Here, the effect $E_f = \theta(H/100)^k$, s.t. $\beta = \gamma(1 - E_f)$. Simulation forecasts based on the calibrated M_{HV} model indicate how many more get infected from the status quo (i.e., as of today) for a choice of management scenarios of daily $H(t)\%$ and $V(t)$ administered. The simulations further show how an increase in the vaccinated plus recovered, $V_p\%$, forces the R_0 to shift lower with respect to $H\%$. The graphs for the 124 countries are given in the Appendix.

Table 1: **The projected percentages of homestay $H\%$ and vaccinations plus recovered, $V_p\%$, required to bring R_0 below 1, for the ten island nations (the prototype)**

The Akaike Information Criteria (AIC) values of the fitted alternative M_H , M_V and M_{HV} models, and the critical values of $H(R_0 = 1)\%$ and $V_p(R_0 = 1)\%$ computed based on the all-representative M_{HV} model are given (see graphs in the Appendix for all nations). The coefficient ν , a proxy for the efficacy of the vaccines, was set at 0.8 in island estimations. Thus, the degrees of freedom (df) in both M_H and M_{HV} models become 4. NLL-Negative log likelihood of the model fits. And μ is the daily death rate. Other parameter values are given in the Table.1 in the Appendix. The graphs of $H(R_0 = 1)\%$ with respect to $V_p\%$, and R_0 with respect to $H\%$ based on the M_{HV} are given in the Appendix. Note: *ap* stands for, as at present.

Island	Model	Parameters and Metrics						
		$H(R_0 < 1)$ @ $V_p\% = ap$	$V_p(R_0 < 1)$ @ $H\% = 0$	μ (d^{-1})	df	NLL	AIC	Working Rank
United Kingdom	M_H	—	—	0.002	4	7.02E2	1.41E3	3
	M_V	—	—	0.002	2	6.12E2	1.23E3	2
	M_{HV}	> 30	> 52	0.002	4	6.01E2	1.21E3	1
Taiwan	M_H	—	—	0.003	4	3.70E2	7.47E2	2
	M_V	—	—	0.053	2	4.65E2	9.34E2	3
	M_{HV}	> 13	> 72	0.043	4	3.53E2	7.13E2	1
Sri Lanka	M_H	—	—	0.022	4	4.57E2	9.23E2	1
	M_V	—	—	0.024	2	4.98E2	1.00E3	3
	M_{HV}	> 28	> 52	0.024	4	4.59E2	9.27E2	2
Philippines	M_H	—	—	0.017	4	5.23E2	1.05E3	1
	M_V	—	—	0.017	2	5.38E2	1.08E3	3
	M_{HV}	> 20	> 70	0.017	4	5.28E2	1.06E3	2
Japan	M_H	—	—	0.005	4	5.68E2	1.14E3	1
	M_V	—	—	0.005	2	6.24E2	1.25E3	3
	M_{HV}	> 15	> 50	0.005	4	5.88E2	1.18E3	2
Ireland	M_H	—	—	0.002	4	3.72E2	7.52E2	1
	M_V	—	—	0.002	2	4.46E2	8.97E2	3
	M_{HV}	> 10	> 55	0.003	4	3.99E2	8.05E2	2
Indonesia	M_H	—	—	0.036	4	6.34E2	1.28E3	2
	M_V	—	—	0.040	2	6.62E2	1.33E3	3
	M_{HV}	> 15	> 80	0.037	4	6.32E2	1.27E3	1
Haiti	M_H	—	—	0.002	4	4.25E2	8.59E2	2
	M_V	—	—	0.044	2	4.37E2	8.78E2	3
	M_{HV}	—	> 50	0.037	4	4.24E2	8.56E2	1
Dominican Republic	M_H	—	—	0.007	4	4.45E2	8.97E2	3
	M_V	—	—	0.007	2	4.22E2	8.49E2	2
	M_{HV}	> 20	> 70	0.006	4	4.15E2	8.37E2	1
Australia	M_H	—	—	0.007	4	2.93E2	5.95E2	1
	M_V	—	—	0.007	2	3.17E2	6.37E2	2
	M_{HV}	—	> 50	0.007	4	3.23E2	6.54E2	3

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [AppendixScientificReports.pdf](#)