THE LANCET Infectious Diseases

Supplementary appendix

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13 **1.** Additional information on data collection

Dengue. The incidence of dengue fever is calculated by dividing the number of dengue cases by the total population that year. The dengue incidence in 2020 is subtracted from the average of the incidence in the same time from 2014 to 2019 in the corresponding country and then divided by the average of the incidence to obtain the net change of dengue incidence in 2020.

2m temperature. The temperature of the air 2 meters above the earth's surface. Taking atmospheric conditions into account, 2m temperature is calculated using the interpolation method between the lowest model layer and the surface. The Kelvin temperature minus 273.15 is converted to degrees Celsius (°C).

Surface temperature. The temperature of the earth's surface. Surface temperature is the theoretical temperature required to satisfy the surface energy balance. It represents the temperature at the top layer, which has no heat capacity and therefore responds instantly to changes in surface flux. The Kelvin temperature minus 273.15 is converted to degrees Celsius (°C).

Relative humidity. The humidity of the air 2 meters above the surface. Its original data
is the dew point temperature of 2 meters. Combined with temperature and pressure, it
can be used to calculate the relative humidity.

31 Total precipitation. Liquid and frozen water, including rain and snow, falling on the 32 earth's surface. It is the sum of mass precipitation (precipitation produced by large-scale 33 weather patterns, such as troughs and cold fronts) and convective precipitation 34 (precipitation produced by convection when the air in the lower part of the atmosphere 35 is warmer and less dense than the air in the upper part of the atmosphere). The 36 precipitation variable does not include fog, dew, or precipitation that evaporates in the 37 atmosphere before it falls to the Earth's surface. Precipitation is measured at a depth of 38 meters.

39 Convective precipitation. The cumulative amount of convective precipitation falling 40 to the Earth's surface. It is the precipitation phenomenon caused by atmospheric 41 convection movement, and the rainfall is large in a short period of time. The units of 42 precipitation are depth in metres.

Government stringency index (SI). SI is the simple average of 9 component indicators, including 8 indexes of containment and closure policies and 1 public information campaigns of health system policies. OxCGRT published the calculation formula and detailed definition of specific indicators.¹ The indexes range from 0 to 100. A higher score indicates a more stringent COVID-19 response policy (0 for no response policy and 100 for the most stringent response policy).

Human mobility. The Google Mobility Trends data set measures the number of visitors
per day in a particular site category and compares this change to the baseline day before
the outbreak of the COVID-19 pandemic. The baseline is the median value of the first
five-week period of 2020 (3 January to 6 February). The baseline human mobility was
defined as 100% in this study.

54

55 2. Detailed information on the analytical framework

56 2.1 Computation on Mann-Kendall test

57 In the Mann - Kendall test, the null hypothesis H_0 for climate time series data

58 $(X_1,...,X_{12})$ were independent of n, random variable with the distribution of the sample. 59 The alternative hypothesis H_1 is bilateral inspection, to $k, j \le 12$, and $k \ne n$, X_i 60 and X_j distributed is not the same, the test statistic S calculation is as follows:

61
$$S = \sum_{k=1}^{n-1} \sum_{j=k+1}^{n} Sgn(X_j - X_{12})$$

62 S is a normal distribution with a mean of 0 and a variance of 63 Var(S) = n(n-1)(2n+5)/18.

64 When n > 10, the standard positive system variable is calculated by the following 65 formula:

$$Z\begin{cases} \frac{s-1}{\sqrt{\operatorname{var}(s)}} & S > 0\\ 0 & S = 0\\ \frac{s+1}{\sqrt{\operatorname{var}(s)}} & S < 0 \end{cases}$$

66

67 So, in the trend of the bilateral inspection, on a given a confidence level α , if 68 $|Z| \ge Z_{(1-\sigma/2)}$, the null hypothesis is not acceptable. On a confidence level, the time 69 series data exist obvious up or down trend. For statistic Z, when it is greater than zero, 70 it has an upward trend, and when it is less than zero, it has a downward trend. The 71 absolute value of Z in greater than or equal to 1.28, 1, 64 and 2.32, respectively by 72 the reliability of 90%, 95%, 99% of the test of significance.

73 **2.2 Details on the Spatiotemporal Bayesian hierarchical model**

We specified a spatiotemporal Bayesian hierarchical model that responded to the
monthly dengue cases in 23 countries from 2014 to 2019.² Hypothesis of negative
binomial distribution explains the possible overdistribution of dengue cases:

77

$$y_{c,t}$$
 | dengue case_{c,t}, $\kappa \sim NegBin(dengue \ case_{c,t}, \kappa)$

78 $\log(\text{dengue } case_{c,t}) = NS(\text{climate } factors_{c,t}, \text{var } df, lag \ df) + \beta_{c,m(t)} + \varphi_{c,a(t)} + \upsilon_{c,a(t)} + \alpha_{c,a(t)} + \sigma_{c,a(t)} + \sigma_{c,a(t)}$

79

80 Where, $y_{c,t}$ is the number of dengue cases, and is equal to $a_{(t)} = 2014,...,2019$, the 81 number of annual population per 100,000 *population*_{c, a(t)} multiplied by the estimated 82 value of country c = 1,...,23 for the incidence of unknown dengue fever 83 *dengue case*_{c,t}, κ is an over-discrete parameter. At the same time, we also test the 84 Poisson distribution model, but the goodness of fit standard, including the deviance 85 information criterion (DIC) is higher, so we use the negative binomial formula to 86 consider residual over-discreteness.

We first construct a baseline model that includes spatiotemporal random effects to explain inter-annual variability in seasonal and spatiotemporal correlation structures at national levels. Using cyclic first-order random walk priors, which allow each month to depend on the previous month. Interannual variations and long-term trends are explained by annual spatial random effects, which make any annual trend different over 92 the entire time period at a given location. Unstructured random effects allow for 93 independent region-specific noise, such as differences in media ecology, healthcare 94 access, and reporting rates. Structured spatial random effects allow for dependence 95 between adjacent countries due to common environmental and socio-economic 96 characteristics such as climatic zones and mobility of people.

97 The model parameters are estimated using the integrated nested Laplace approximation 98 in the Bayesian framework. INLA is directly used for full Bayesian inference in disease 99 mapping, avoiding the computationally intensive Markov chain Monte Carlo 100 technique.³ Parametric uncertainty is resolved by assigning prior distributions to parameters. Month autocorrelation random effects were used for 23 countries, in which 101 each month's effect was derived from the effect of the immediately preceding month. 102 103 This country-specific monthly random effect, $\beta_{c, m(t)}$ was assigned a cyclic random walk of order one, or first difference prior distribution, in which each effect is derived 104 from the immediately preceding effect, 105

106
$$\beta_{c, m(t)} - \beta_{c, m(t)-1} \sim N(0, \sigma^2_{\beta})$$

107 where $\beta_{c, m(1)}$ represents the parameter estimate for the month of January for 108 country c.

109 Fig.S13 shows the marginal posterior distribution of the monthly random effects in each 110 country using the best-fit "historical" model. Spatial unstructured and structured 111 random effects with specific countries can account for inter-annual variations due to unknown and unmeasurable spatial characteristics (e.g., the introduction of new dengue 112 113 serotypes or arboviruses at specific times and places) and long-term trends. For the 114 spatial components, we use a modified Besag-York-Mollie (BYM) model with a scaled 115 spatial component, which helps to assign interpretive superpriors and make these 116 superpriors transferable across different geographic environments. The modified BYM 117 model consists of one precision parameter and one mixing parameter. The precision 118 parameter represents the marginal precision and controls the variability explained by the spatial effect. The mixing parameter distributes existing variables between an 119 unstructured and structured component, $\varphi_{c, a(t) + \mathcal{O}_{c, a(t)}}$. The unstructured component 120 121 helps explain unknown or unobserved confounders, such as population immunity, quality of health care, and local vector control interventions. In addition to the single-122 123 scale parameters in the negative binomial model, it introduces an additional source of 124 variability (potential effects) into the model, which helps to model excessive dispersion. 125 Structured components assume that if regions share boundaries, there is spatial 126 dependency that acts as a substitute for spatial autocorrelation between nearby regions 127 due to shared environmental or socio-economic characteristics.⁴

128 **2.3 Details on the DLNM**

The influence of meteorological factors on human health is nonlinear (such as J, V or U shaped relationship) and shows lagged effect. Gasparrini introduced the Distributed Lag non-linear model (DLNM) into the study of the health effects of air temperature for the first time.^{5,6} Based on the ideas of traditional models such as generalized linear model and generalized additive model, they introduced a cross basis process to describe the distribution of dependent variables in the independent variable dimension and lag dimension at the same time, so as to evaluate the lag effect and nonlinear effect of exposure factors at the same time.

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138 We used a distributed lag nonlinear model (DLNM) to establish a negative binomial 139 distribution to derive an estimate of a specific variable-dengue cases association, expressed as relative risk (RR). This model can describe complex nonlinearity and lag 140 141 correlation by defining a combination of two functions that define the traditional 142 exposure - response correlation and the additional lag - response correlation, 143 respectively. Lag-response associations represent temporal changes in given exposure 144 risk and estimates the distribution of immediate and delayed effects that accumulate during the lag. 145 The technical details and terminology are explained in detail in literature and tutorials.⁶ 146

147

148 Basis function refers to the function that converts the independent variable into a new 149 variable set and includes it in the design matrix of the model to estimate its effect.

150

The dependent variable is the number of dengue cases.⁶ In this study, the exposure factors were 2m temperature, convective precipitation environmental factors and PHSM policy factors. For environmental covariates, we used population-weighted averages to reduce the biases particular for sparsely populated countries with big meteorological gradients:

156
$$PrEnv_{c} = \frac{\sum_{i=1}^{n} pop_{i} \times Env_{i}}{\sum_{i=1}^{n} pop_{i}}$$

157 Where $PrDen_c$ is the population-weighted environmental factors in country c, pop_i 158 is the population in pixel i, and Env_i is the environmental factor in pixel i, and n is 159 the total number of pixels in country c.

160

161 The new variable generated by the transformation of the basis function of the 162 independent variable is called the change relationship between the basis variable and 163 the dependent variable can be described in a more detailed way through the 164 transformation of the independent variable, and a more accurate exposure response 165 relationship can be obtained. The basis functions of the independent variable dimension include the meteorological cross basis function of a natural cubic spline of time with 3 166 167 degrees of freedom (df), and the cross basis function of PHSM and human mobility of 168 a natural cubic spline of time with 1 df. Their boundary sections are the minimum and 169 maximum values of their respective variables, respectively.

170

171 Due to the hysteresis of the influence of exposure, the outcome of the day may be affected by the exposure L months ago at the longest. In order to describe the hysteresis 172 effect of exposure, it is also necessary to select a basis function to transform the 173 174 hysteresis to form a matrix. Based on the available literature and knowledge of the 175 vector-borne process of human disease transmission, the lag time for weather variables is up to three months.⁷⁻⁹ In order to describe the lag effect of exposure, the basis function 176 of the lag dimension is a natural cubic spline of time with 1 df, and the maximum lag 177 178 is 3 months. The boundary nodes are placed at 0 and 3 months respectively, and two 179 internal nodes are distributed for 1 month and 2 months. The difference between cases 180 reported in last year and mean annual cases 2013-2019 were introduce to account for 181 population immunity built up. Since dengue risk and vulnerability to COVID-19 related disruptions is likely to be affected by wealth, GDP per capita was also included in the
 model. Population size was included as an offset variable. Q AIC information criteria
 are used to evaluate the model.

185 **2.4 Computation of the preventive fraction**

Measuring attributable risk and prevention is an integral part of epidemiological analysis, especially when it is aimed at planning and evaluating public health interventions. Forward attribution is well suited to separating the risks attributable to different ranges of components because their sum matches the overall risk. In addition, from current exposures to future risks, a forward-looking view seems better suited to quantifying the health burden and prevention from a specific exposure event, as it is based on more consistent counterfactual conditions.⁷

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We select the forward attribution method to quantify the preventive fraction (PF) for COVID-19 dengue transmission. For a particular month t in 2020, the dengue prevention attributable to a policy index or human mobility X_t is defined as the fraction $PF_{x,t}$ of dengue cases with 3 months as the maximum lag period, defined by:

198
$$PF_{x,t} = 1 - \exp(\sum_{l=0}^{L} \beta_{xt}, l)$$

199 With $\sum \beta_{x_{t,1}}$ as the overall cumulative log-relative risk for policy index or human 200 mobility x_t in month t. The risk estimate $\sum \beta_{x_{t,1}}$ is calculated by the cumulative 201 correlation of the policy index or human mobility over three months and re-centered on 202 the base values of the non-PHSM. The basic value is the counterfactual condition to 203 define the culpable protective factors. Therefore, the attributable prevention can be 204 interpreted as the excess cases due to non-basic value.

205 This method is described in detail in Gasparrini's previous article.⁷

206 **2.5 Model variable description table**

| Variable | Description |
|-------------------------------|---|
| <i>c</i> = 1,,23 | Number of countries |
| <i>t</i> = 1,,72 | Number of months between January 2014 and December 2019 |
| $a_{(t)} = 2014, \dots, 2019$ | Annual |
| m(t) = 1,, 12 | January to December |
| К | Overdispersion parameter |
| NS | Natural cubic spline |
| var df | Degree of freedom of variable |
| lag df | Degree of freedom of lag |

| Yc, t | Number of reported cases |
|---|--|
| annual anomaly $(a(t) - 1)$ | Short-term immunity |
| $\beta_{c,m(t)}$ | Country-specific monthly random effect |
| $\boldsymbol{\varphi}_{c,a(t)} + \boldsymbol{\mathcal{U}}_{c,a(t)}$ | Yearly spatial random effects. |
| Climate factors | Surface temperature and convective precipitation |
| Population | Per 100 000 population in each country |
| PHSM | Public health and social measures |
| HMB | Human movement behaviours |
| ŷ | The mean predicted case counts for 2020 from the historical model on the log scale |
| | |

1. Supplementary Table S1-S4

Table S1: 2014-2019 Monthly Dengue - Environment (i.e., non-PHSM, non-HMB) covariate DLNM model adequacy results for models of increasing complexity. The deviance information criterion (DIC) and the cross-validated (CV) mean logarithmic score for models of increasing complexity. Lower scores indicate a better fitting model.

| Model | Dengue incidence rate estimate | DIC | CV mean log score |
|----------|---|----------|----------------------|
| Baseline | Environmental covariates + Spatiotemporal random effects | 27345.71 | 8.288 |
| mt | Base model + mt DLNM | 27302.61 | 8.27 |
| st | Base model + st DLNM | 27301.43 | 8.269 |
| rh | Base model + rt DLNM | 27320.72 | 8.275 |
| tp | Base model + tp DLNM | 27335.83 | 8.28 |
| cp | Base model + cp DLNM | 27328.32 | 8.275 |
| mt+rh | Base model $+$ (mt $+$ rh) DLNM | 27276.04 | 8.259 |
| mt+tp | Base model $+$ (mt $+$ tp) DLNM | 27279.92 | 8.26 |
| mt+cp | Base model + ($mt + cp$) DLNM | 27274.22 | 8.256 |
| st+rh | Base model $+$ (st $+$ rh) DLNM | 27275.17 | 8.259 |
| st+tp | Base model $+$ (st $+$ tp) DLNM | 27275.15 | 8.258 |
| st+cp | Base model + (st + cp) DLNM | 27269.41 | 8.255 |
| rh+tp | Base model + $(rh + tp)$ DLNM | 27323.98 | 8.274 |
| rh+cp | Base model $+$ (rh $+$ cp) DLNM | 27312.84 | 8.268 |
| mt+rh+tp | Base model + $(mt + rh + tp)$ DLNM | 27278.59 | 8.259 |
| mt+rh+cp | Base model + $(mt + rh + cp)$ DLNM | 27275.31 | 8.256 |
| st+rh+tp | Base model + $(st + rh + tp)$ DLNM | 27275.33 | 8.258 |
| st+rh+cp | Base model + $(st + rh + cp)$ DLNM | 27270.91 | 8.255 |

Environmental covariates: population immunity;

mt: 2*m* temperature; st: Surface temperature; rh: Relative humidity; tp: Total precipitation; cp: Convective precipitation.

Table S2: 2014-2019 Monthly Dengue - Environment (i.e., non-PHSM, non-HMB) covariate DLNM model including per capita GDP adequacy results for models of increasing complexity. The deviance information criterion (DIC) and the cross-validated (CV) mean logarithmic score for models of increasing complexity. Lower scores indicate a better fitting model.

| Model | Dengue incidence rate estimate | DIC | CV mean log score |
|--------------|---|----------|-------------------|
| Baseline+GDP | Environmental covariates + Spatiotemporal random effects | 27344.83 | 8.287 |
| mt+GDP | Base model + mt DLNM | 27302.15 | 8.27 |
| st+GDP | Base model + st DLNM | 27301.64 | 8.269 |
| rh+GDP | Base model + rt DLNM | 27320.67 | 8.275 |
| tp+GDP | Base model + tp DLNM | 27336.96 | 8.28 |
| cp+GDP | Base model + cp DLNM | 27329.10 | 8.276 |
| mt+rh+GDP | Base model + (mt + rh) DLNM | 27275.46 | 8.259 |
| mt+tp+GDP | Base model + (mt + tp) DLNM | 27279.23 | 8.26 |
| mt+cp+GDP | Base model + (mt + cp) DLNM | 27274.69 | 8.256 |
| st+rh+GDP | Base model $+$ (st $+$ rh) DLNM | 27275.22 | 8.259 |
| st+tp+GDP | Base model + (st + tp) DLNM | 27275.34 | 8.258 |
| st+cp+GDP | Base model + (st + cp) DLNM | 27269.45 | 8.254 |
| rh+tp+GDP | Base model $+$ (rh $+$ tp) DLNM | 27324.94 | 8.275 |
| rh+cp+GDP | Base model + $(rh + cp)$ DLNM | 27312.86 | 8.268 |
| mt+rh+tp+GDP | Base model + $(mt + rh + tp) DLNM$ | 27278.65 | 8.259 |
| mt+rh+cp+GDP | Base model + $(mt + rh + cp)$ DLNM | 27274.75 | 8.256 |
| st+rh+tp+GDP | Base model $+$ (st $+$ rh $+$ tp) DLNM | 27274.08 | 8.257 |
| st+rh+cp+GDP | Base model + (st + rh + cp) DLNM | 27271.13 | 8.255 |

Environmental covariates: population immunity + *GDP per capita;*

mt: 2*m* temperature; st: Surface temperature; rh: Relative humidity; tp: Total precipitation; cp: Convective precipitation.

Table S3: Overall cumulative 4-month association between PHSM, HMB and dengue transmission relative risk. 95% CI = 95% confidence interval.

| | PHSM | M (%) | | HMB (%) | | | | |
|-----|--------------------|--------------------|-----------------------------|--------------------|--------------------|--------------------|--------------------|--|
| CHI | SI (95% CI) | C1 (95% CI) | Non-Residential (95% CI) | Transit (95% CI) | Park (95% CI) | Grocery (95% CI) | Retail (95% CI) | |
| 0 | 1 | 1 | / | / | / | / | / | |
| 10 | 0.86 (0.8 - 0.93) | 0.84 (0.79 - 0.89) | / | / | / | / | / | |
| 20 | 0.74 (0.63 - 0.87) | 0.7 (0.62 - 0.79) | / | 0.03 (0 - 0.23) | / | / | 0.03 (0 - 0.25) | |
| 30 | 0.64 (0.5 - 0.81) | 0.59 (0.49 - 0.7) | 0.28 (0.13 - 0.59) | 0.05 (0.01 - 0.28) | 0.05 (0.01 - 0.31) | 0.01 (0 - 0.04) | 0.05 (0.01 - 0.3) | |
| 40 | 0.55 (0.4 - 0.76) | 0.49 (0.38 - 0.62) | 0.33 (0.17 - 0.63) | 0.08 (0.02 - 0.33) | 0.08 (0.02 - 0.36) | 0.01 (0 - 0.07) | 0.08 (0.02 - 0.36) | |
| 50 | 0.48 (0.32 - 0.71) | 0.41 (0.3 - 0.56) | 0.4 (0.23 - 0.68) | 0.12 (0.03 - 0.4) | 0.12 (0.03 - 0.43) | 0.03 (0.01 - 0.1) | 0.12 (0.03 - 0.42) | |
| 60 | 0.41 (0.25 - 0.66) | 0.34 (0.24 - 0.49) | 0.48 (0.31 - 0.74) | 0.18 (0.07 - 0.48) | 0.19 (0.07 - 0.51) | 0.06 (0.02 - 0.16) | 0.18 (0.07 - 0.5) | |
| 70 | 0.35 (0.2 - 0.62) | 0.29 (0.19 - 0.44) | 0.58 (0.42 - 0.8) | 0.28 (0.13 - 0.58) | 0.28 (0.13 - 0.6) | 0.12 (0.06 - 0.26) | 0.28 (0.13 - 0.6) | |
| 80 | 0.31 (0.16 - 0.58) | 0.24 (0.15 - 0.39) | 0.69 (0.56 - 0.86) | 0.43 (0.26 - 0.69) | 0.43 (0.26 - 0.71) | 0.25 (0.15 - 0.4) | 0.43 (0.26 - 0.71) | |
| 90 | 0.26 (0.13 - 0.54) | 0.2 (0.12 - 0.35) | 0.83 (0.75 - 0.93) | 0.65 (0.51 - 0.83) | 0.66 (0.51 - 0.84) | 0.5 (0.39 - 0.64) | 0.65 (0.51 - 0.84) | |
| 100 | 0.23 (0.1 - 0.51) | 0.17 (0.09 - 0.31) | 1 | 1 | 1 | 1 | 1 | |
| 110 | / | / | / | / | 1.52 (1.18 - 1.96) | 2.01 (1.57 - 2.58) | / | |
| 120 | / | / | / | / | / | 4.06 (2.47 - 6.65) | / | |

C1-School closing; HMB-Reduction in human mobility; '/'- Without the intervention; RR of the baseline values of PHSM=0 and Mobility=100 is 1.

| | Table S4: Overall cumulative proportion of dengue cases averted by PHSM and HMB in each countries and region. | | | | | | |
|-------------------|---|-----------------------|--------------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| A #22.5 | PHSM (%) | | HMB (%) | | | | |
| Areas | SI (95% CI) | C1 (95% CI) | Non-Residential (95% CI) | Transit (95% CI) | Park (95% CI) | Grocery (95% CI) | Retail (95% CI) |
| All | 54.18 (32.76 - 69.13) | 70.95 (55.55 - 80.48) | 30.95 (15.75 - 43.65) | 75.37 (44.21 - 90.91) | 70.51 (41.41 - 87.44) | 29.48 (12.17 - 49.03) | 75.56 (44.89 - 91.15) |
| Americas | 53.6 (33.27 - 69.93) | 71.53 (58.11 - 81.42) | 30.66 (15.75 - 45.38) | 73.54 (43.45 - 89.04) | 71.25 (41.51 - 87.11) | 29.05 (12.54 - 50.04) | 75.55 (45.02 - 90.55) |
| Southeast Asia | 56.46 (36.39 - 70.94) | 67.73 (53.38 - 78.03) | 32.1 (16.64 - 47.15) | 81.08 (53.28 - 93.79) | 66.56 (37.13 - 83.6) | 31.5 (13.76 - 51.1) | 75.64 (43.14 - 91.92) |
| Belize | 51.75 (31.44 - 67.71) | 71.88 (57.55 - 82.1) | 30.66 (15.87 - 45.23) | 82.7 (51.05 - 94.44) | 54.34 (25.4 - 77.34) | 38.99 (18.2 - 61.94) | 69.73 (35.9 - 88.99) |
| Bolivia | 31.04 (16.21 - 47.52) | 44.27 (30.84 - 57.34) | 28.81 (12.45 - 45.28) | 76.86 (42.03 - 93.55) | 70.58 (32.2 - 91.59) | 59.31 (26.96 - 84.8) | 77.19 (36.29 - 94.12) |
| Brazil | 46.38 (25.21 - 63.3) | 57.91 (42.66 - 68.71) | 27.41 (14.34 - 40.03) | 69.86 (42.56 - 85.98) | 71.64 (42.73 - 87.83) | 14.92 (6.98 - 23.29) | 74.9 (43.91 - 89.68) |
| Colombia | 55.37 (33.69 - 71.37) | 69.69 (54.23 - 80.08) | 43.26 (23.24 - 60.57) | 85.61 (57.54 - 96.23) | 81.28 (50.33 - 94.1) | 63.49 (35.7 - 82.69) | 86.6 (57.61 - 96.4) |
| Costa Rica | 60.59 (39.89 - 75.46) | 79.43 (67.16 - 87.24) | 49.14 (27.74 - 64.82) | 87.37 (65.3 - 96.03) | 87.02 (63.37 - 95.92) | 60.4 (35.7 - 76.39) | 84.5 (59.4 - 94.94) |
| DR | 45.05 (23.94 - 62.4) | 60.11 (44.73 - 72.92) | 30.19 (15.92 - 45.37) | 80.03 (48.73 - 94.45) | 63.43 (31.18 - 84.33) | 44.69 (22 - 65.73) | 71.47 (39.5 - 90.08) |
| Ecuador | 56.35 (33.67 - 72.99) | 70.86 (56.64 - 81.22) | 47.15 (24.43 - 64.37) | 87.31 (59.09 - 96.36) | 83.72 (54.21 - 95.26) | 69.2 (37.76 - 87.82) | 86.27 (56.76 - 96.44) |
| ES | 63.84 (39.82 - 78.75) | 75.17 (61.89 - 84.36) | 50.25 (30.94 - 66.95) | 88.73 (62.92 - 97.1) | 85.7 (57.62 - 95.93) | 69.49 (42.19 - 86.35) | 88.91 (63.47 - 96.95) |
| Guatemala | 61.6 (39.68 - 77.7) | 71.74 (58.04 - 81.98) | 42.42 (21.31 - 59.1) | 88.26 (61.97 - 96.81) | 74.33 (44.47 - 89.17) | 60.77 (33.72 - 78.69) | 81.05 (51.1 - 93.65) |
| Honduras | 65.33 (39.23 - 80.26) | 75.5 (63.64 - 84.9) | 50.8 (28.25 - 66.31) | 90.92 (67.44 - 97.8) | 77.98 (49.59 - 90.7) | 73.46 (43.15 - 88.86) | 89.65 (60.87 - 97.57) |
| Jamaica | 47.18 (28.92 - 63.72) | 61.15 (45.21 - 72.96) | 24.45 (12.51 - 36.21) | 57.64 (31.23 - 77.43) | 63.23 (34.84 - 83.51) | 36.6 (17.91 - 53.89) | 59.14 (31.91 - 78.82) |
| Mexico | 62.47 (41.39 - 76.74) | 80.53 (68.91 - 87.96) | 42.12 (23.62 - 56.82) | 84.17 (60.96 - 94.18) | 78.02 (50.89 - 90.6) | 35.67 (19.18 - 49.41) | 80.92 (55.87 - 93.04) |
| Nicaragua | 17.67 (10.46 - 24.72) | 47.72 (36.15 - 58.61) | 25.08 (13.48 - 35.86) | 64.6 (39.72 - 80.35) | 50.37 (27.4 - 66.84) | 31.1 (16.52 - 43.74) | 60.87 (35.27 - 77.45) |
| Panama | 52.71 (30.22 - 69.71) | 67.61 (52.13 - 78.44) | 46.6 (24.19 - 65.17) | 87.79 (59.7 - 96.49) | 84.22 (50.1 - 95.92) | 69.57 (39.35 - 87.62) | 88.5 (59.73 - 97.21) |
| Peru | 63.29 (40.49 - 77.26) | 72.11 (58.74 - 81.01) | 52.78 (29.61 - 70.39) | 90.28 (66.05 - 97.36) | 84.71 (53.8 - 95.47) | 73.31 (43.77 - 88.69) | 90.63 (66.71 - 97.83) |
| Venezuela | 61.66 (38.19 - 76.13) | 75.88 (61.91 - 84.76) | 39.29 (19.9 - 55.09) | 81.64 (54.11 - 93.05) | 74.24 (47.27 - 88.4) | 52.61 (29.17 - 70.38) | 79.38 (49.02 - 91.81) |
| | | | | | | | |

Table S4: Overall cumulative proportion of dengue cases averted by PHSM and HMB in each countries and region.

| Cambodia | 46.54 (28.51 - 60.75) | 79.68 (67.18 - 87.31) | 31.73 (17.08 - 43.58) | 83.47 (60.77 - 93.46) | 44.8 (25.36 - 60.14) | 37.9 (20.9 - 53) | 57.61 (34.21 - 74.03) |
|-------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| Laos | 50.39 (29.12 - 66) | 61.73 (47.71 - 72.53) | 22.06 (11.99 - 32.5) | 75.6 (46.96 - 89.94) | 28.07 (14.98 - 39.57) | 28.89 (12.27 - 46.78) | 60.86 (28.41 - 81.09) |
| Malaysia | 52.43 (31.54 - 66.74) | 68.61 (54.06 - 78.75) | 38.24 (19.45 - 53.67) | 85.35 (56.52 - 95.53) | 71.64 (43.26 - 89.38) | 44.79 (21.13 - 65.4) | 84.65 (55.09 - 96) |
| Philippines | 59.48 (36.64 - 74.35) | 73.58 (60 - 83.04) | 45.07 (24.45 - 62.68) | 89.92 (67.51 - 97.47) | 70.77 (40.97 - 86.72) | 61.32 (33.37 - 81.22) | 87.88 (59.57 - 96.99) |
| Singapore | 56.42 (37.27 - 70.09) | 61.78 (48.19 - 73.33) | 45.63 (26.63 - 61.58) | 86.75 (62.57 - 95.9) | 83.25 (55.51 - 94.62) | 31.78 (16.35 - 44.88) | 84.43 (57.96 - 94.98) |
| Thailand | 57.24 (36.84 - 72.11) | 71.22 (57.3 - 80.5) | 30.47 (16.53 - 43.08) | 80 (55.49 - 92.02) | 68.4 (41.06 - 84.67) | 9.55 (3.79 - 16.57) | 64.32 (36.53 - 82.42) |
| Vietnam | 62.02 (41.83 - 75.74) | 69.1 (55.56 - 78.64) | 17.11 (9.16 - 25.16) | 54.59 (28.57 - 75.77) | 56.03 (33.07 - 71.65) | 8.37 (1.62 - 19.83) | 57.65 (29.59 - 76.84) |

DR, Dominican Republic; ES, El Salvador; HMB-Reduction in human mobility; '/'- Without the intervention.

2. Supplementary Figure S1-S20

Figure S1: Seasonal variation in monthly dengue incidence for 2020 and average monthly dengue incidence for 2014-2019 in Latin America and Southeast Asia. (A) Seasonal variation of monthly dengue incidence for countries in Latin America. (B) Seasonal variation of monthly dengue incidence for countries in Southeast Asia. The percentage is the relative change ratio of annual dengue incidence in 2020 to the mean of 2014-2019. The gray dotted line is when countries started taking COVID-19 PHSM.

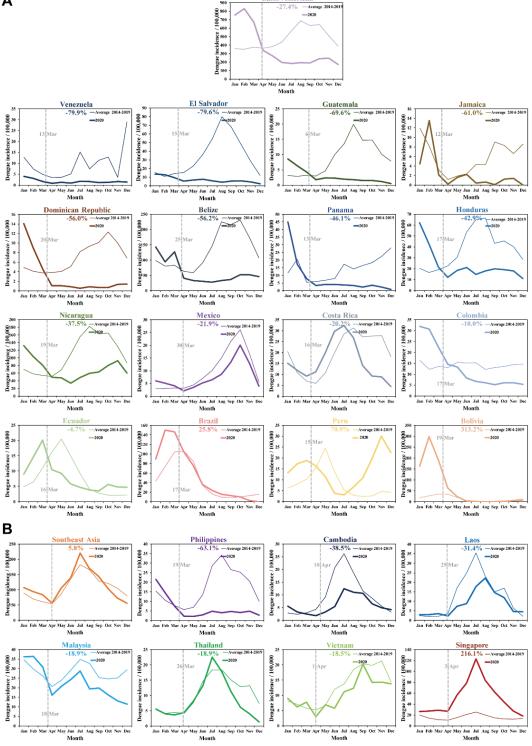
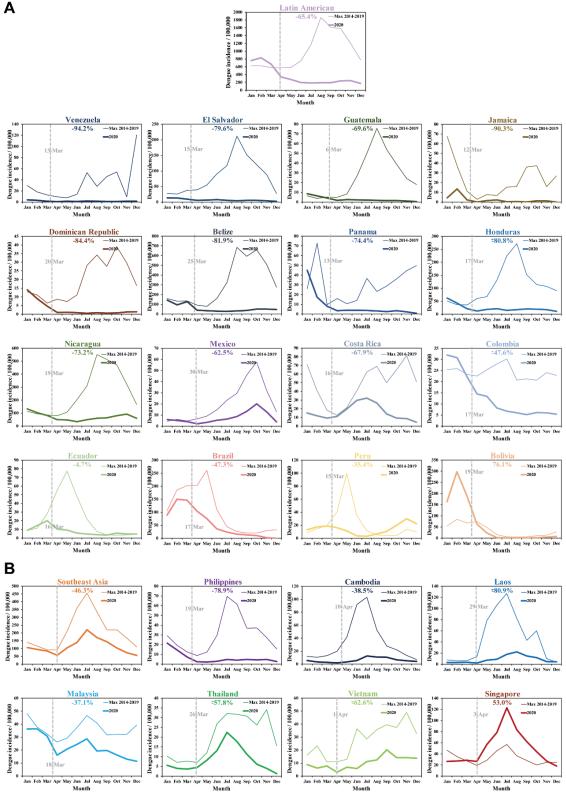


Figure S2: Seasonal variation in monthly dengue incidence for 2020 and maximum monthly dengue incidence for 2014-2019 in Latin America and Southeast Asia. (A) Seasonal variation of monthly dengue incidence for countries in Latin America. (B) Seasonal variation of monthly dengue incidence for countries in Southeast Asia. The percentage is the relative change ratio of annual dengue incidence in 2020 to the maximum value of 2014-2019. The gray dotted line is when countries started taking COVID-19 PHSM.



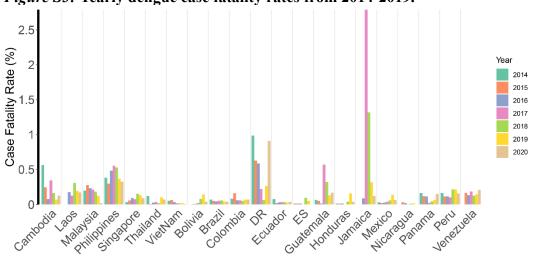


Figure S3: Yearly dengue case fatality rates from 2014-2019.

DR, Dominican Republic; ES, El Salvador.

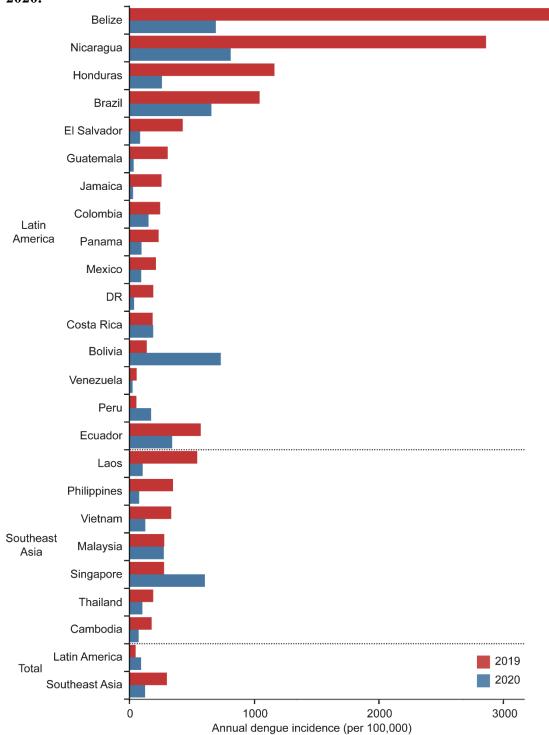


Figure S4: Distribution of annual dengue incidence for each country in 2019 and 2020.

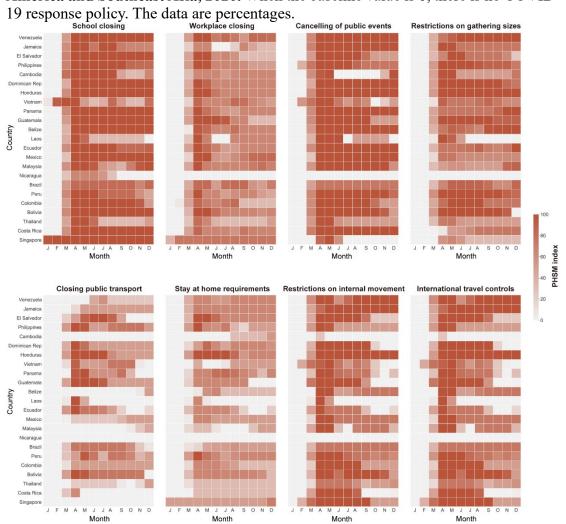


Figure S5: The change of 8 PHSM index response to COVID-19 in the Latin America and Southeast Asia, 2020. When the baseline value is 0, there is no COVID-19 response policy. The data are percentages.

Figure S6: The change of HMB response to COVID-19 in the Latin America and Southeast Asia, 2020. There are six categories of community mobility: residential, workplace, transit stations, park, grocery and pharmacy, retail and recreation. Global human mobility data is obtained from Google Community Mobility Reports. The selected observation time period is the mean value within 35 days after the national emergency response. The baseline is the median value, for the corresponding day of the week, during January 3, 2020 to February 6, 2020. The baseline value is 100 and data are percentages.

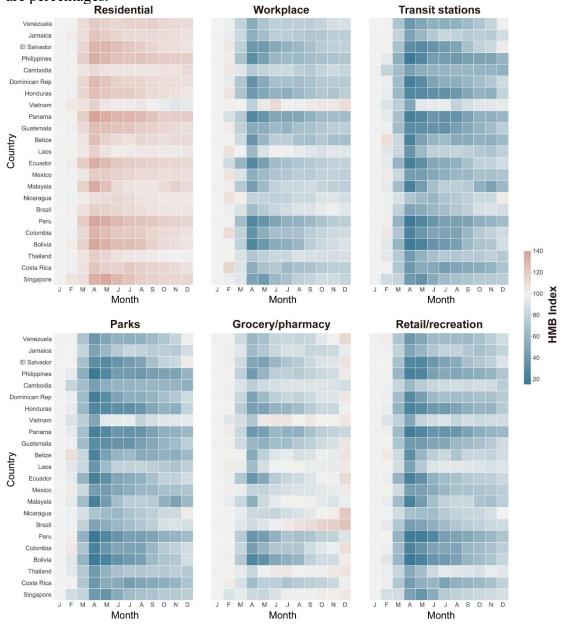
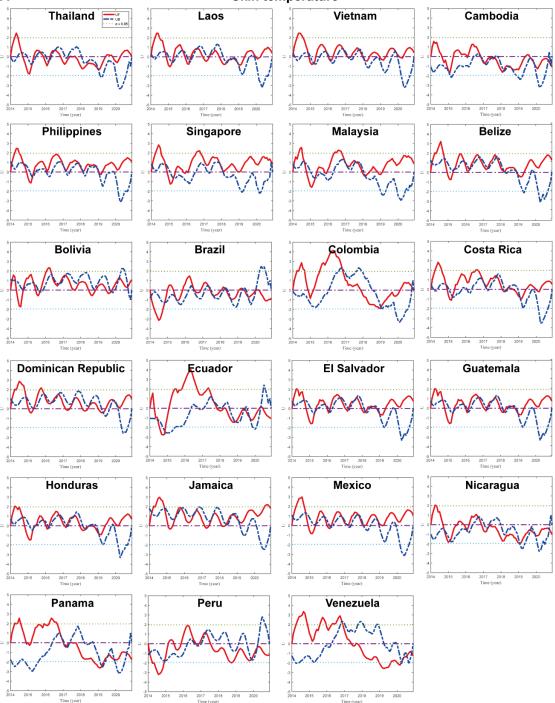


Figure S7: Mann-Kendall test for significance of trends in meteorological factor for each country in the Latin America and Southeast Asia, 2014-2020. (A) Mann-Kendall significance test for surface temperature. (B) Mann-Kendall significance test for convective precipitation. The red line represents the UF value, the blue line represents the UB value, and the dashed line represents the 95% CI. When the red line exceeds the critical line of I, the variable has a significant change trend at this time. **A Skin temperature**



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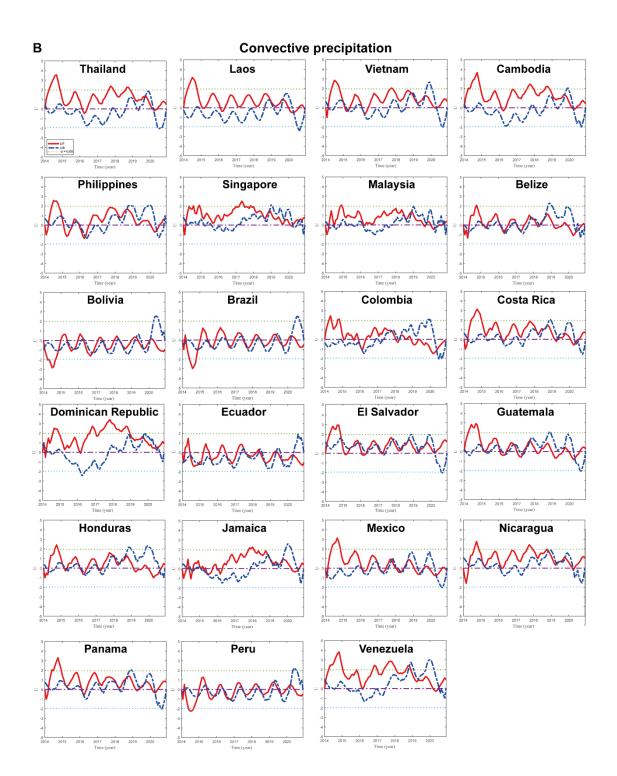
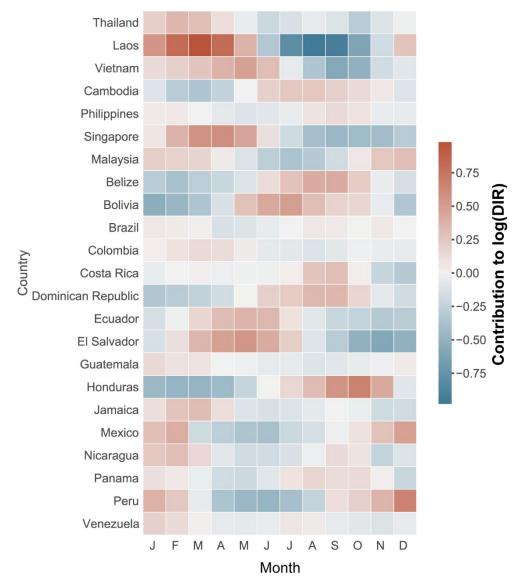


Figure S8: Posterior distributions of country-specific autocorrelated monthly random effects. Posterior mean of marginal posterior distribution of the autocorrelated month random effects (e.g., the annual cycle) at the linear predictor scale from January to December for the 23 countries in Latin America and Southeast Asia. This shows the contribution of the random effects to the log of the dengue incidence rate (DIR) using the "historical" model.



"Historical" model

Figure S9: Contribution of year-specific spatial random effects to dengue incidence rate estimates. Marginal posterior mean of the combined spatially structured and unstructured random effects at the linear predictor scale in 2020. This shows the contribution of the spatial random effects to the log of the dengue incidence rate using the "historical" model.

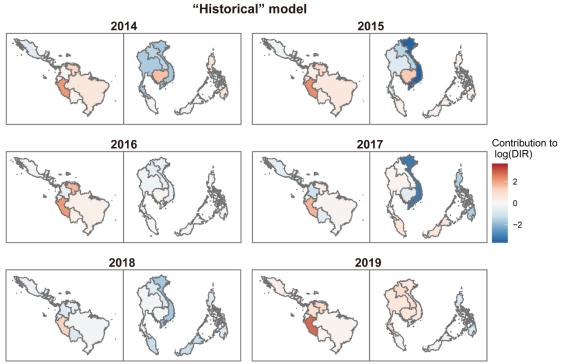
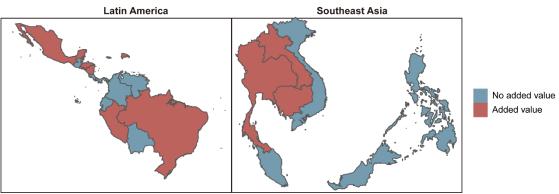
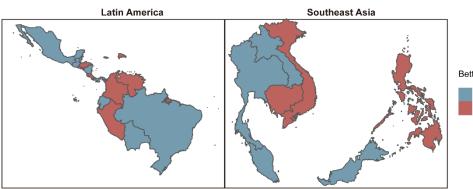


Figure S10: Added value of using "historical" model compared to baseline model. Difference between mean absolute error (MAE) for the baseline model (state-specific monthly random effects and year-specific spatial random effects) and MAE for the "historical" model. Countries with positive values (red) suggest that capturing the nonlinear and delayed impacts of climate factors, improves the model in these areas. Countries with negative values (blue) suggest that climate factors information did not improve the model fit and other unexplained factors may dominate space-time dynamics in these countries. The MAE of the "Historical" model was smaller than the baseline model for 12 of the 23 countries (52%).



"Historical" model

Figure S11: Sensitivity testing of "historical" models using complete and seperate (Latin American and Southeast Asian) datasets. Countries with positive MAE values (red) indicate that modeling independently of countries in two large regions can improve these regional models. Countries with negative values (blue) indicate that modeling independently for two large regions does not improve the model fit, and is better for all countries. In 12 of the 23 countries (52%), the MAE of the complete dataset model was smaller than that of the two-region dataset model.



Better model

Using complete data Using separate data *Figure S12:* The association between different selected intervention variables with dengue risk over different lags. (A) Contour plot of the association between PHSM and risk of dengue, relative to the baseline without government interventions (PHSM = 0). The deeper the shade of red, the greater the increase in relative risk (RR) of dengue compared with the baseline. The deeper the shade of blue, the greater the decrease in RR of dengue compared with the baseline. (B) Dengue lag–response association for loose (PHSM = 10), moderate (PHSM = 50), and strict (PHSM = 90) government interventions relative to the baseline. (C) Cumulative lags over the three month associations between PHSM and risk of dengue, relative to the baseline without government interventions. Shaded regions mark the prediction with 95% empirical CI. Predictions are from the "intervention" models. The PHSM index ranges from 0 to 100. A higher score indicates a more stringent, more geographically comprehensive COVID-19 response policy (0 for no response policy and 100 for the most stringent response policy).

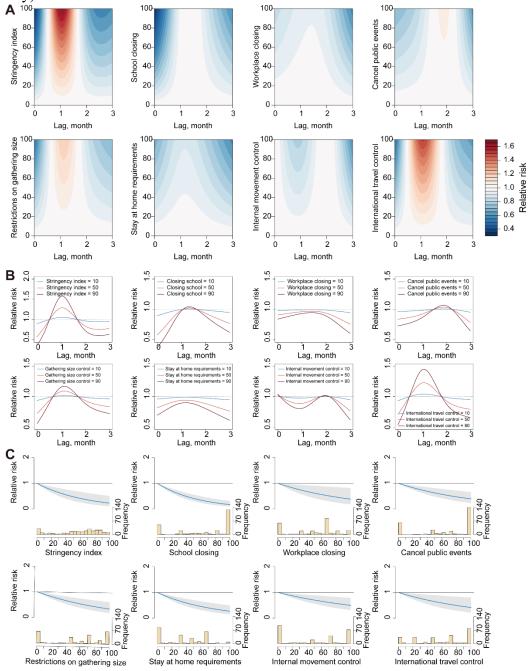


Figure S13: The association between different selected human movement variables with dengue risk over different lags. (A) Contour plot of the association between HMB and risk of dengue, relative to the baseline without government interventions (HMB = 100). The deeper the shade of red, the greater the increase in relative risk (RR) of dengue compared with the baseline. The deeper the shade of blue, the greater the decrease in RR of dengue compared with the baseline. (B) Dengue lag–response association for loose (HMB = max), moderate (HMB = 80), and strict (HMB = 30) government interventions relative to the baseline. (C) Cumulative lags over the three month associations between HMB and risk of dengue, relative to the baseline without government interventions. Shaded regions mark the prediction with 95% empirical CI. Predictions are from the "intervention" models. The baseline of human mobility was the median for the first five weeks of 2020 (3 January to 6 February), which was defined as 100%.

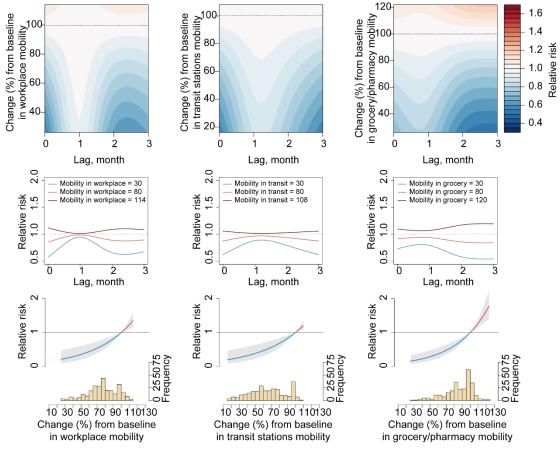
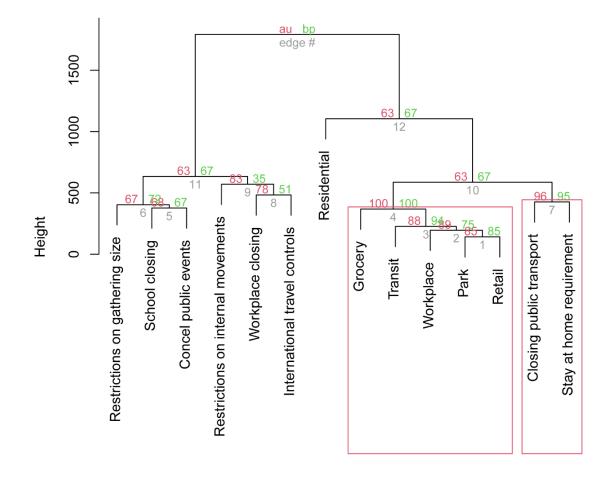


Figure S14: The uncertainty in hierarchical cluster analysis of PHSM and human mobility time series. The height of nodes connecting two variables on the dendrogram represents the degree of similarity. For each cluster in hierarchical clustering, quantities called p-values are calculated via multiscale bootstrap resampling. P-value of a cluster is a value between 0 and 1, which indicates how strong the cluster is supported by data. Red values are AU (Approximately Unbiased) p-values, and green values are BP (Bootstrap Probability) values. AU p-value, which is computed by multiscale bootstrap resampling, is a better approximation to unbiased p-value than BP value computed by normal bootstrap resampling. Clusters with AU larger than 95% are highlighted by rectangles, which are strongly supported by data.



Cluster dendrogram with p-values (%)

Distance: euclidean Cluster method: ward.D2 *Figure S15:* Heat map of correlations between variables in the Latin America and Southeast Asia, 2020. C1 - C8 is 8 specific indicators of the containment and closure policies, namely "school closing", "workplace closing", "cancelling of public events", "restrictions on gathering sizes", "closure of public transport", "stay at home requirements", "restrictions on internal movement" and "international travel controls". Red indicates a positive correlation between the two variables, blue indicates a negative correlation between the two variables, blue indicate correlation coefficients.

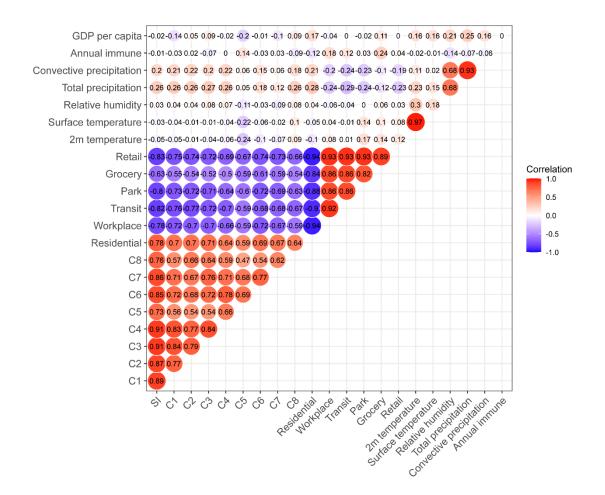
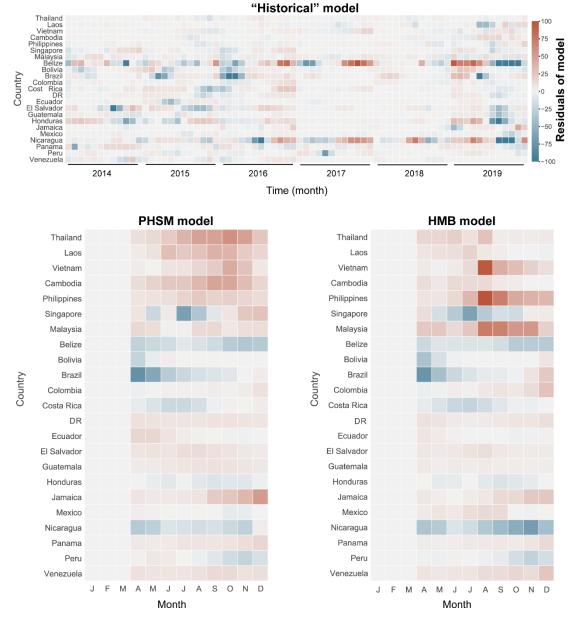


Figure S16: Distributions of residuals between model prediction and observed dengue incidence rate (DIR). The residuals between "historical" and "intervention" model prediction and observed DIR per 100,000 population from January to December for the 23 countries in Latin America and Southeast Asia.



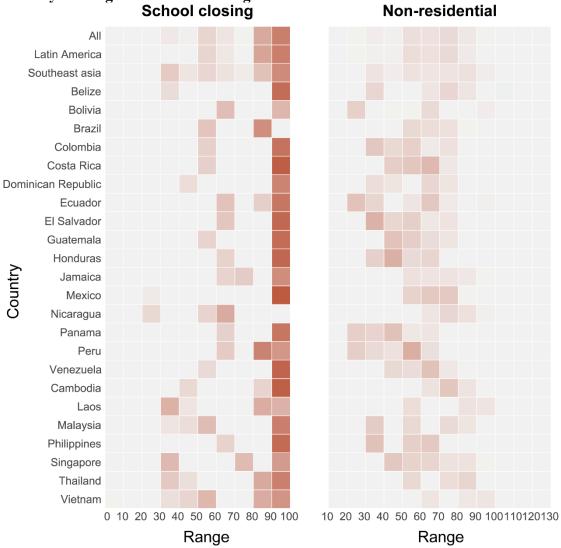


Figure S17: Proportion of dengue cases averted by PHSM/ human mobility in each country and region at different ranges. School closing Non-residential

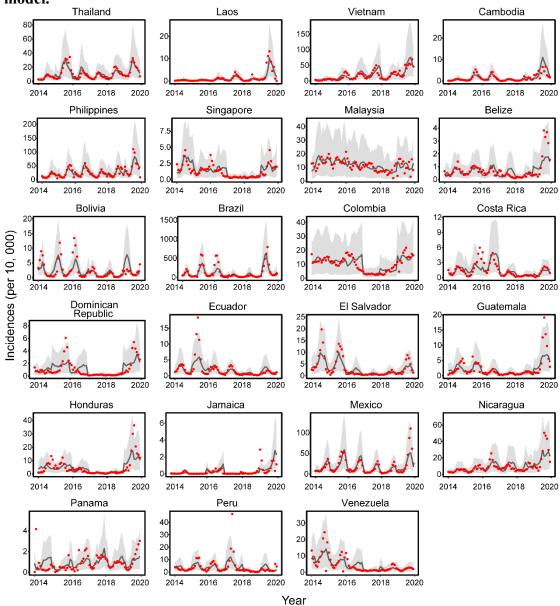


Figure S18: Predicted and observed monthly dengue cases from the "historical" model.

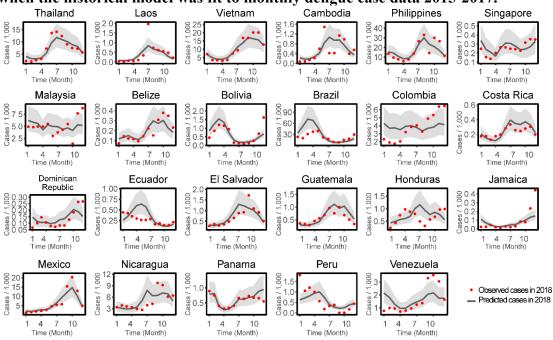


Figure S19: Predicted and estimated case numbers for the example year 2018 when the historical model was fit to monthly dengue case data 2015-2017.

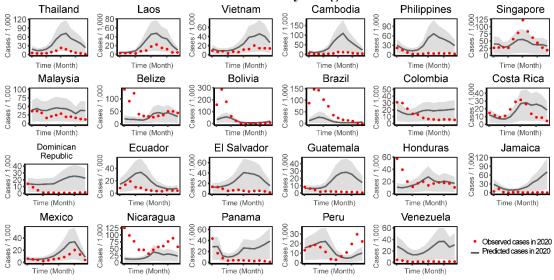


Figure S20: Predicted and estimated case numbers for the example year 2020 when the historical model was fit to monthly dengue case data 2014-2019.

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References

1. Hale T, Angrist N, Goldszmidt R, et al. A global panel database of pandemic policies (Oxford COVID-19 Government Response Tracker). *Nat Hum Behav* 2021; **5**(4): 529-38.

2. Lowe R, Barcellos C, Coelho CA, et al. Dengue outlook for the World Cup in Brazil: an early warning model framework driven by real-time seasonal climate forecasts. *Lancet Infect Dis* 2014; **14**(7): 619-26.

3. Schrödle B, Held L. A primer on disease mapping and ecological regression using INLA. *Computation Stat* 2011; **26**(2): 241-58.

4. Riebler A, Sørbye SH, Simpson D, Rue H. An intuitive Bayesian spatial model for disease mapping that accounts for scaling. *Stat Methods Med Res* 2016; **25**(4): 1145-65.

5. Gasparrini A. Distributed Lag Linear and Non-Linear Models in R: The Package dlnm. *J Stat Softw* 2011; **43**(8): 1-20.

6. Gasparrini A, Armstrong B, Kenward MG. Distributed lag non-linear models. *Stat Med* 2010; **29**(21): 2224-34.

7. Naish S, Dale P, Mackenzie JS, McBride J, Mengersen K, Tong S. Climate change and dengue: a critical and systematic review of quantitative modelling approaches. *BMC Infect Dis* 2014; **14**: 167.

8. Lowe R, Bailey TC, Stephenson DB, et al. The development of an early warning system for climate-sensitive disease risk with a focus on dengue epidemics in Southeast Brazil. *Stat Med* 2013; **32**(5): 864-83.

9. Hii YL, Rocklöv J, Wall S, Ng LC, Tang CS, Ng N. Optimal lead time for dengue forecast. *PLoS Negl Trop Dis* 2012; **6**(10): e1848.