Age could be driving variable SARS-CoV-2 epidemic trajectories worldwide

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Abstract

Background Current geographic spread of documented severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections shows heterogeneity. This study explores the role of age in potentially driving differentials in infection spread, epidemic potential, and rates of disease severity and mortality across countries.

Methods An age-stratified deterministic mathematical model that describes SARS-CoV-2 transmission dynamics was applied to 159 countries and territories with a population ≥1 million.

Results Assuming worst-case scenario for the pandemic, the results indicate that there could be stark regional differences in epidemic trajectories driven by differences in the distribution of the population by age. In the African Region (median age: 18.9 years), the median R_0 was 1.05 versus 2.05 in the European Region (median age: 41.7 years), and the median (per 100 persons) for the infections rate was 22.5 (versus 69.0), for severe and/or critical disease cases rate was 3.3 (versus 13.0), and for death rate was 0.5 (versus 3.9).

Conclusions Age could be a driver of variable SARS-CoV-2 epidemic trajectories worldwide. Countries with sizable adult and/or elderly populations and smaller children populations may experience large and rapid epidemics in absence of interventions. Meanwhile, countries with predominantly younger age cohorts may experience smaller and slower epidemics. These predictions, however, should not lead to complacency, as the pandemic could still have a heavy toll nearly everywhere.

INTRODUCTION

The current geographic spread of the documented severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [1] infections and associated Coronavirus Disease 2019 (COVID-2019) [1] shows heterogeneity [2]. This remains unexplained but may possibly reflect delays in virus introduction into the population, differentials in testing and/or reporting, differentials in the implementation, scale, adherence, and timing of public health interventions, or other epidemiological factors. In this study, we explore the role of age in explaining the differential spread of the infection and its future epidemic potential.

As our understanding of the SARS-CoV-2 transmission dynamics is rapidly evolving [3], the role of age in the epidemiology of this infection is becoming increasingly apparent [4-7]. In a recent study examining SARS-CoV-2 epidemiology in China [4], we quantified the effect of age on the *biological* susceptibility to infection acquisition. We found that *relative* to individuals aged 60-69 years, susceptibility was 0.06 in those aged 0-19 years, 0.34 in those aged 20-29 years, 0.57 in those aged 30-39 years, 0.69 in those aged 40-49 years, 0.79 in those aged 50-59 years, 0.94 in those aged 70-79 years, and 0.88 in those aged ≥80 years (Supplementary Figure S1). Notably, this age-dependence was estimated after accounting for the assortativeness in population mixing by age [4].

Age also affects disease progression [7-10] and mortality risk [11-13] among those infected. The proportion of infections that eventually progress to severe disease, critical disease, or death, increases rapidly with age, especially among those ≥50 years of age (Supplementary Figure S2) [8-12]. Since the demographic structure of the population (that is the distribution of the population across the different age groups) varies by country and region, this poses a question as

to the extent to which age effects can drive geographic differentials in the reproduction number (R_0), epidemic potential, and rates of disease severity and mortality.

We aimed here to answer this question and to estimate for each country (with a population ≥1 million), region, and globally, R_0, and the rate per 100 persons (out of the total population by the end of the epidemic cycle) of each of the cumulative number of incident infections, mild infections, severe and/or critical disease cases, and deaths, in addition to the number of days needed for the national epidemic to reach its incidence peak (a measure of how fast the epidemic will grow). We also aimed to introduce indices for infection severity, mortality, and susceptibility across countries.

METHODS

We adapted and applied our recently developed deterministic mathematical model [4] describing SARS-CoV-2 transmission dynamics in China (Supplementary Figure S3), to 159 countries and territories, virtually covering the world population [14]. Since our focus was on investigating the natural course of the SARS-CoV-2 epidemic and on assessing its full epidemic potential, the model was applied assuming the *worst-case* scenario for the epidemic in each country, that is in absence of any intervention.

The model stratified the population into compartments according to age (0-9, 10-19, …, ≥80 years), infection status (uninfected, infected), infection stage (mild, severe, critical), and disease stage (severe, critical), using a system of coupled nonlinear differential equations (Supplementary Section 1). Susceptible individuals in each age group were assumed at risk of acquiring the infection at a hazard rate that varies based on the age-specific susceptibility to the infection (Supplementary Figure S1), the infectious contact rate per day, and the transmission

mixing matrix between the different age groups (Supplementary Section 1). Following a latency period of 3.69 days [15-18], infected individuals develop mild, severe, or critical infection, as informed by the observed age-specific distribution of cases across these infection stages in China [8-10]. The duration of infectiousness was assumed to last for 3.48 days [8, 15, 17, 18] after which individuals with mild infection recover, while those with severe and critical infection develop, respectively, severe and critical disease over a period of 28 days [8] prior to recovery. Individuals with critical disease have the additional risk of disease mortality, as informed by the age-stratified disease mortality rate in China [11, 12].

Model parameters were based on current data for SARS-CoV-2 natural history and epidemiology, or through model fitting to the China outbreak data [4] (Supplementary Section 2 and Table S1). Namely, the overall infectious contact rate, age-specific biological susceptibility profile, and age-specific mortality rate were assumed as those in China [4]. The population size, demographic structure, and life expectancy in countries and territories with a population of ≥1 million, as of 2020, were extracted from the United Nations World Population Prospects database [14]. Model parameters, definitions, values, and justifications are in Supplementary Section 2 and Tables S1 and S2. Indices for mortality, infection severity, and susceptibility were derived by weighting each of these factors in each age group by the fraction of the population in that age group, and then summing the contributions of all ages.

Ranges of uncertainty around model-predicted outcomes were determined using five-hundred simulation runs that applied Latin Hypercube sampling [19, 20] from a multidimensional distribution of the model parameters. At each run, input parameter values were selected from ranges specified by assuming ±30% uncertainty around parameters' point estimates. The resulting distribution for each model-predicted outcome was then used to derive the most

probable estimate and 95% uncertainty interval (UI). Mathematical modelling analyses were performed in MATLAB R2019a [21], while statistical analyses were performed in STATA/SE 16.1 [22].

RESULTS

In what follows, we highlight results for select (mostly populous) countries that are of broad geographic representation and characterized by diverse demographic structures. These include Brazil, China, Egypt, India, Indonesia, Italy, Niger, Pakistan, and USA. Detailed results for all 159 countries and territories are in Supplementary Tables S3-S8.

Figure 1A shows the estimated R_0 in these select countries, which was highest in Italy at 2.30, followed by USA and China at 1.95, Brazil at 1.75, Indonesia at 1.55, India at 1.45, Egypt at 1.35, Pakistan at 1.25, and lowest in Niger at 0.93. Country-specific estimates of R_0 grouped by World Health Organization (WHO) region are illustrated in Figure 2. The median R_0 was 1.05 (range: 0.93-1.95) in African Region (AFRO), 1.45 (range: 0.98-1.75) in Eastern Mediterranean Region (EMRO), 1.55 (range: 1.15-1.95) in South-East Asia Region (SEARO), 1.65 (range: 1.25-2.28) in Region of the Americas (AMRO), 1.85 (range: 1.25-2.30) in Western pacific Region (WPRO), and 2.05 (range: 1.25-2.30) in European Region (EURO). Globally, the median R_0 was 1.55 with a range of 0.93-2.30.

Figure 1B shows the estimated number of days needed for the national epidemic to reach its incidence peak. In Italy, the peak was reached after 122 days (~4 months), whereas in Pakistan it was reached after 350 days (nearly a year). Meanwhile, since $R_0 < 1$, no epidemic would emerge in Niger. Of note that the number of days needed for the national epidemic to reach its incidence

peak depends on the population size in addition to R_0 — it takes more time for the epidemic to reach its peak in larger nations (Supplementary Tables S3-S8).

The estimated incidence rate per 100 persons, defined as the *cumulative* number of infections by the end of the epidemic cycle out of the total population, was highest in Italy at 75.5 and lowest in Pakistan at 33.0 (Figure 3A). Across world regions, the median incidence rate per 100 persons was 22.5 (range: 0.25-63.5) in AFRO, 45.0 (range: 1.5-65.0) in EMRO, 49.0 (range: 25.0-66.5) in SEARO, 53.0 in AMRO (range: 35.0-70.5), 63.5 (range: 31.0-76.5) in WPRO, and 69.0 (range: 31.0-75.5) in EURO, and 49.0 (range: 0.25-76.5) globally.

The estimated death rate per 100 persons followed the same pattern, where it was highest in Italy at 4.7 and lowest in Pakistan at 0.9 (Figure 3B). Across world regions, the median death rate per 100 persons was 0.5 (range: 0.0-2.8) in AFRO, 0.9 (range: 0.0-2.0) in EMRO, 1.6 (range: 0.8-2.9) in SEARO, 2.0 in AMRO (range: 1.0-4.2), 2.7 (range: 0.8-5.3) in WPRO, and 3.9 (range: 0.8-4.7) in EURO, and 1.6 (range: 0.0-5.3) globally.

The estimated rate of mild infections per 100 persons was highest in Italy at 60.5 and lowest in Pakistan at 27.0 (Figure 4A). Across world regions, the median per 100 persons was 17.0 (range: 0.25-52.5) in AFRO, 39.0 (range: 1.5-55.0) in EMRO, 41.0 (range: 23.0-54.5) in SEARO, 43.5 in AMRO (range: 29.0-56.5), 51.5 (range: 27.0-61.5) in WPRO, and 56.5 (range: 25.0-65.0) in EURO, and 41.0 (range: 0.25-61.5) globally.

Meanwhile, the estimated rate of severe and/or critical disease cases per 100 persons was highest in Italy at 14.7 and lowest in Pakistan at 5.0 (Figure 4B). Across world regions, the median per 100 persons was 3.3 (range: 0.0-11.3) in AFRO, 7.1 (range: 0.3-9.5) in EMRO, 7.7 (range: 4.1-

11.9) in SEARO, 8.7 in AMRO (range: 5.0-13.5), 11.5 (range: 5.0-15.5) in WPRO, and 13.0

(range: 4.7-14.7) in EURO, and 8.0 (range: 0.0-15.5) globally.

The indices for mortality, infection severity, and susceptibility varied across countries and

regions (Figure 5 and Supplementary Figure S4). The medians for the mortality, critical

infections, and susceptibility indices were lowest in AFRO at 0.5%, 2.7%, and 28.2%,

respectively, and highest in EURO at 2.4%, 7.4%, and 53.7%, respectively (Figure 5).

Meanwhile, the medians for mild infections and severe infections indices were lowest in EURO

at 83.1% and 9.6%, respectively and highest in AFRO at 87.2% and 10.2%, respectively

(Supplementary Figure S4).

DISCUSSION

The above results suggest that although this pandemic is a formidable challenge globally, its

intensity and toll in terms of morbidity and mortality may vary substantially by country and

regionally. While some countries, particularly in resource-rich countries, may experience large

and rapid epidemics, other countries, particularly in resource-poor countries, may experience

smaller and slower epidemics. While the scale of the epidemic may be smallest in sub-Saharan

Africa with its young population, it could be intense in countries with small children population

and sizable adult and/or elderly population.

The key finding of this study is the role of age in potentially driving divergent SARS-CoV-2

epidemic trajectories and disease burdens. The effect of age reflects the interplay of three main

factors: the variation in susceptibility by age (Supplementary Figure S1), variation in disease

severity and mortality by age (Supplementary Figure S2), and variation in demographic structure

across countries (Supplementary Tables S3-S8). The combined effect of these factors can result

in stark variations in R_0 (Figure 2), and consequently epidemic potential, disease severity, and disease mortality—there was strong correlation between R_0 and median age across countries (Supplementary Figure S5). Incidentally, the globally diagnosed cases as of April 9th, 2020 show a correlation with median age across countries (Spearman correlation coefficient: 0.71 (95% CI: 0.62-0.78), p<0.001). A linear regression analysis using these data indicated an increase in the number of diagnosed infections by 1058.0 (95% CI: 386.0-1729.9; p: 0.002) for every one-year increase in median age. Although this may be explained by most diagnosed infections being reported by countries with advanced testing infrastructure, this may support the role of age presented here. Importantly, as infection transmission dynamics is a non-linear phenomenon, even small changes in R_0, when R_0 is in the range of 1-2, can drive considerable differences in epidemic size and trajectory (Supplementary Figure S6).

An illustration of the role of age can be seen in Niger, a nation with a median age of only 15 years, where the exclusion of children from the population would have increased R_0 from 0.93 to 2.6. This demonstrates how the lower susceptibility among younger persons, particularly children, acts as a "herd immunity" impeding the ferocious strength of the force of infection of an otherwise very infectious virus. This epidemiological feature contrasts that of other respiratory infections, such as the 2009 influenza A (H1N1) pandemic (H1N1pdm) infection (Supplementary Figure S7) [23], where the cumulative incidence was found to be highest among children and young adults, and much smaller among older adults.

One possible inference to be drawn from the above results is that epidemic size and associated disease burden could be highest in settings with sizable mid-age and/or elderly populations, as currently exemplified by Italy. This may also possibly explain sub-national patterns, such as the

large number of diagnosed cases in the city of New York, although additional fine-grained analyses are needed to delineate within-country heterogeneities in transmission dynamics.

Another possible inference of relevance to containment efforts relates to the likelihood of the infection establishing itself in a population. The probability of a major outbreak upon introduction of one infection is given approximately by $1 - 1/R_0$ [24, 25]. Accordingly, in countries where R_0 is just above the epidemic threshold of $R_0 = 1$, the virus will need to be introduced multiple times before it can generate sustainable chains of transmission (Supplementary Figure S8 provides an illustration of this effect). In such countries, less disruptive social distancing measures may be sufficient to contain the epidemic compared to countries with larger R_0.

Our study explores the potential effect of age on the epidemiology of SARS-CoV-2, but other factors that remain poorly understood, may also contribute to driving different epidemic trajectories. Transmission of the virus may be affected by seasonality, environmental and genetic factors, differences in social network structure and cultural norms (such as shaking hands, kissing, and other person-to-person contacts), and underlying co-morbidities which also impact disease severity and mortality. These factors may have contributed to a slowly growing epidemic in Japan, despite its demographic structure, as opposed to fast growing epidemics in the European Region and the USA.

This study has limitations. Model estimations are contingent on the validity and generalizability of input data. Our estimates were based on SARS-CoV-2 natural history and disease progression data from China, but these may not be applicable to other countries. The key factor driving the heterogeneity in transmission dynamics is the age-specific biological susceptibility profile. We

used the susceptibility profile as derived from the China outbreak data [4], but this may not be generalizable to other countries. More estimates from other countries are needed to investigate the potential variation in this profile. While current data on the attack rate from different countries supports age heterogeneity and lower exposure among children, different countries show still variation in the age-stratified attack rate (Supplementary Figures S9 and S10). Of note that the observed lower susceptibility to the infection at younger age [4] does not necessarily imply absence of infection, but may reflect rapid infection clearance or subclinical infection. This may impact our estimates depending on these infections' degree of infectiousness. A sensitivity analysis assuming a 50% increase in the susceptibility of younger age cohorts (to somewhat reflect the effect of subclinical infections) resulted in smaller differences in R_0 across countries, but still supported our findings of wide heterogeneity in R_0 (supplementary Figure S11). It is conceivable that such subclinical infections may have lower viral load, and therefore rapid infection clearance and limited transmission potential. Data on infection clusters from China and other countries suggested that children do not appear to play a significant role in the transmission of this infection [7, 8, 26].

Our study may have overestimated disease mortality by basing mortality rates on estimates of crude case fatality rate in China, as suggested by a recent study [13]. Our results are based on the most probable value for R_0 as estimated through 500 runs of uncertainty analysis. The latter may have biased our reported results towards lower R_0. For instance, the most probable value for R_0 in China was 1.95, but the point estimate assuming the baseline values of the input parameters was higher at 2.10 [4]. Despite these limitations, our parsimonious model, tailored to the nature of available data, was able to reproduce the epidemic as observed in China [4], and generated results that are valid to a wide range of model assumptions.

CONCLUSION

Age appears to be a driver of variable SARS-CoV-2 epidemic trajectories worldwide. Countries with sizable adult and/or elderly populations and smaller children populations may experience large and rapid epidemics in absence of interventions, necessitating disruptive social distancing measures to contain the epidemic. Meanwhile, countries with predominantly younger age cohorts may experience smaller and slower epidemics and may require less disruptive social distancing measures to contain the epidemic. These predictions, however, should not lead to complacency, and should not affect national response in strengthening preparedness plans and in implementing prevention interventions. Once established, and even if smaller in scale due to their predominantly younger population, the SARS-CoV-2 epidemic would still cause a heavy toll on developing countries with resource-poor healthcare infrastructure.

Data availability

All data generated or analysed during this study are included in this article and its Supplementary Information file.

Acknowledgements

Author contributions

HHA constructed and parameterized the mathematical model and conducted the mathematical modelling analyses. HC contributed to the parameterization of the mathematical model, conducted the statistical analyses, and wrote the first draft of the manuscript. LJA conceived and led the design of the study, construct and parameterization of the mathematical model, conduct of analyses, and drafting of the article. All authors contributed to discussion and interpretation of the results and to the writing of the manuscript. All authors have read and approved the final manuscript.

Competing interests

We declare no competing interests.

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Figure 1: Estimates for the basic reproduction number, R_0, and the number of days needed for the national epidemic to reach its incidence peak, in select countries.
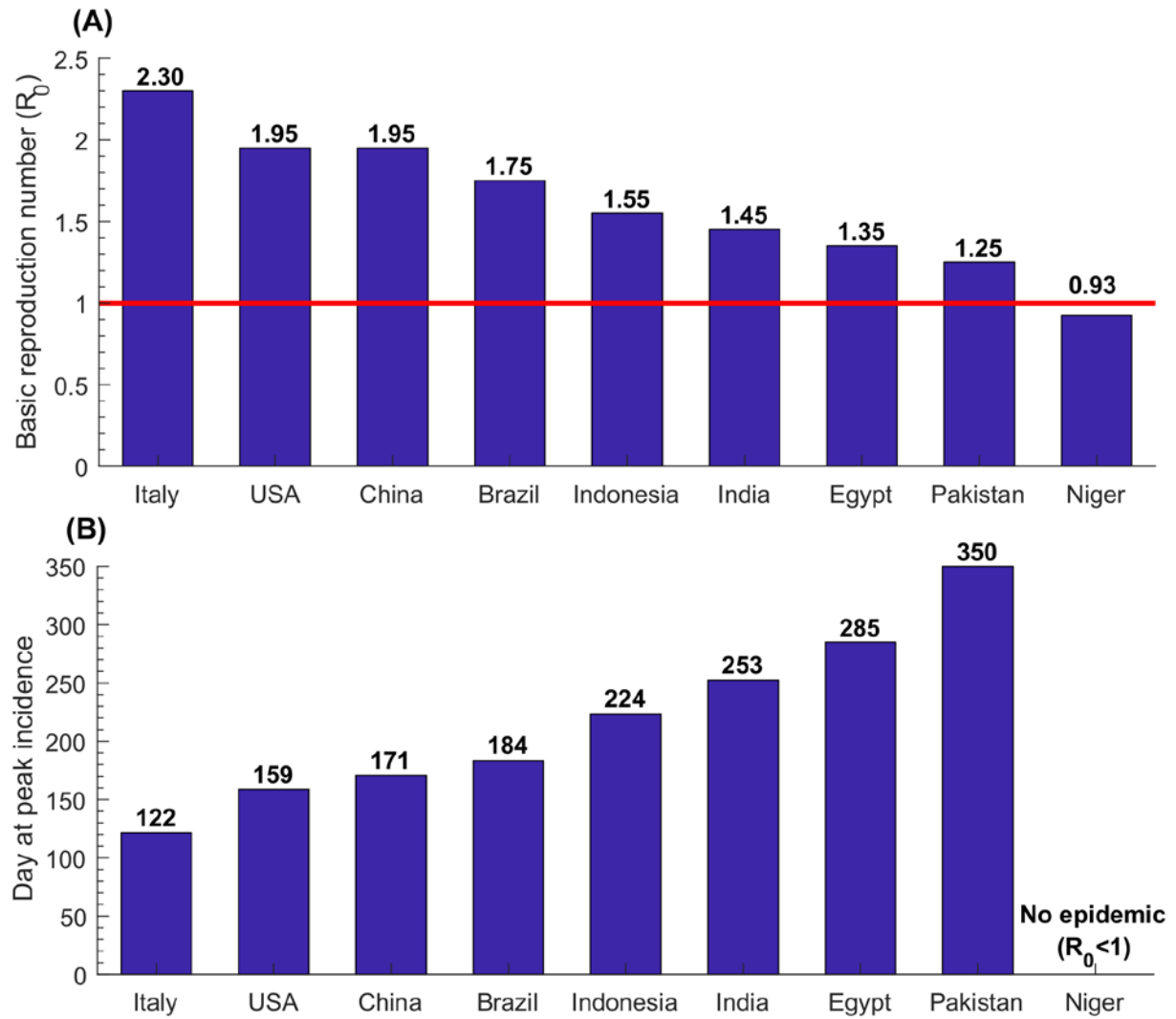
Figure 2: Estimates for the basic reproduction number R_0 in 159 countries and territories with a population of at least one million, across World Health Organization regions. These are the African Region (AFRO), Eastern Mediterranean Region (EMRO), South-East Asia Region (SEARO), Region of the Americas (AMRO), Western Pacific Region (WPRO), and European Region (EURO). The figure shows also the median age in years and the median R_0 for each world region.
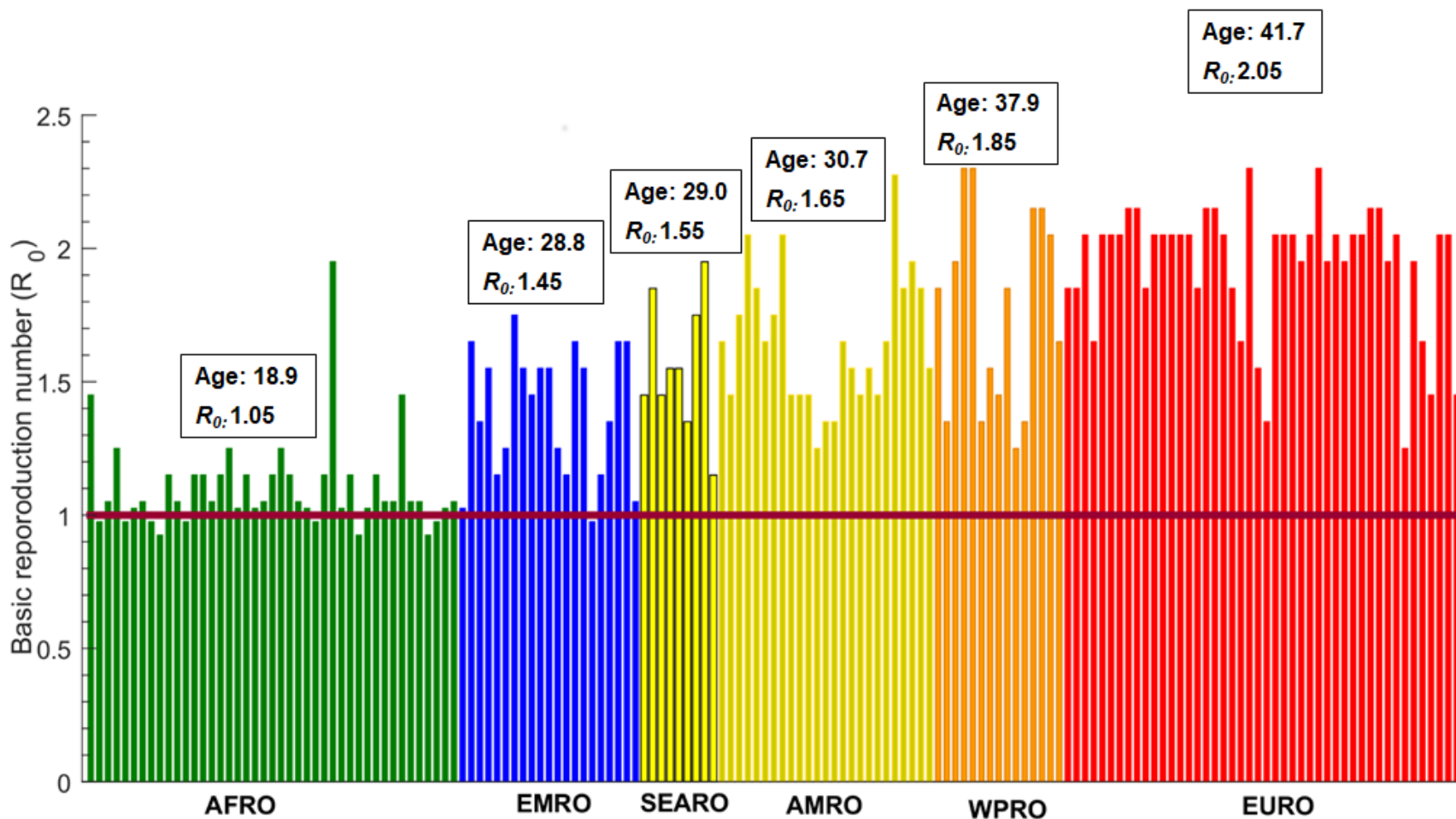
Figure 3: Estimates for the number of infections and the number of deaths per 100 persons in select countries.
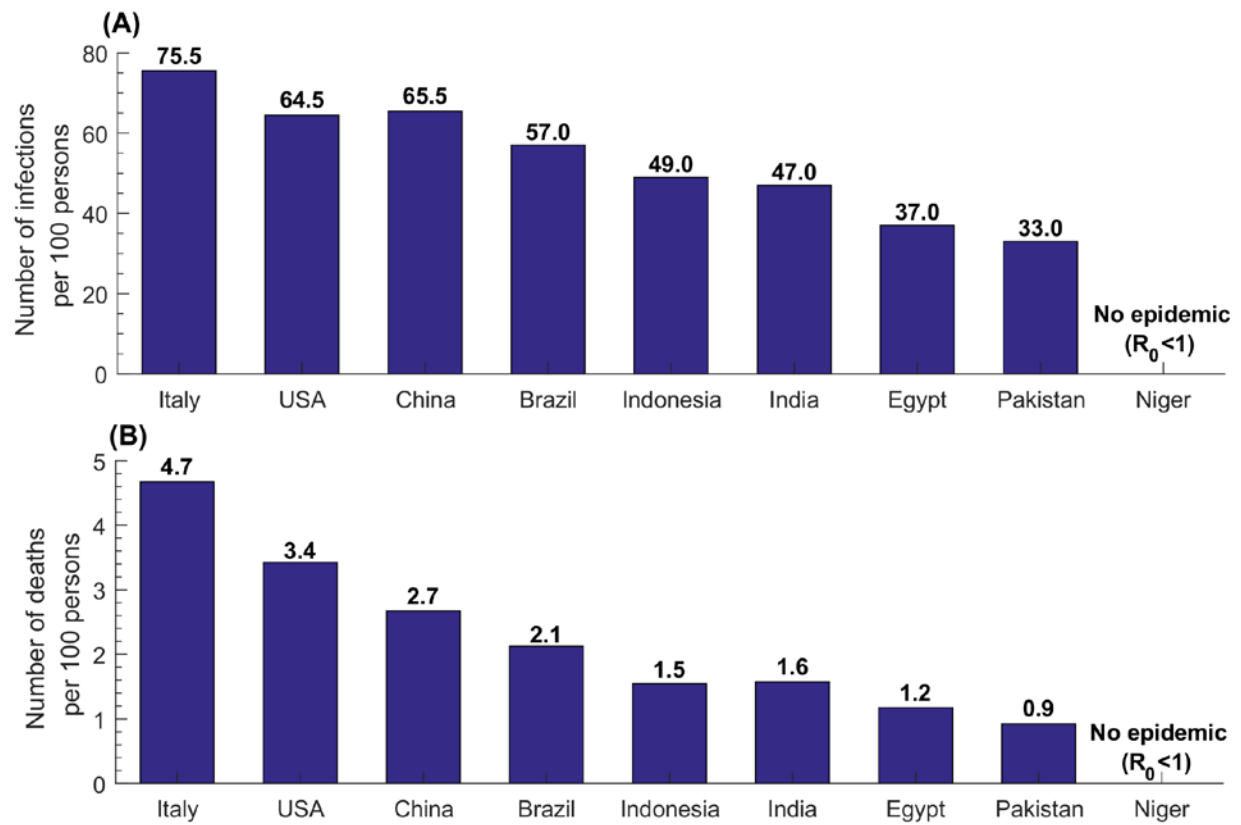
Figure 4: Estimates for the number of mild infections and the number of severe and/or critical diseases cases per 100 persons in select countries.
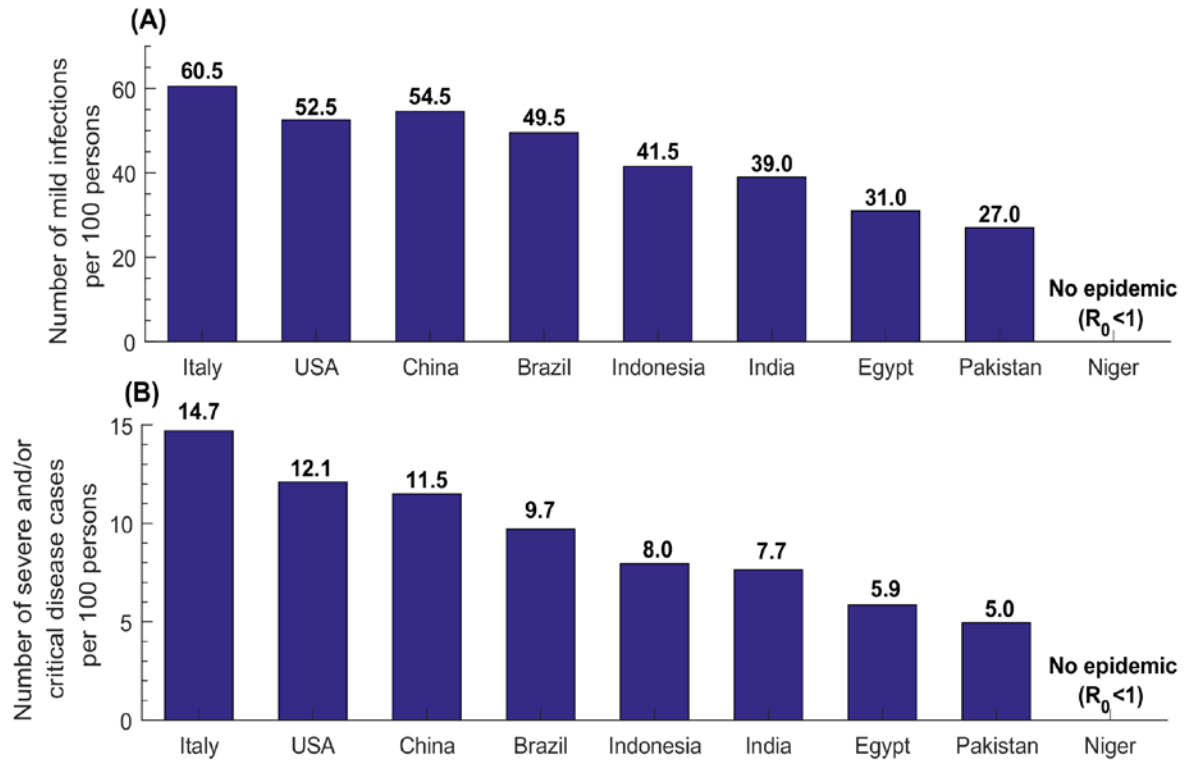
Figure 5: Estimates for the A) disease mortality index, B) critical infections index, and C) susceptibility index in 159 countries and territories with a population of at least one million, across World Health Organization regions. These are the African Region (AFRO), Eastern Mediterranean Region (EMRO), South-East Asia Region (SEARO), Region of the Americas (AMRO), Western Pacific Region (WPRO), and European Region (EURO). The figure shows also the median index for each world region.

Age could be driving variable SARS-CoV-2 epidemic trajectories worldwide

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Figure S1: Age-specific susceptibility to SARS-CoV-2 acquisition relative to individuals aged 60-69 years [1].

Figure S2: Key attributes of SARS-CoV-2 disease progression stratified by age. Distribution by age of: A) the proportion of infections that will progress to be mild or asymptomatic, severe, or critical [2-4] and B) crude case fatality rate [5, 6].
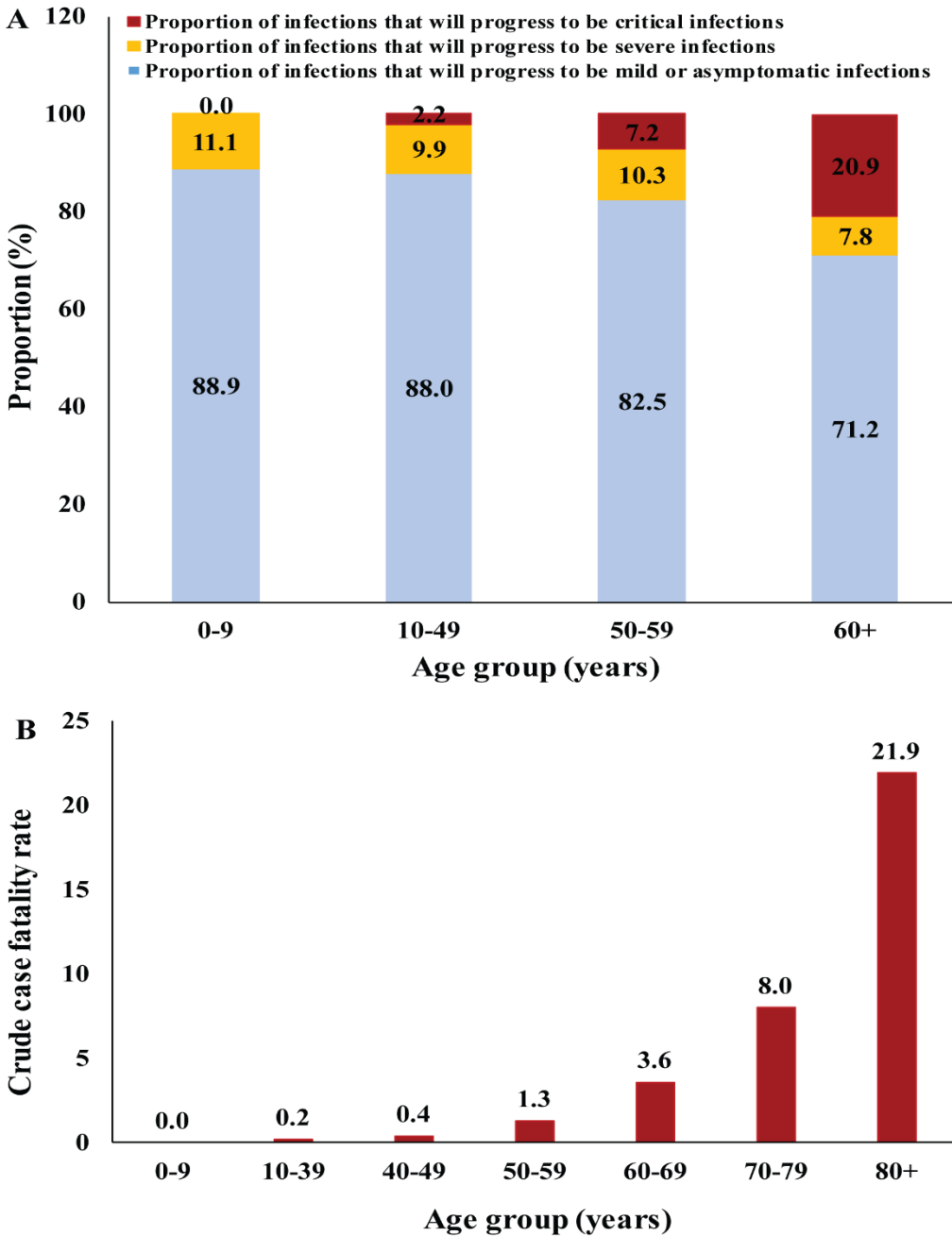
1. Mathematical model structure

We applied a recently developed deterministic compartmental mathematical model that describes the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission dynamics and disease progression in a population [1], to all countries and territories with a population of at least one million, as of 2020 [7]. An illustration of the basic model structure can be found in Figure S3. The model stratifies the population into compartments based on age (0-9, 10-19, 20-29,…, ≥80 years), infection status (uninfected, infected), infection stage (mild, severe, critical), and disease stage (severe, critical).

Figure S3: Schematic diagram illustrating the basic structure of the SARS-CoV-2 model.
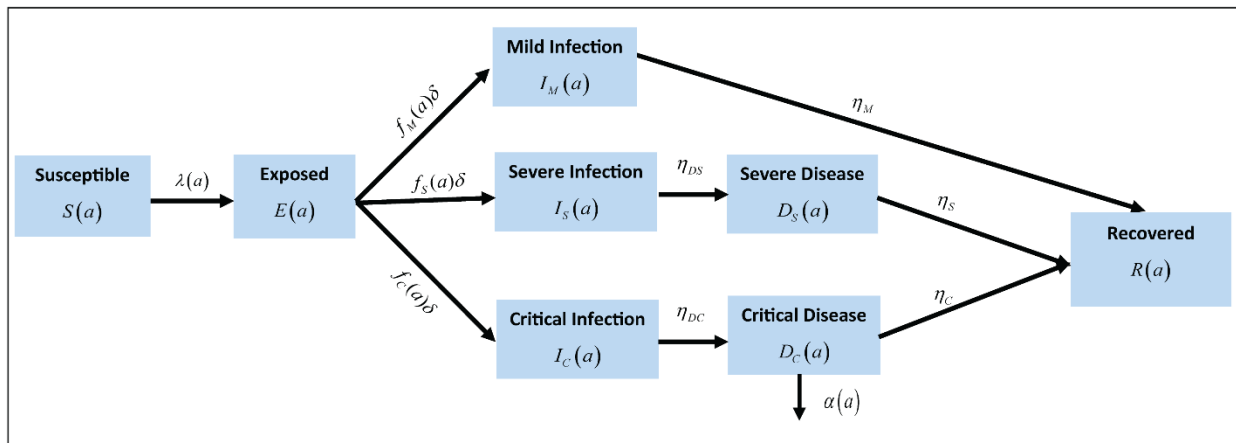
A system of coupled nonlinear differential equations is used to describe SARS-CoV-2 transmission dynamics. Nine age cohorts were considered $(a = 1, 2, ..., 9)$, each representing a ten-year age band apart from the last cohort which includes individuals aged ≥80 years. The age-specific distribution for each country/territory, as of the year 2020, was obtained from the United Nations World Population Prospects database [7]. All disease-related mortality was assumed to occur in individuals that are in the critical disease stage, as informed by the China outbreak data [5].

The epidemic dynamics in the first age group was described using:

Population aged 0-9 years:

$$\frac{dS(1)}{dt} = -\left(\lambda(1) + \mu + \xi(1)\right)S(1)$$

$$\frac{dE(1)}{dt} = \lambda(1)S(1) - \left(\delta + \mu + \xi(1)\right)E(1)$$

$$\frac{dI_M(1)}{dt} = f_M(1)\delta E(1) - \left(\eta_M + \mu + \xi(1)\right)I_M(1)$$

$$\frac{dI_S(1)}{dt} = f_S(1)\delta E(1) - \left(\eta_{DS} + \mu + \xi(1)\right)I_S(1)$$

$$\frac{dI_C(1)}{dt} = f_C(1)\delta E(1) - \left(\eta_{DC} + \mu + \xi(1)\right)I_C(1)$$

$$\frac{dD_S(1)}{dt} = \eta_{DS}I_S(1) - \left(\eta_S + \mu + \xi(1)\right)D_S(1)$$

$$\frac{dD_C(1)}{dt} = \eta_{DC}I_C(1) - \left(\eta_C + \mu + \xi(1) + \alpha(1)\right)D_C(1)$$

$$\frac{dR(1)}{dt} = \eta_M I_M(1) + \eta_S D_S(1) + \eta_C D_C(1) - \left(\mu + \xi(1)\right)R(1)$$

and in subsequent age groups, using:

Populations aged 10+ years:

$$\frac{dS(a)}{dt} = \xi(a-1)S(a-1) - \left(\lambda(a) + \mu + \xi(a)\right)S(a)$$

$$\frac{dE(a)}{dt} = \xi(a-1)E(a-1) + \lambda(a)S(a) - \left(\delta + \mu + \xi(a)\right)E(a)$$

$$\frac{dI_M(a)}{dt} = \xi(a-1)I_M(a-1) + f_M(a)\delta E(a) - \left(\eta_M + \mu + \xi(a)\right)I_M(a)$$

$$\frac{dI_S(a)}{dt} = \xi(a-1)I_S(a-1) + f_S(a)\delta E(a) - \left(\eta_{DS} + \mu + \xi(a)\right)I_S(a)$$

$$\frac{dI_C(a)}{dt} = \xi(a-1)I_C(a-1) + f_C(a)\delta E(a) - \left(\eta_{DC} + \mu + \xi(a)\right)I_C(a)$$

$$\frac{dD_S(a)}{dt} = \xi(a-1)D_S(a-1) + \eta_{DS}I_S(a) - \left(\eta_S + \mu + \xi(a)\right)D_S(a)$$

$$\frac{dD_C(a)}{dt} = \xi(a-1)D_C(a-1) + \eta_{DC}I_C(a) - \left(\eta_C + \mu + \xi(a) + \alpha(a)\right)D_C(a)$$

$$\frac{dR(a)}{dt} = \xi(a-1)R(a-1) + \eta_M I_M(a) + \eta_S D_S(a) + \eta_C D_C(a) - \left(\mu + \xi(a)\right)R(a)$$

The definitions of the population variables and symbols used in the equations are listed in Table

S1.

Table S1: Definitions of population variables and symbols used in the model.

Symbol	Definition
$S(a)$	Susceptible population
$E(a)$	Latently infected population
$I_M(a)$	Population with mild infection
$I_S(a)$	Population with severe infection
$I_C(a)$	Population with critical infection
$D_S(a)$	Population with severe disease
$D_C(a)$	Population with critical disease
$R(a)$	Recovered population
N	Total population size
n_{age}	Number of age groups
$\xi(a)$	Transition rate from one age group to the next age group
$\sigma(a)$	Susceptibility profile to the infection in each age group
$\beta(t)$	Average infectious contact rate
e_{Age}	Degree of assortativeness in the age group mixing
$1/\delta$	Duration of latent infection
$1/\eta_M$	Duration of mild infection infectiousness
$1/\eta_{DS}$	Duration of severe infection infectiousness before isolation and/or hospitalization
$1/\eta_S$	Duration of severe disease following onset of severe disease
$1/\eta_{DC}$	Duration of critical infection infectiousness before isolation and/or hospitalization
$1/\eta_C$	Duration of critical disease following onset of critical disease
$1/\mu$	Natural death rate
$CFR(a)$	*Relative* case fatality rate in each age group
$\alpha(a)$	Mortality rate in each age group
$f_M(a)$	Proportion of infections that will progress to be mild or asymptomatic infections
$f_S(a)$	Proportion of infections that will progress to be severe infections
$f_C(a)$	Proportion of infections that will progress to be critical infections

The force of infection (hazard rate) for each susceptible population in each age group $S(a)$ is

given by

$$\lambda(a)=\beta(t)\sigma(a)\sum_{a'=1}^{n_{age}}\mathcal{H}_{a,a'}\frac{I_M(a')+I_S(a')+I_C(a')}{\left[S(a')+E(a')+I_M(a')+I_S(a')+I_C(a')+D_S(a')+D_C(a')+R(a')\right]},$$

where $\beta(t)$ is the overall infectious contact rate per day, $\sigma(a)$ is the susceptibility profile to the infection in each age group, and $\mathcal{H}_{a,a'}$ is the mixing matrix which provides the probability that an individual in the a age group will mix with (that is contact) an individual in the a' age group. The mixing matrix is given by

$$\mathcal{H}_{a,a'}=e_{Age}\delta_{a,a'}+(1-e_{Age})\frac{S(a')+E(a')+I_M(a')+I_S(a')+I_C(a')+D_S(a')+D_C(a')+R(a')}{\sum_{a''=1}^{n_{age}}\left[S(a'')+E(a'')+I_M(a'')+I_S(a'')+I_C(a'')+D_S(a'')+D_C(a'')+R(a'')\right]}$$

Here, $\delta_{a,a'}$ is the identity matrix, and $e_{Age}\in[0,1]$ is the degree of assortativeness in the mixing. At the extreme $e_{Age}=0$, the mixing is fully proportional, while at the other extreme $e_{Age}=1$, the mixing is fully assortative, that is individuals mix only with members in their own age group.

2. Parameter values

The input parameters of the model were chosen based on current empirical data for SARS-CoV-2 natural history and epidemiology. The parameter values are listed in Table S2.

Table S2: Model assumptions in terms of parameter values.

Parameter	Symbol	Value	Justification
Duration of latent infection	$1/\delta$	3.69 days	Based on existing estimate [8] and based on a median incubation period of 5.1 days [9] adjusted by observed viral load among infected persons [10] and reported transmission before onset of symptoms [11]
Duration of infectiousness	$1/\eta_M$; $1/\eta_{DS}$; $1/\eta_{DC}$	3.48 days	Based on existing estimate [8] and based on observed time to recovery among persons with mild infection [4, 8] and observed viral load in infected persons [10, 11]
Duration of severe disease following onset of severe disease	$1/\eta_S$	28 days	Observed duration from onset of severe disease to recovery [4]
Duration of hospitalization for critical infection	$1/\eta_C$	28 days	Observed duration from onset of critical disease to recovery [4]

Life expectancy for each country	$1/\mu$	Table S3	United Nations World Population Prospects database [7]
Relative case fatality rate in each age group	$CFR(a)$		Observed crude case fatality rate based on China data [5, 6]
Age 0-9 years		0%	
Age 10-39 years		0.2%	
Age 40-49 years		0.4%	
Age 50-59 years		1.3%	
Age 60-69 years		3.6%	
Age 70-79 years		8.0%	
Age 80+ years		21.9%	
Proportion of infections that will progress to be mild or asymptomatic infections	$f_M(a)$		Observed proportion of infections that eventually develop mild or asymptomatic in China [2-4]
Age 0-9 years		88.9%	
Age 10-49 years		88.0%	
Age 50-59 years		82.5%	
Age 60+ years		71.2%	
Proportion of infections that will progress to be severe infections	$f_S(a)$		Observed proportion of infections that eventually develop severe disease in China [2-4]
Age 0-9 years		11.1%	
Age 10-49 years		9.9%	
Age 50-59 years		10.3%	
Age 60+ years		7.8%	
Proportion of infections that will progress to be critical infections	$f_C(a)$		Observed proportion of infections that eventually develop critical disease in China [2-4]
Age 0-9 years		0.0%	
Age 10-49 years		2.2%	
Age 50-59 years		7.2%	
Age 60+ years		20.9%	
Susceptibility profile to the infection in each age group	$\sigma(a)$		Estimates based on fitting the epidemic in China [1]
Age 0-9 years		0.05	
Age 10-19 years		0.05	
Age 20-29 years		0.32	
Age 30-39 years		0.53	
Age 40-49 years		0.65	
Age 50-59 years		0.74	
Age 60-69 years		0.93	
Age 70-79 years		0.88	
Age 80+ years		0.83	
Overall infectious contact rate	$\beta(t)$	0.59 contacts per day	Estimate based on fitting the epidemic in China [1]
Degree of assortativeness in the age group mixing	e_{Age}	0.004	Estimate based on fitting the epidemic in China [1]

3. The basic reproduction number R_0

Using the second generation matrix method described by Heffernan *et al.* [12], the basic reproduction number was derived to be:

$$R_0 = \sum_{a=1}^{n_{age}} \begin{bmatrix} w(a)f_M(a)\left(\dfrac{\delta}{\delta+\mu+\xi(a)}\dfrac{\beta\sigma(a)}{\eta_M+\mu+\xi(a)}\right) \\ +w(a)f_S(a)\left(\dfrac{\delta}{\delta+\mu+\xi(a)}\dfrac{\beta\sigma(a)}{\eta_{DS}+\mu+\xi(a)}\right) \\ +w(a)f_C(a)\left(\dfrac{\delta}{\delta+\mu+\xi(a)}\dfrac{\beta\sigma(a)}{\eta_{DC}+\mu+\xi(a)}\right) \end{bmatrix},$$

where $w(a)$ is the proportion of the population in each age group.

Table S3: Model estimates for key SARS-CoV-2 epidemiologic indicators for countries and territories with a population of at least one million [7] in the World Health Organization African Region (AFRO).

African Region	Total population [7]	Med-ian age [7]	Life expec-tancy [7]	R_0[a]	Infections per 100 persons[a]	Deaths per 100 persons[a]	Mild infections per 100 persons[a]	Severe and/or critical disease cases per 100 persons[a]	Day at peak incidence[a]
Country	Thousands	Years	Years	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)
Algeria	43,851,043	28.5	77.5	1.45 (1.35-2.21)	45.0 (35.2-52.6)	1.4 (1.2-1.6)	37.0 (29.5-44.3)	7.4 (5.7-8.3)	217.5 (206.0-246.0)
Angola	32,866,268	16.7	62.2	0.98 (0.88-1.46)	1.5 (0.0-23.4)	0.0 (0.0-0.5)	1.0 (0.0-20.0)	0.2 (0.0-3.4)	697.5 (518.0-700[b])
Benin	12,123,198	18.8	62.8	1.05 (0.98-1.61)	19.5 (0.1-29.8)	0.6 (0.0-0.7)	17.0 (0.1-25.4)	3.3 (0.0-4.5)	675.0 (360.0-700[b])
Botswana	2,351,625	24.0	69.9	1.25 (1.18-1.94)	35.0 (23.6-43.6)	0.9 (0.7-1.1)	29.0 (19.9-37.0)	5.3 (3.7-6.6)	235.0 (212.0-306.0)
Burkina Faso	20,903,278	17.6	63.0	0.98 (0.91-1.51)	2.5 (0.0-25.6)	0.1 (0.0-0.5)	1.5 (0.0-21.9)	0.3 (0.0-3.8)	700[b] (453.0-700[b])
Burundi	11,890,781	17.3	62.7	1.03 (0.90-1.49)	2.5 (0.0-24.8)	0.1 (0.0-0.5)	1.5 (0.0-21.1)	0.3 (0.0-3.6)	700[b] (454.0-700[b])
Cameroon	26,545,864	18.7	60.3	1.05 (0.96-1.59)	2.5 (0.0-29.2)	0.1 (0.0-0.6)	17.5 (0.0-24.9)	0.3 (0.0-4.3)	675.0 (397.0-700[b])
Cent. Afr. Rep.	4,829,764	17.6	54.4	0.98 (0.91-1.50)	2.5 (0.0-24.7)	0.1 (0.0-0.6)	1.5 (0.0-21.0)	0.3 (0.0-3.7)	700[b] (420.0-700[b])
Chad	16,425,859	16.6	55.2	0.92 (0.86-1.43)	1.0 (0.0-22.0)	0.0 (0.0-0.5)	1.0 (0.0-18.7)	0.2 (0.0-3.2)	697.5 (532.0-700[b])
Congo	5,518,092	19.2	65.2	1.15 (1.01-1.66)	23.0 (2.5-31.7)	0.5 (0.1-0.7)	19.0 (2.2-27.0)	3.4 (0.4-4.7)	405.0 (316.0-700[b])
Côte d'Ivoire	26,378,275	18.9	58.8	1.05 (0.97-1.60)	22.5 (0.0-29.6)	0.6 (0.0-0.7)	1.5 (0.0-25.2)	3.3 (0.0-4.4)	675.0 (389.0-700[b])
D. Rep. Congo	89,561,404	17.0	61.6	0.98 (0.91-1.51)	2.5 (0.0-25.4)	0.1 (0.0-0.6)	1.5 (0.0-21.6)	0.3 (0.0-3.8)	690.0 (497.0-700[b])
Equ. Guinea	1,402,985	22.3	59.8	1.15 (1.05-1.74)	27.0 (14.7-36.7)	0.5 (0.3-0.6)	23.0 (12.6-31.6)	3.8 (2.1-5.2)	310.0 (259.0-534.0)
Eritrea	3,546,427	19.2	67.5	1.15 (1.01-1.67)	23.0 (6.1-31.7)	0.7 (0.2-0.9)	19.0 (5.2-26.9)	3.5 (1.0-4.9)	345.0 (303.0-700[b])
Ethiopia	114,963,583	19.5	67.8	1.05 (0.99-1.63)	22.5 (0.0-31.5)	0.7 (0.0-0.8)	19.5 (0.0-26.8)	3.8 (0.0-4.7)	675.0 (402.0-700[b])
Eswatini	1,160,164	20.7	61.1	1.15 (1.04-1.72)	25.0 (13.7-34.5)	0.7 (0.4-0.8)	23.0 (11.6-29.4)	3.8 (2.1-5.1)	330.0 (261.0-547.0)
Gabon	2,225,728	22.5	67.0	1.25 (1.11-1.83)	29.0 (18.4-39.1)	0.7 (0.5-0.9)	25.0 (15.6-33.3)	4.4 (2.8-5.8)	275.0 (239.0-404.0)
Gambia	2,416,664	17.8	63.3	1.03 (0.92-1.52)	2.5 (0.0-25.5)	0.1 (0.0-0.5)	1.5 (0.0-21.8)	0.3 (0.0-3.7)	675.0 (383.0-700[b])
Ghana	31,072,945	21.5	64.9	1.15 (1.09-1.79)	29.0 (17.7-37.7)	0.7 (0.5-0.8)	25.0 (15.0-32.1)	4.4 (2.7-5.6)	350.0 (298.0-538.0)
Guinea	13,132,792	18.0	62.6	1.03 (0.93-1.53)	2.5 (0.0-26.4)	0.1 (0.0-0.6)	2.5 (0.0-22.4)	0.3 (0.0-3.9)	700[b] (423.0-700[b])
Guinea-Bissau	1,967,998	18.8	59.4	1.05 (0.97-1.60)	19.0 (0.1-29.0)	0.5 (0.0-0.6)	17.0 (0.1-24.7)	2.9 (0.0-4.3)	675.0 (326.0-700[b])
Kenya	53,771,300	20.1	67.5	1.15 (1.01-1.67)	25.0 (0.6-33.5)	0.5 (0.0-0.6)	21.0 (0.5-28.6)	3.4 (0.1-4.9)	425.0 (361.0-700[b])
Lesotho	2,142,252	24.0	55.7	1.25 (1.18-1.95)	37.0 (23.9-43.9)	1.0 (0.7-1.2)	29.0 (20.2-37.2)	5.6 (3.8-6.7)	235.0 (210.0-299.0)
Liberia	5,057,677	19.4	65.0	1.15 (1.01-1.67)	23.0 (4.0-31.9)	0.6 (0.1-0.7)	21.0 (3.4-27.1)	3.4 (0.6-4.8)	375.0 (312.0-700[b])
Madagascar	27,691,019	19.6	68.2	1.05 (1.00-1.66)	23.0 (0.6-32.1)	0.6 (0.0-0.7)	19.0 (0.5-27.3)	3.4 (0.1-4.8)	425.0 (355.0-700[b])
Malawi	19,129,955	18.1	65.6	1.03 (0.92-1.53)	2.5 (0.0-26.7)	0.1 (0.0-0.6)	2.5 (0.0-22.8)	0.3 (0.0-3.9)	700[b] (434.0-700[b])
Mali	20,250,834	16.3	60.5	0.98 (0.87-1.44)	1.0 (0.0-22.3)	0.0 (0.0-0.5)	1.0 (0.0-19.0)	0.2 (0.0-3.3)	697.5 (526.0-700[b])
Mauritania	4,649,660	20.1	65.6	1.15 (1.03-1.70)	25.0 (11.1-33.6)	0.6 (0.3-0.8)	21.0 (9.4-28.7)	3.8 (1.7-5.0)	375.0 (294.0-642.0)
Mauritius	1,271,767	37.5	75.5	1.95 (1.72-2.80)	63.5 (56.7-69.9)	2.8 (2.6-3.1)	52.5 (46.6-57.7)	11.3 (10.1-12.2)	116.0 (115.0-117.0)
Mozambique	31,255,435	17.6	62.1	1.03 (0.92-1.51)	2.5 (0.0-25.8)	0.1 (0.0-0.6)	1.5 (0.0-22.0)	0.3 (0.0-3.8)	700[b] (462.0-700[b])
Namibia	2,540,916	21.8	64.9	1.15 (1.08-1.79)	31.0 (17.0-37.6)	0.7 (0.5-0.9)	19.0 (14.4-32)	4.4 (2.6-5.6)	290.0 (253.0-457.0)
Niger	24,206,636	15.2	63.6	0.92 (0.83-1.37)	0.3 (0.0-17.0)	0.0 (0.0-0.4)	0.3 (0.0-14.4)	0.1 (0.0-2.5)	697.5 (624.0-700[b])
Nigeria	206,139,587	18.1	55.8	1.03 (0.95-1.57)	2.5 (0.0-28.6)	0.1 (0.0-0.6)	2.5 (0.0-24.4)	0.5 (0.0-4.3)	705.0 (459.0-700[b])
Rwanda	12,952,209	20.0	70.0	1.15 (1.03-1.69)	25.0 (6.5-33.5)	0.6 (0.2-0.8)	19.0 (5.5-28.5)	3.7 (1.0-5.0)	405.0 (320.0-700[b])
Senegal	16,743,930	18.5	68.9	1.05 (0.96-1.59)	22.5 (0.0-29.0)	0.6 (0.0-0.7)	1.5 (0.0-24.7)	3.3 (0.0-4.3)	675.0 (382.0-700[b])
Sierra Leone	7,976,985	19.4	55.9	1.05 (0.99-1.64)	21.0 (0.4-31.1)	0.5 (0.0-0.7)	19.0 (0.4-26.5)	3.2 (0.1-4.6)	425.0 (338.0-700[b])
South Africa	59,308,690	27.6	64.9	1.45 (1.32-2.16)	45.0 (33.7-52.0)	1.2 (1.0-1.4)	37.0 (28.4-44.0)	7.1 (5.4-8.0)	232.5 (217.0-268.0)

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African Region	Total population [7]	Median age [7]	Life expectancy [7]	R_0[a]	Infections per 100 persons[a]	Deaths per 100 persons[a]	Mild infections per 100 persons[a]	Severe and/or critical disease cases per 100 persons[a]	Day at peak incidence[a]
Country	**Thousands**	**Years**	**Years**	**N (95% UI)**	**N (95% UI)**	**N (95% UI)**	**N (95% UI)**	**N (95% UI)**	**N (95% UI)**
South Sudan	11,193,729	19.0	58.7	1.05 (0.98-1.62)	21.0 (0.2-30.3)	0.6 (0.0-0.7)	17.0 (0.1-25.8)	3.2 (0.0-4.5)	675.0 (353.0-700[b])
Togo	8,278,737	19.4	62.1	1.05 (1.00-1.65)	23.0 (1.1-31.6)	0.6 (0.0-0.7)	19.0 (1.0-27.0)	3.4 (0.2-4.7)	375.0 (330.0-700[b])
Uganda	45,741,000	16.7	64.4	0.92 (0.86-1.42)	0.5 (0.0-22.0)	0.0 (0.0-0.4)	0.5 (0.0-18.8)	0.1 (0.0-3.2)	697.5 (575.0-700[b])
Tanzania	59,734,213	18.0	66.4	0.98 (0.94-1.55)	2.5 (0.0-27.7)	0.1 (0.0-0.6)	2.5 (0.0-23.6)	0.5 (0.0-4.1)	705.0 (443.0-700[b])
Zambia	18,383,956	17.6	64.7	1.03 (0.89-1.48)	2.5 (0.0-24.9)	0.1 (0.0-0.5)	1.5 (0.0-21.3)	0.3 (0.0-3.6)	690.0 (472.0-700[b])
Zimbabwe	14,862,927	18.7	62.2	1.05 (0.97-1.60)	22.5 (0.0-29.3)	0.6 (0.0-0.7)	16.5 (0.0-25.0)	3.3 (0.0-4.3)	675.0 (377.0-700[b])
AFRO	**1,118,418,151**	**18.9**	**63.3**[c]	**1.05 (0.93-1.95)**[c]	**22.5 (0.25-63.5)**[c]	**0.5 (0.0-2.8)**[c]	**17.0 (0.25-52.5)**[c]	**3.3 (0.0-11.3)**[c]	**675 (116.0-700**[b]**)**[c]

Cent Afr Rep, Central African Republic. D Rep Congo, Democratic Republic of the Congo. Equ Guinea, Equatorial Guinea. N, number. NA, not applicable. Tanzania, United Republic of Tanzania. UI, uncertainty interval.

[a]For each epidemiologic indicator, the table reports the most probable estimate and the 95% uncertainty interval. For a number of countries, R_0 was close to 1 in some of the uncertainty runs leading to an estimated time for peak incidence beyond the simulation duration of two years (delayed epidemic peak). For these countries, the upper limit of the uncertainty interval was set at 700 days, that is the end day of the simulation. Uncertainty runs in which R_0 was less than 1 led to no epidemic emergence, and thus were excluded from further analysis. Reported ranges for the epidemic indicators did not include these runs, except for the range of R_0.

[b]The estimated time for peak incidence was beyond the simulation duration of two years. The upper limit of the uncertainty interval was set at 700 days, that is the end day of the simulation.

[c]Estimates are for the median (and range).

Table S4: Model estimates for key SARS-CoV-2 epidemiologic indicators for countries and territories with a population of at least one million [7] in the World Health Organization Region of the Americas (AMRO).

Region of the Americas	Total population [7]	Median age [7]	Life expectancy [7]	R_0[a]	Infections per 100 persons[a]	Deaths per 100 persons[a]	Mild infections per 100 persons[a]	Severe and/or critical disease cases per 100 persons[a]	Day at peak incidence[a]
Country	Thousands	Years	Years	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)
Argentina	45,195,777	31.5	77.2	1.65 (1.51-2.47)	53.0 (44.8-60.0)	2.3 (2.0-2.5)	45.5 (37.0-49.8)	9.1 (7.8-10.2)	180.5 (174.0-188.0)
Bolivia	11,673,029	25.6	72.4	1.45 (1.28-2.10)	41.0 (30.3-48.6)	1.5 (1.2-1.6)	33.0 (25.3-40.8)	6.8 (5.0-7.8)	227.5 (207.0-262.0)
Brazil	212,559,409	33.5	76.6	1.75 (1.57-2.57)	57.0 (49.3-64.3)	2.1 (2.0-2.4)	49.5 (41.0-53.7)	9.7 (8.4-10.6)	183.5 (180.0-190.0)
Canada	37,742,157	41.1	83.0	2.05 (1.86-3.02)	69.5 (63.0-74.5)	3.7 (3.6-4.1)	56.5 (51.1-60.7)	13.1 (11.9-13.8)	131.3 (127.0-133.0)
Chile	19,116,209	35.3	80.7	1.85 (1.66-2.71)	61.5 (54.0-67.7)	2.6 (2.4-2.9)	51.5 (44.5-56.1)	10.7 (9.5-11.6)	146.9 (145.0-148.0)
Colombia	50,882,884	31.3	77.9	1.65 (1.50-2.46)	55.0 (45.4-61.1)	2.0 (1.8-2.2)	45.5 (37.7-51.1)	9.1 (7.7-10.0)	182.5 (176.0-191.0)
Costa Rica	5,094,114	33.5	80.9	1.75 (1.58-2.59)	59.0 (49.9-64.6)	2.3 (2.1-2.5)	48.5 (41.4-53.8)	9.9 (8.6-10.8)	144.3 (142.0-148.0)
Cuba	11,326,616	42.2	79.2	2.05 (1.84-2.99)	68.5 (62.4-74.1)	3.3 (3.2-3.7)	56.5 (50.9-60.7)	12.5 (11.5-13.4)	122.3 (120.0-125.0)
Dom. Rep.	10,847,904	28.0	74.7	1.45 (1.37-2.24)	47.0 (36.5-53.8)	1.6 (1.4-1.8)	39.0 (30.4-45.1)	7.7 (6.1-8.7)	196.5 (184.0-215.0)
Ecuador	17,643,060	27.9	77.7	1.45 (1.36-2.24)	47.0 (36.4-53.7)	1.7 (1.4-1.8)	39.0 (30.4-45.1)	7.7 (6.0-8.6)	202.5 (191.0-224.0)
El Salvador	6,486,201	27.6	74.1	1.45 (1.37-2.25)	47.0 (36.8-54.0)	1.7 (1.5-1.9)	39.0 (30.6-45.2)	7.7 (6.2-8.8)	187.5 (178.0-207.0)
Guatemala	17,915,567	22.9	75.1	1.25 (1.14-1.88)	35.0 (21.3-41.3)	1.0 (0.7-1.1)	29.0 (18.0-35.1)	5.0 (3.4-6.3)	305.0 (262.0-410.0)
Haiti	11,402,533	24.0	65.0	1.35 (1.19-1.96)	35.0 (24.7-44.3)	1.1 (0.8-1.2)	31.0 (20.8-37.5)	5.6 (3.9-6.8)	265.0 (233.0-332.0)
Honduras	9,904,608	24.3	75.9	1.35 (1.20-1.98)	37.0 (25.8-45.6)	1.0 (0.8-1.2)	31.0 (21.7-38.7)	5.9 (4.1-6.9)	255.0 (227.0-318.0)
Jamaica	2,961,161	30.7	74.9	1.65 (1.48-2.43)	53.0 (43.9-59.9)	2.0 (1.8-2.2)	45.5 (36.5-50.0)	9.1 (7.5-9.9)	155.5 (150.0-162.0)
Mexico	128,932,753	29.2	75.4	1.55 (1.41-2.31)	49.0 (39.5-56.2)	1.7 (1.5-1.9)	40.5 (32.9-47.2)	8.0 (6.5-9.1)	214.5 (204.0-234.0)
Nicaragua	6,624,554	26.5	75.2	1.45 (1.28-2.11)	41.0 (31.1-49.8)	1.2 (1.0-1.4)	35.0 (26.1-42.1)	6.5 (5.0-7.7)	212.5 (198.0-250.0)
Panama	4,314,768	29.7	79.1	1.55 (1.42-2.34)	49.0 (39.9-56.4)	1.8 (1.6-2.0)	40.5 (33.2-47.2)	8.3 (6.7-9.2)	171.0 (163.0-182.0)
Paraguay	7,132,530	26.3	74.6	1.45 (1.29-2.13)	43.0 (31.8-50.3)	1.4 (1.1-1.6)	35.0 (26.6-42.3)	7.1 (5.2-8)	212.5 (196.0-244.0)
Peru	32,971,846	31.0	77.4	1.65 (1.47-2.41)	53.0 (43.3-59.4)	2.0 (1.7-2.1)	43.5 (36.1-49.7)	8.7 (7.3-9.7)	185.0 (177.0-195.0)
Puerto Rico	2,860,840	44.5	80.7	2.28 (1.99-2.61)	70.5 (64.0-74.7)	4.2 (4.0-4.6)	56.5 (51.5-60.4)	13.5 (12.5-14.3)	106.3 (103.0-110.0)
Trin. and Tob.	1,399,491	36.2	73.9	1.85 (1.66-2.72)	61.5 (54.0-67.6)	2.5 (2.3-2.8)	51.5 (44.5-56.1)	10.7 (9.4-11.6)	121.9 (121.0-123.0)
USA	331,002,647	38.3	79.1	1.95 (1.76-2.86)	64.5 (57.9-70.2)	3.4 (3.2-3.8)	52.5 (47.1-57.4)	12.1 (10.9-12.9)	158.9 (156.0-160.0)
Uruguay	3,473,727	35.8	78.4	1.85 (1.66-2.71)	60.5 (53.3-66.6)	3.2 (2.8-3.3)	49.5 (43.5-54.8)	10.9 (9.7-11.9)	130.9 (129.0-132.0)
Venezuela	28,435,943	29.6	72.3	1.55 (1.41-2.32)	49.0 (39.2-55.5)	1.8 (1.5-2.0)	40.5 (32.6-46.4)	8.0 (6.6-9.1)	195.0 (185.0-210.0)
AMRO	**1,017,900,328**	**30.7**	**76.6**[c]	**1.65 (1.25-2.28)**[c]	**53.0 (35.0-70.5)**[c]	**2.0 (1.0-4.2)**[c]	**43.5 (29.0-56.5)**[c]	**8.7 (5.0-13.5)**[c]	**183.5 (106.3-305.0)**[c]

Dom Rep, Dominican Republic. N, number. Trin. and Tob., Trinidad and Tobago. UI, uncertainty interval. USA, United States of America.

[a]For each epidemiologic indicator, the table reports the most probable estimate and the 95% uncertainty interval. For a number of countries, R_0 was close to 1 in some of the uncertainty runs leading to an estimated time for peak incidence beyond the simulation duration of two years (delayed epidemic peak). For these countries, the upper limit of the uncertainty interval was set at 700 days, that is the end day of the simulation. Uncertainty runs in which R_0 was less than 1 led to no epidemic emergence, and thus were excluded from further analysis. Reported ranges for the epidemic indicators did not include these runs, except for the range of R_0.

[c]Estimates are for the median (and range).

Table S5: Model estimates for key SARS-CoV-2 epidemiologic indicators for countries and territories with a population of at least one million [7] in the World Health Organization Eastern Mediterranean Region (EMRO).

Eastern Mediterranean Region	Total population [7]	Median age [7]	Life expectancy [7]	R_0[a]	Infections per 100 persons[a]	Deaths per 100 persons[a]	Mild infections per 100 persons[a]	Severe and/or critical disease cases per 100 persons[a]	Day at peak incidence[a]
Country	Thousands	Years	Years	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)
Afghanistan	38,928,341	18.4	66.0	1.03 (0.94-1.55)	2.5 (0.0-27.8)	0.1 (0.0-0.6)	2.5 (0.0-23.7)	0.5 (0.0-4.1)	700[b] (436.0-700[b])
Bahrain	1,701,583	32.5	77.7	1.65 (1.50-2.48)	61.0 (49.0-66.7)	0.9 (0.8-1.1)	51.0 (42.1-57.4)	8.7 (7.0-9.4)	146.5 (141.0-154.0)
Egypt	102,334,403	24.6	72.5	1.35 (1.22-2.01)	37.0 (26.7-45.5)	1.2 (0.9-1.3)	31.0 (22.4-38.4)	5.9 (4.3-7.1)	285.0 (255.0-350.0)
Iran	83,992,953	32.0	77.3	1.55 (1.47-2.41)	53.0 (43.9-60.2)	1.7 (1.4-1.8)	44.5 (36.8-50.8)	8.7 (7.1-9.4)	195.0 (187.0-207.0)
Iraq	40,222,503	21.0	71.1	1.15 (1.06-1.75)	27.0 (14.3-36.2)	0.7 (0.4-0.8)	23.0 (12.1-30.8)	4.1 (2.2-5.4)	375.0 (320.0-628.0)
Jordan	10,203,140	23.8	75.0	1.25 (1.17-1.93)	37.0 (23.5-43.5)	0.9 (0.6-1.0)	29.0 (19.9-37.0)	5.3 (3.6-6.5)	265.0 (238.0-353.0)
Kuwait	4,270,563	36.8	75.9	1.75 (1.59-2.61)	61.0 (51.6-67.0)	1.2 (1.1-1.4)	51.5 (43.9-57.1)	9.1 (7.8-9.9)	143.5 (139.0-147.0)
Lebanon	6,825,442	29.6	79.3	1.55 (1.43-2.34)	51.0 (40.5-57.2)	1.8 (1.5-1.9)	41.5 (33.8-48.0)	8.3 (6.7-9.2)	175.0 (168.0-188.0)
Libya	6,871,287	28.8	73.4	1.45 (1.34-2.20)	45.0 (35.4-53.7)	1.1 (0.9-1.2)	39.0 (29.9-45.7)	7.1 (5.4-8.0)	196.5 (184.0-222.0)
Morocco	36,910,558	29.5	77.4	1.55 (1.42-2.33)	49.0 (39.7-56.2)	1.7 (1.5-1.9)	40.5 (33.1-47.1)	8.3 (6.7-9.2)	197.0 (188.0-213.0)
Oman	5,106,622	30.6	78.6	1.55 (1.39-2.30)	53.0 (41.9-61.4)	0.7 (0.7-0.9)	47.0 (36.1-53.0)	7.4 (5.9-8.4)	178.5 (170.0-199.0)
Pakistan	220,892,331	22.8	67.8	1.25 (1.14-1.88)	33.0 (21.8-41.3)	0.9 (0.7-1.1)	27.0 (18.3-35.0)	5.0 (3.4-6.3)	350.0 (303.0-479.0)
Palestine	5,101,416	20.8	74.6	1.15 (1.04-1.71)	25.0 (12.3-34.5)	0.6 (0.3-0.8)	19.0 (10.4-29.4)	3.8 (1.9-5.1)	345.0 (293.0-627.0)
Qatar	2,881,060	32.3	80.7	1.65 (1.54-2.55)	65.0 (53.6-71.5)	0.8 (0.7-0.9)	55.0 (46.3-61.8)	8.9 (7.4-9.7)	147.5 (141.0-153.0)
Saudi Arabia	34,813,867	31.8	75.7	1.55 (1.42-2.35)	53.0 (42.1-59.7)	1.0 (0.9-1.1)	45.0 (35.9-51.1)	7.9 (6.2-8.7)	193.5 (185.0-212.0)
Somalia	15,893,219	16.7	58.3	0.98 (0.88-1.45)	1.5 (0.0-22.8)	0.0 (0.0-0.5)	1.5 (0.0-19.4)	0.3 (0.0-3.4)	697.5 (501.0-700[b])
Sudan	43,849,269	19.7	66.1	1.15 (1.02-1.68)	23.0 (1.7-32.9)	0.7 (0.0-0.8)	21.0 (1.5-27.9)	3.7 (0.3-5.0)	405.0 (352.0-700[b])
Syria	17,500,657	25.6	76.1	1.35 (1.24-2.05)	39.0 (28.6-48.0)	1.1 (0.8-1.2)	33.0 (24.2-40.7)	6.2 (4.5-7.3)	242.5 (222.0-295.0)
Tunisia	11,818,618	32.8	77.4	1.65 (1.53-2.50)	55.0 (46.3-61.5)	2.0 (1.8-2.2)	45.5 (38.4-51.3)	9.5 (7.8-10.2)	162.5 (158.0-168.0)
UAE	9,890,400	32.6	78.5	1.65 (1.53-2.54)	63.0 (52.8-70.6)	0.7 (0.6-0.8)	55.0 (45.6-61.2)	8.7 (7.2-9.5)	161.0 (154.0-169.0)
Yemen	29,825,968	20.2	66.4	1.05 (1.00-1.66)	23.0 (0.4-32.8)	0.6 (0.0-0.7)	19.0 (0.4-28.0)	3.4 (0.1-4.8)	425.0 (357.0-700[b])
EMRO	**729,834,200**	**28.8**	**75.7[c]**	**1.45 (0.98-1.75)[c]**	**45.0 (1.5-65.0)[c]**	**0.9 (0.0-2.0)[c]**	**39.0 (1.5-55.0)[c]**	**7.1 (0.3-9.5)[c]**	**197.0 (143.5-700[b])[c]**

N, number. Syria, Syrian Arab Republic. UAE, United Arab Emirates. UI, uncertainty interval.

[a]For each epidemiologic indicator, the table reports the most probable estimate and the 95% uncertainty interval. For a number of countries, R_0 was close to 1 in some of the uncertainty runs leading to an estimated time for peak incidence beyond the simulation duration of two years (delayed epidemic peak). For these countries, the upper limit of the uncertainty interval was set at 700 days, that is the end day of the simulation. Uncertainty runs in which R_0 was less than 1 led to no epidemic emergence, and thus were excluded from further analysis. Reported ranges for the epidemic indicators did not include these runs, except for the range of R_0.

[b]The estimated time for peak incidence was beyond the simulation duration of two years. The upper limit of the uncertainty interval was set at 700 days, that is the end day of the simulation.

[c]Estimates are for the median (and range).

Table S6: Model estimates for key SARS-CoV-2 epidemiologic indicators for countries and territories with a population of at least one million [7] in the World Health Organization European Region (EURO).

European Region	Total population [7]	Median age [7]	Life expectancy [7]	R_0[a]	Infections per 100 persons[a]	Deaths per 100 persons[a]	Mild infections per 100 persons[a]	Severe and/or critical disease cases per 100 persons[a]	Day at peak incidence[a]
Country	Thousands	Years	Years	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)
Albania	2,877,800	36.4	79.0	1.85 (1.73-2.82)	63.5 (57.1-69.9)	3.1 (2.9-3.5)	52.5 (46.6-57.3)	11.7 (10.5-12.6)	122.0 (120.0-123.0)
Armenia	2,963,234	35.4	75.6	1.85 (1.67-2.72)	61.5 (53.8-67.4)	2.7 (2.5-3.0)	50.5 (44.2-55.7)	10.9 (9.6-11.8)	128.9 (127.0-130.0)
Austria	9,006,400	43.5	82.1	2.05 (1.91-3.11)	71.5 (65.7-76.6)	4.0 (3.8-4.4)	58.5 (53.2-62.3)	13.5 (12.5-14.3)	114.3 (111.0-118.0)
Azerbaijan	10,139,175	32.3	73.3	1.65 (1.52-2.49)	55.0 (46.5-62.1)	1.8 (1.6-2.0)	46.5 (38.8-52.1)	9.3 (7.7-10.0)	161.5 (157.0-168.0)
Belarus	9,449,321	40.3	75.2	2.05 (1.84-2.99)	68.5 (62.2-73.8)	3.4 (3.2-3.7)	55.5 (50.7-60.4)	12.7 (11.5-13.4)	121.3 (119.0-124.0)
Belgium	11,589,616	41.9	82.2	2.05 (1.85-3.01)	68.5 (62.1-73.5)	4.1 (3.7-4.3)	55.5 (50.2-59.7)	13.1 (11.9-13.8)	121.3 (119.0-124.0)
Bosnia & Herz.	3,280,815	43.1	77.9	2.05 (1.91-3.11)	71.5 (65.5-76.5)	3.8 (3.6-4.2)	58.5 (53.1-62.3)	13.5 (12.4-14.2)	108.3 (104.0-110.0)
Bulgaria	6,948,445	44.6	75.5	2.15 (1.96-3.19)	71.5 (67.3-77.7)	4.3 (4.1-4.6)	58.5 (54.3-63.0)	14.1 (13.0-14.8)	110.5 (105.0-113.0)
Croatia	4,105,268	44.3	79.0	2.15 (1.95-3.16)	72.5 (66.6-77.2)	4.3 (4.1-4.7)	58.5 (53.7-62.4)	14.1 (13.0-14.7)	106.5 (103.0-110.0)
Cyprus	1,207,361	37.3	81.5	1.85 (1.74-2.84)	65.5 (58.2-71.2)	3.0 (2.8-3.3)	55.5 (47.8-58.8)	11.7 (10.4-12.5)	113 (112.0-115.0)
Czech Republic	10,708,982	43.2	79.9	2.05 (1.92-3.11)	71.5 (65.4-76.3)	3.9 (3.7-4.3)	57.5 (53.0-62.1)	13.3 (12.4-14.2)	115.3 (112.0-119.0)
Denmark	5,792,203	42.3	81.4	2.05 (1.85-3.01)	68.5 (62.3-73.6)	4.0 (3.8-4.3)	55.5 (50.3-59.7)	13.1 (12.0-13.9)	117.3 (113.0-119.0)
Estonia	1,326,539	42.4	79.2	2.05 (1.89-3.07)	71.5 (64.1-75.1)	4.0 (3.8-4.4)	57.5 (51.8-61.0)	13.3 (12.3-14.1)	103.3 (99.0-105.0)
Finland	5,540,718	43.1	82.5	2.05 (1.91-3.09)	71.5 (64.3-75.1)	4.3 (4.1-4.8)	56.5 (51.6-60.6)	13.7 (12.7-14.5)	111.3 (108.0-115.0)
France	65,273,512	42.3	83.1	2.05 (1.85-3.00)	67.5 (61.5-72.7)	4.0 (3.8-4.4)	55.5 (49.6-58.9)	12.9 (12.0-13.9)	136.3 (132.0-138.0)
Georgia	3,989,175	38.3	74.2	1.85 (1.74-2.83)	63.5 (57.0-69.5)	3.2 (3.0-3.5)	52.5 (46.4-56.9)	11.7 (10.5-12.6)	122.9 (122.0-125.0)
Germany	83,783,945	45.7	81.9	2.15 (1.97-3.19)	73.5 (67.5-77.8)	4.5 (4.3-4.9)	59.5 (54.3-62.9)	14.1 (13.2-15.0)	127.5 (122.0-130.0)
Greece	10,423,056	45.6	82.8	2.15 (1.98-3.21)	73.5 (68.1-78.3)	4.5 (4.3-4.9)	59.5 (54.8-63.3)	14.1 (13.2-15.0)	112.5 (107.0-115.0)
Hungary	9,660,350	43.3	77.3	2.05 (1.92-3.13)	71.5 (66.0-76.8)	4.0 (3.8-4.4)	58.5 (53.4-62.5)	13.7 (12.6-14.3)	115.3 (111.0-118.0)
Ireland	4,937,796	38.2	82.8	1.85 (1.70-2.77)	60.5 (55.1-68.0)	2.9 (2.7-3.2)	49.5 (45.1-56.0)	11.1 (10.0-12.0)	128.8 (128.0-130.0)
Israel	8,655,541	30.5	83.5	1.65 (1.47-2.40)	49.0 (41.6-56.9)	2.4 (2.1-2.6)	41.5 (34.2-47.1)	8.9 (7.5-9.9)	169.5 (163.0-178.0)
Italy	60,461,828	47.3	84.0	2.30 (2.02-3.27)	75.5 (69.6-79.5)	4.7 (4.5-5.1)	60.5 (55.9-64.1)	14.7 (13.7-15.4)	121.5 (116.0-124.0)
Kazakhstan	18,776,707	30.7	73.9	1.55 (1.44-2.36)	49.0 (40.6-56.6)	1.9 (1.6-2.0)	41.5 (33.8-47.3)	8.3 (6.9-9.3)	185.0 (176.0-197.0)
Kyrgyzstan	6,524,191	26.0	72.0	1.35 (1.26-2.07)	39.0 (29.1-47.9)	1.2 (0.9-1.3)	33.0 (24.5-40.5)	6.2 (4.7-7.4)	222.5 (203.0-263.0)
Latvia	1,886,202	43.9	75.7	2.05 (1.92-3.11)	69.5 (65.1-75.8)	4.4 (4.0-4.6)	57.5 (52.5-61.4)	13.7 (12.6-14.4)	103.3 (99.0-106.0)
Lithuania	2,722,291	45.1	76.4	2.05 (1.93-3.13)	71.5 (65.9-76.5)	4.2 (4.0-4.6)	57.5 (53.1-61.9)	13.9 (12.8-14.6)	104.3 (101.0-108.0)
Netherlands	17,134,873	43.3	82.8	2.05 (1.88-3.06)	69.5 (63.5-74.5)	4.0 (3.8-4.4)	56.5 (51.3-60.4)	13.5 (12.3-14.1)	121.3 (118.0-125.0)
Norway	5,421,242	39.8	82.9	1.95 (1.80-2.92)	66.5 (60.1-72.1)	3.7 (3.3-3.9)	54.5 (48.9-58.9)	12.3 (11.2-13.2)	120.3 (118.0-123.0)
Poland	37,846,605	41.7	79.3	2.05 (1.90-3.09)	71.5 (65.1-76.2)	3.9 (3.7-4.2)	58.5 (52.8-62.1)	13.3 (12.3-14.1)	127.3 (123.0-129.0)
Portugal	10,196,707	46.2	82.7	2.30 (1.99-3.24)	74.5 (68.7-78.8)	4.5 (4.3-4.9)	60.5 (55.3-63.6)	14.5 (13.4-15.1)	109.5 (106.0-113.0)
Rep. Moldova	4,033,963	37.6	72.3	1.95 (1.78-2.91)	67.5 (60.8-73.4)	2.8 (2.6-3.1)	56.5 (50.1-60.8)	12.1 (10.7-12.6)	119.3 (118.0-122.0)
Romania	19,237,682	43.2	76.5	2.05 (1.90-3.09)	71.5 (64.9-75.8)	4.0 (3.7-4.3)	57.5 (52.5-61.7)	13.5 (12.3-14.1)	120.3 (117.0-124.0)
Russia	145,934,460	39.6	73.0	1.95 (1.81-2.95)	67.5 (60.8-72.6)	3.3 (3.2-3.7)	54.5 (49.6-59.5)	12.3 (11.2-13.1)	145.3 (143.0-147.0)
Serbia	8,737,370	41.6	76.5	2.05 (1.87-3.03)	69.5 (63.2-74.6)	3.8 (3.6-4.1)	56.5 (51.3-60.7)	13.1 (12.0-13.8)	119.3 (115.0-121.0)
Slovakia	5,459,643	41.2	78.0	2.05 (1.87-3.04)	71.5 (63.9-75.4)	3.5 (3.3-3.8)	57.5 (52.2-61.8)	12.9 (11.8-13.6)	114.3 (112.0-117.0)
Slovenia	2,078,932	44.5	81.8	2.15 (1.96-3.17)	72.5 (67.0-77.3)	4.2 (4.0-4.6)	59.5 (54.0-62.7)	13.9 (12.9-14.7)	102.3 (97.0-104.0)
Spain	46,754,783	44.9	84.0	2.15 (1.95-3.17)	71.5 (67.2-77.7)	4.1 (3.9-4.5)	59.5 (54.4-63.2)	13.9 (12.8-14.5)	123.5 (119.0-127.0)

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European Region	Total population [7]	Med-ian age [7]	Life expec-tancy [7]	R_0[a]	Infections per 100 persons[a]	Deaths per 100 persons[a]	Mild infections per 100 persons[a]	Severe and/or critical disease cases per 100 persons[a]	Day at peak incidence[a]
Country	Thousands	Years	Years	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)
Sweden	10,099,270	41.1	83.3	1.95 (1.83-2.98)	67.5 (61.3-72.8)	4.0 (3.7-4.3)	55.5 (49.5-59.1)	12.9 (11.8-13.7)	122.3 (119.0-125.0)
Switzerland	8,654,618	43.1	84.2	2.05 (1.9-3.09)	71.5 (65.2-76.1)	3.9 (3.7-4.3)	58.5 (52.8-62.0)	13.5 (12.4-14.2)	116.3 (112.0-118.0)
Tajikistan	9,537,642	22.4	71.8	1.25 (1.12-1.84)	31.0 (19.4-39.5)	0.8 (0.5-0.9)	25.0 (16.4-33.6)	4.7 (3.0-5.9)	310 (260.0-431.0)
Macedonia	2,083,380	39.1	76.3	1.95 (1.79-2.92)	67.5 (60.5-72.8)	3.1 (2.9-3.4)	55.5 (49.6-59.9)	12.1 (10.9-12.9)	113.3 (111.0-115.0)
Turkey	84,339,067	31.5	78.5	1.65 (1.49-2.44)	55.0 (44.3-60.0)	2.0 (1.7-2.2)	44.5 (36.8-50.1)	9.1 (7.5-9.9)	189 (183.0-200.0)
Turkmenistan	6,031,187	26.9	68.6	1.45 (1.29-2.12)	41.0 (31.2-49.8)	1.2 (0.9-1.3)	37.0 (26.2-42.1)	6.5 (5.0-7.7)	212.5 (195.0-245.0)
Ukraine	43,733,759	41.2	72.5	2.05 (1.87-3.05)	70.5 (64.1-75.5)	3.6 (3.4-3.9)	57.5 (52.2-61.8)	12.9 (11.9-13.7)	129.3 (127.0-132.0)
United Kingdom	67,886,004	40.5	81.8	2.05 (1.82-2.95)	65.5 (60.8-72.5)	3.8 (3.5-4.1)	54.5 (49.3-59.1)	12.5 (11.5-13.4)	138.3 (136.0-141.0)
Uzbekistan	33,469,199	27.8	72.0	1.45 (1.33-2.18)	45.0 (34.4-52.6)	1.2 (1.0-1.4)	37.0 (28.9-44.6)	7.1 (5.5-8.1)	222.5 (207.0-253.0)
EURO	**930,700,857**	**41.7**	**79.0[c]**	**2.05 (1.25-2.30)[c]**	**69.0 (31.0-75.5)[c]**	**3.9 (0.8-4.7)[c]**	**56.5 (25.0-65.0)[c]**	**13.0 (4.7-14.7)[c]**	**121.3 (102.3-310.0)[c]**

Bosnia & Herz, Bosnia and Herzegovina. Macedonia, Republic of North Macedonia. N, number. Rep Moldova, Republic of Moldova. Russia, Russian Federation. UI, uncertainty interval.

[a]For each epidemiologic indicator, the table reports the most probable estimate and the 95% uncertainty interval. For a number of countries, R_0 was close to 1 in some of the uncertainty runs leading to an estimated time for peak incidence beyond the simulation duration of two years (delayed epidemic peak). For these countries, the upper limit of the uncertainty interval was set at 700 days, that is the end day of the simulation. Uncertainty runs in which R_0 was less than 1 led to no epidemic emergence, and thus were excluded from further analysis. Reported ranges for the epidemic indicators did not include these runs, except for the range of R_0.

[c]Estimates are for the median (and range).

Table S7: Model estimates for key SARS-CoV-2 epidemiologic indicators for countries and territories with a population of at least one million [7] in the World Health Organization South-East Asia Region (SEARO).

South-East Asia Region	Total population [7]	Med-ian age [7]	Life expec-tancy [7]	R_0[a]	Infections per 100 persons[a]	Deaths per 100 persons[a]	Mild infections per 100 persons[a]	Severe and/or critical disease cases per 100 persons[a]	Day at peak incidence[a]
Country	Thousands	Years	Years	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)
Bangladesh	164,689,383	27.6	73.6	1.45 (1.32-2.18)	45.0 (34.6-53.0)	1.2 (1.0-1.4)	39.0 (29.2-44.9)	7.1 (5.5-8.1)	242.5 (228.0-281.0)
DPR. Korea	25,778,815	35.3	72.9	1.85 (1.63-2.66)	61.5 (52.2-66.3)	2.3 (2.1-2.6)	49.5 (43.2-55.1)	10.3 (9-11.2)	154.3 (151.0-156.0)
India	1,380,004,385	28.4	70.4	1.45 (1.37-2.25)	47.0 (37.7-55.0)	1.6 (1.3-1.7)	39.0 (31.6-46.3)	7.7 (6.2-8.7)	252.5 (240.0-283.0)
Indonesia	273,523,621	29.7	72.3	1.55 (1.41-2.32)	49.0 (39.9-56.6)	1.5 (1.3-1.7)	41.5 (33.4-47.6)	8.0 (6.5-9.0)	223.5 (211.0-242.0)
Myanmar	54,409,794	29.0	67.8	1.55 (1.39-2.29)	49.0 (38.7-55.8)	1.6 (1.3-1.7)	41.0 (32.4-47.0)	7.7 (6.3-8.8)	208.5 (197.0-227.0)
Nepal	29,136,808	24.6	71.7	1.35 (1.24-2.04)	39.0 (28.7-47.7)	1.2 (1.0-1.4)	33.0 (24.0-40.2)	6.2 (4.6-7.5)	252.5 (229.0-304.0)
Sri Lanka	21,413,250	34.0	77.6	1.75 (1.57-2.56)	55.5 (47.8-62.2)	2.4 (2.2-2.7)	42.5 (39.3-51.4)	9.7 (8.5-10.7)	161.3 (158.0-165.0)
Thailand	69,799,978	40.1	77.7	1.95 (1.78-2.90)	66.5 (59.7-72.2)	2.9 (2.8-3.3)	54.5 (49.0-59.5)	11.9 (10.7-12.7)	143.3 (141.0-145.0)
Timor-Leste	1,318,442	20.8	70.2	1.15 (1.06-1.75)	25.0 (15.3-35.3)	0.8 (0.5-1.0)	23.0 (12.9-29.9)	4.1 (2.5-5.4)	290.0 (251.0-476.0)
SEARO	**2,020,074,476**	**29.0**	**72.3**[c]	**1.55 (1.15-1.95)**[c]	**49.0 (25.0-66.5)**[c]	**1.6 (0.8-2.9)**[c]	**41.0 (23.0-54.5)**[c]	**7.7 (4.1-11.9)**[c]	**223.5 (143.3-290.0)**[c]

DPR Korea, Democratic People's Republic of Korea. N, number. UI, uncertainty interval.

[a]For each epidemiologic indicator, the table reports the most probable estimate and the 95% uncertainty interval. For a number of countries, R_0 was close to 1 in some of the uncertainty runs leading to an estimated time for peak incidence beyond the simulation duration of two years (delayed epidemic peak). For these countries, the upper limit of the uncertainty interval was set at 700 days, that is the end day of the simulation. Uncertainty runs in which R_0 was less than 1 led to no epidemic emergence, and thus were excluded from further analysis. Reported ranges for the epidemic indicators did not include these runs, except for the range of R_0.

[c]Estimates are for the median (and range).

Table S8: Model estimates for key SARS-CoV-2 epidemiologic indicators for countries and territories with a population of at least one million [7] in the World Health Organization Western Pacific Region (WPRO).

Western Pacific Region	Total population [7]	Med-ian age [7]	Life expec-tancy [7]	R_0[a]	Infections per 100 persons[a]	Deaths per 100 persons[a]	Mild infections per 100 persons[a]	Severe and/or critical disease cases per 100 persons[a]	Day at peak incidence[a]
Country	Thousands	Years	Years	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)	N (95% UI)
Australia	25,499,881	37.9	83.9	1.85 (1.74-2.83)	63.5 (57.1-69.7)	3.3 (3.1-3.6)	52.5 (46.6-57.1)	11.7 (10.6-12.6)	139.9 (138.0-141.0)
Cambodia	16,718,971	25.6	70.5	1.35 (1.24-2.04)	39.0 (28.2-47.6)	1.1 (0.8-1.2)	33.0 (23.8-40.3)	6.2 (4.5-7.3)	247.5 (223.0-299.0)
China	1,439,323,774	38.4	77.5	1.95 (1.75-2.86)	65.5 (58.7-71.4)	2.7 (2.5-3.0)	54.5 (48.4-59.1)	11.5 (10.3-12.3)	170.9 (169.0-172.0)
Hong Kong	7,496,988	44.8	85.3	2.30 (1.99-3.24)	75.5 (69.7-80.1)	4.1 (3.8-4.4)	61.5 (56.5-65.2)	14.1 (13.1-14.8)	106.5 (104.0-111.0)
Japan	126,476,458	48.4	85.0	2.30 (2.07-3.35)	76.5 (71.2-80.6)	5.3 (5.1-5.8)	61.5 (56.7-64.5)	15.5 (14.5-16.1)	123.5 (116.0-126.0)
Lao PDR.	7,275,556	24.4	68.9	1.35 (1.19-1.97)	37.0 (25.0-44.9)	0.9 (0.7-1.1)	29.0 (21.1-38.1)	5.6 (3.9-6.8)	255.0 (225.0-321.0)
Malaysia	32,365,998	30.3	76.7	1.55 (1.44-2.37)	51.0 (42.2-58.9)	1.7 (1.4-1.8)	44.5 (35.3-49.6)	8.3 (6.9-9.4)	191.0 (182.0-204.0)
Mongolia	3,278,292	28.2	70.5	1.45 (1.31-2.16)	43.0 (33.1-51.5)	1.1 (0.9-1.3)	37.0 (28.0-43.7)	6.8 (5.2-7.8)	192.5 (181.0-221.0)
New Zealand	4,822,233	38.0	82.8	1.85 (1.73-2.82)	63.5 (56.6-69.1)	3.3 (3.1-3.7)	51.5 (46.1-56.5)	11.7 (10.6-12.6)	125.9 (124.0-127.0)
Pap. New Gui	8,947,027	22.4	65.2	1.25 (1.13-1.86)	31.0 (20.2-40.3)	0.8 (0.6-0.9)	27.0 (17.1-34.2)	5.0 (3.2-6.1)	295.0 (254.0-409.0)
Philippines	109,581,085	25.7	71.7	1.35 (1.27-2.09)	41.0 (30.4-48.9)	1.2 (1.0-1.4)	35.0 (25.5-41.3)	6.5 (4.9-7.6)	262.5 (239.0-308.0)
Rep.Korea	51,269,183	43.7	83.5	2.15 (1.93-3.15)	73.5 (67.4-78.4)	3.6 (3.4-4.0)	59.5 (55.0-64.2)	13.5 (12.4-14.2)	124.5 (122.0-129.0)
Taiwan	23,816,775	42.5	81.0	2.15 (1.91-3.12)	73.5 (66.7-77.8)	3.5 (3.3-3.9)	59.5 (54.4-63.8)	13.3 (12.2-14.0)	120.3 (118.0-125.0)
Singapore	5,850,343	42.2	84.1	2.05 (1.91-3.11)	73.5 (66.9-78.3)	3.2 (3.0-3.5)	60.5 (54.9-64.5)	13.1 (12.0-13.8)	112.3 (109.0-115.0)
Viet Nam	97,338,583	32.5	75.8	1.65 (1.52-2.50)	55.0 (46.7-62.2)	1.9 (1.7-2.1)	47.5 (38.9-52.2)	9.1 (7.8-10.1)	185.5 (179.0-193.0)
WPRO	**1,960,061,147**	**37.9**	**77.5**[c]	**1.85 (1.25-2.30)**[c]	**63.5 (31.0-76.5)**[c]	**2.7 (0.8-5.3)**[c]	**51.5 (27.0-61.5)**[c]	**11.5 (5.0-15.5)**[c]	**170.9 (106.5-295.0)**[c]

Lao PDR, Lao People's Democratic Republic. N, number. Pap New Gui, Papua New Guinea. Rep Korea, Republic of Korea. UI, uncertainty interval.

[a]For each epidemiologic indicator, the table reports the most probable estimate and the 95% uncertainty interval. For a number of countries, R_0 was close to 1 in some of the uncertainty runs leading to an estimated time for peak incidence beyond the simulation duration of two years (delayed epidemic peak). For these countries, the upper limit of the uncertainty interval was set at 700 days, that is the end day of the simulation. Uncertainty runs in which R_0 was less than 1 led to no epidemic emergence, and thus were excluded from further analysis. Reported ranges for the epidemic indicators did not include these runs, except for the range of R_0.

[c]Estimates are for the median (and range).

Figure S4: Estimates for the A) mild infections index, B) severe infections index, and C) severe and/or critical infections index in 159 countries and territories with a population of at least one million, across World Health Organization regions. These are the African Region (AFRO), Eastern Mediterranean Region (EMRO), South-East Asia Region (SEARO), Region of the Americas (AMRO), Western Pacific Region (WPRO), and European Region (EURO). The figure shows also the median index for each world region.
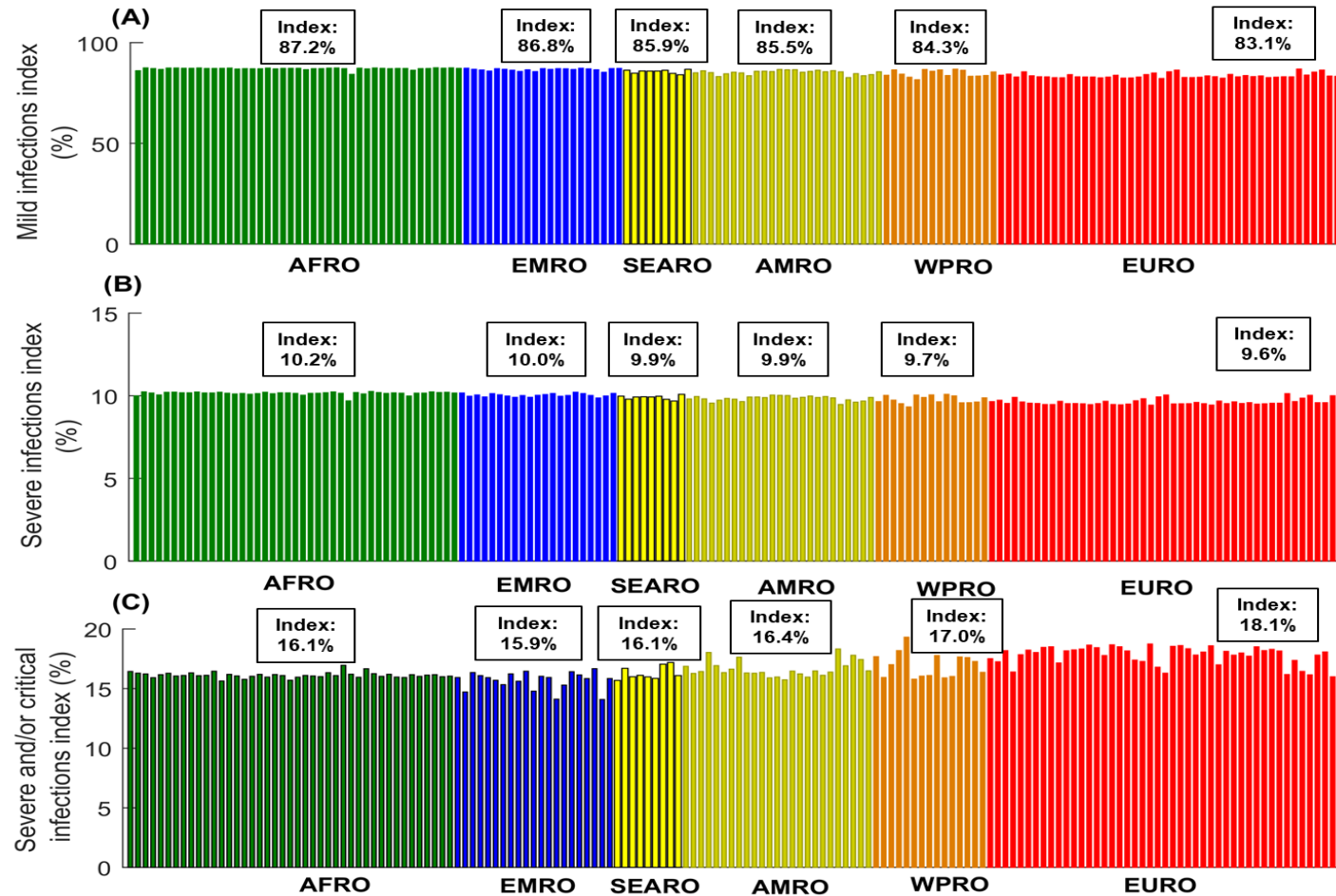
Figure S5: Impact of the variation in median age in any country on the basic reproduction number, R_0. This figure was produced based on the estimates of all countries.
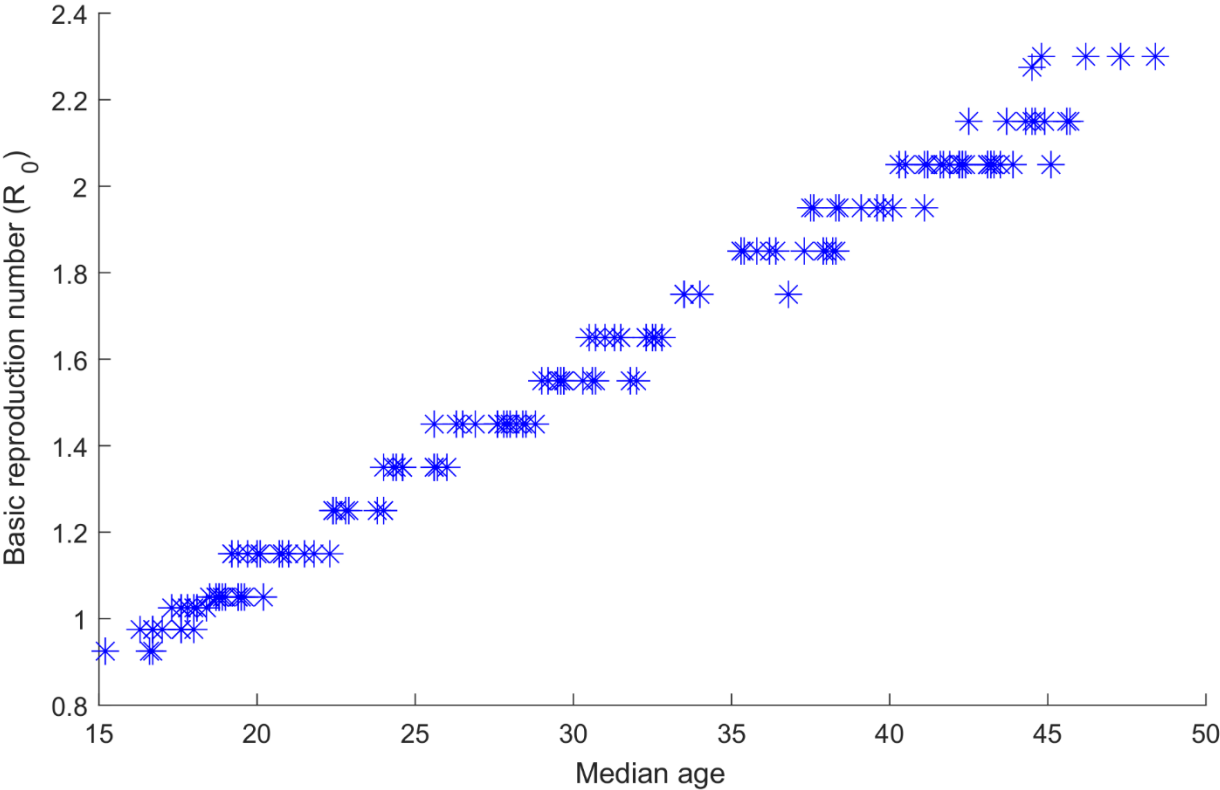
Figure S6: Impact of the variation in the basic reproduction number, R_0, on the attack rate by the end of the epidemic cycle. This figure was produced by curve fitting the estimates of all countries, however, the figure highlights only the specific data points of the select countries presented in the main text.
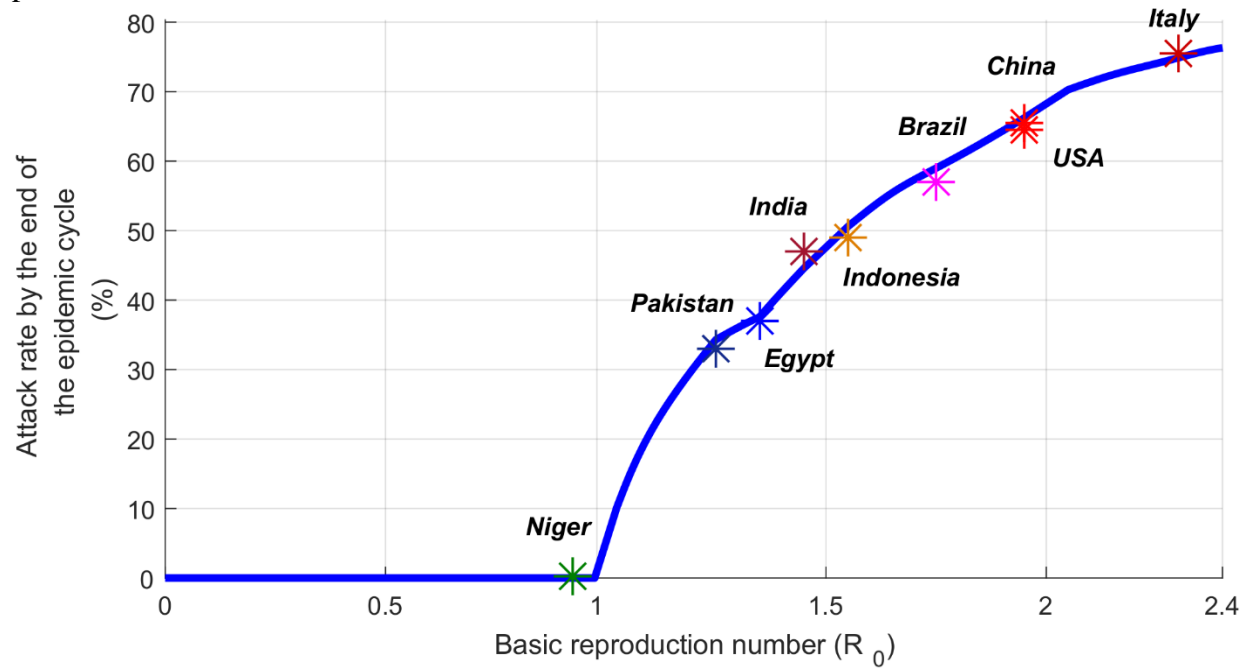
Figure S7: Age-specific cumulative incidence of the 2009 influenza A (H1N1) pandemic (H1N1pdm) virus [13].
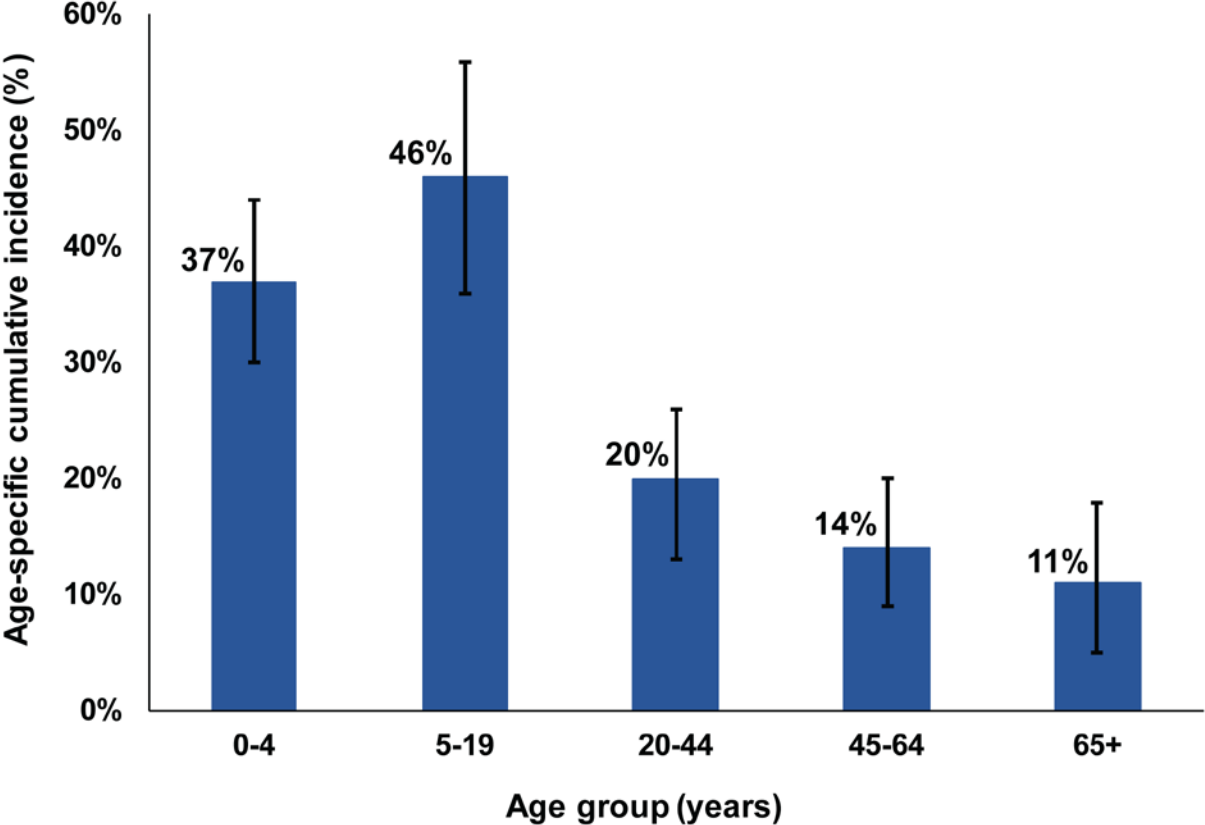
Figure S8: Impact of the variation in the basic reproduction number, R_0, on the probability of occurrence of a major SARS-CoV-2 outbreak upon introduction of one infection into the population.
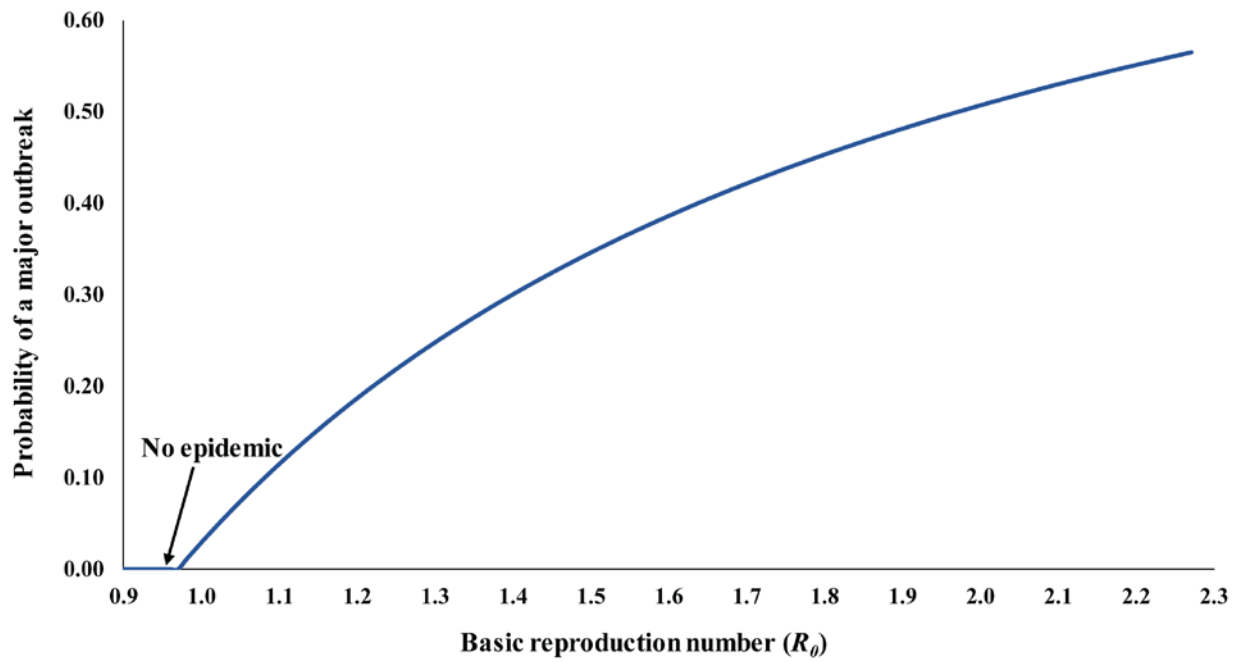
Figure S9: Distribution of SARS-CoV-2 age-specific attack rate per 10,000 persons for Australia, Austria, Denmark, Finland, France, Germany, Iceland and Italy.
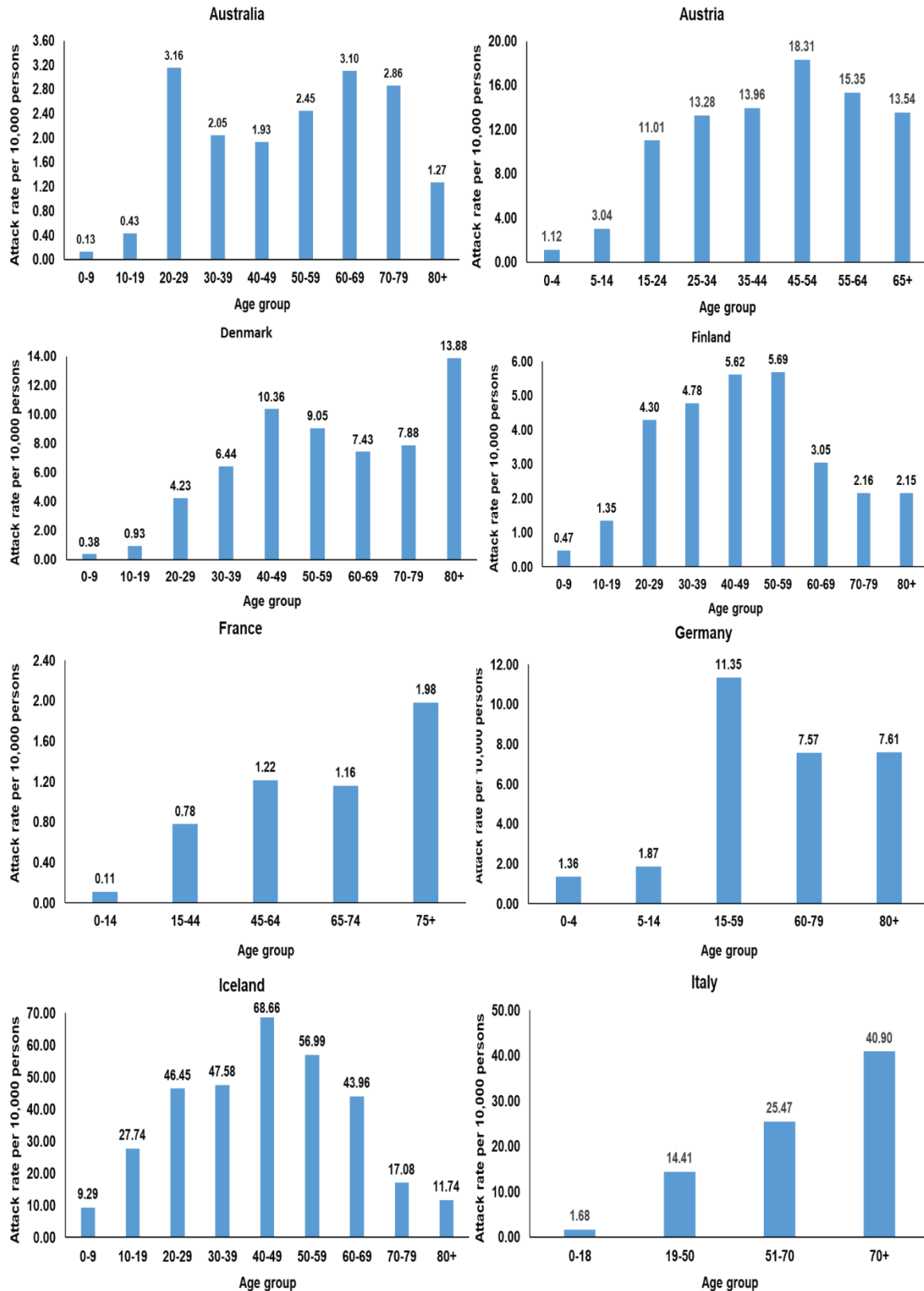
Figure S10: Distribution of SARS-CoV-2 age-specific attack rate per 10,000 persons for Japan, Norway, Singapore, Sweden, and Republic of Korea.
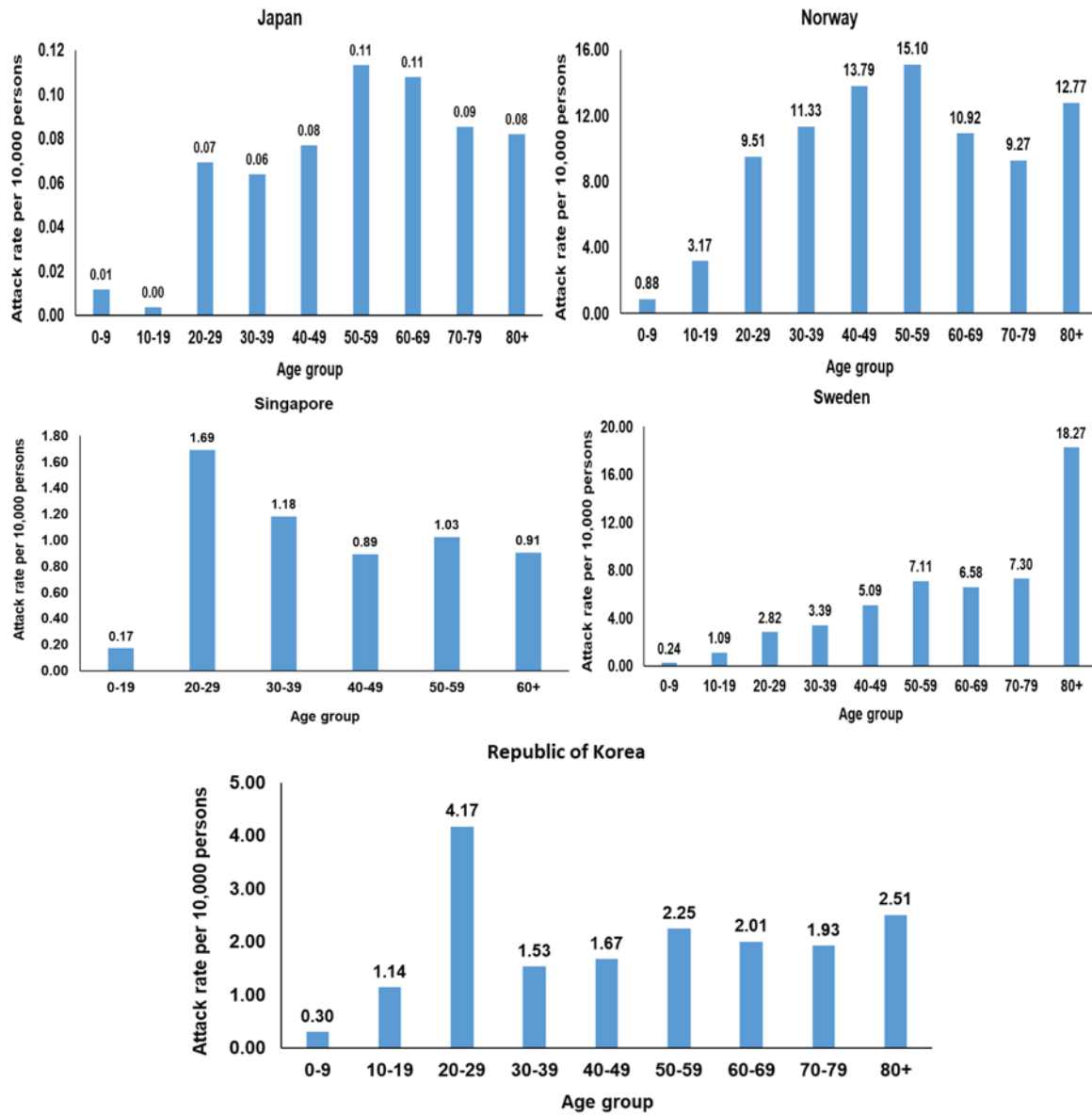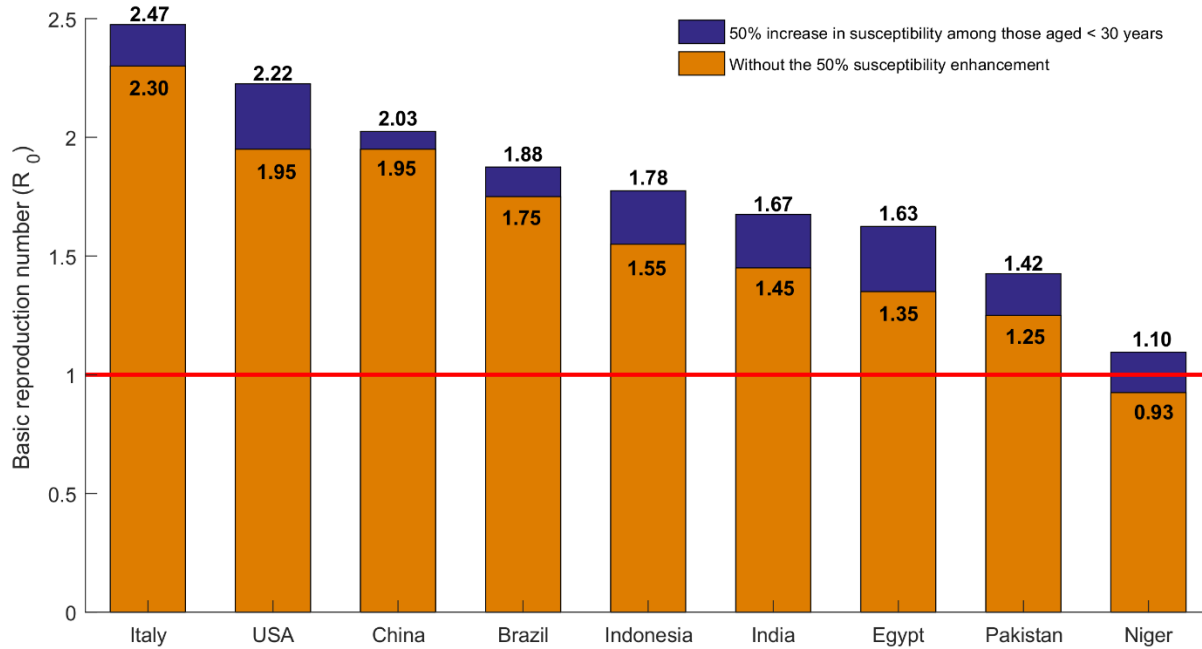
Figure S11: Sensitivity analysis assessing the impact of a 50% increase in the susceptibility to SARS-CoV-2 infection among those aged <30 years on our estimates for the basic reproduction number, R_0, for the select countries presented in the main text. The figure also includes, for comparison, estimates of R_0 without assuming the 50% susceptibility enhancement.

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