COVID-19 Results Briefing

Global

March 31, 2021

This document contains summary information on the latest projections from the IHME model on COVID-19 globally. The model was run on March 31, 2021, with data through March 29, 2021.

The steady increase in daily cases and slower increase in daily deaths reflects four distinct trends. In Brazil and some neighboring countries, a P1-driven surge is unfolding with potentially huge impacts on health systems and deaths. We have revised upward our estimates over the next four months for these locations because of revisions of cross-variant immunity and P.1 transmissibility based on more detailed analysis of the Amazonas state experience. The second area of concern is the northern states of the US and Canada, where a B.1.1.7 surge appears to be unfolding. The rapid increases in cases seen in Michigan may be a marker of what may unfold in other parts of the US and Canada. Overly rapid reopening, well documented in the rapid increases in mobility in the US, increases the risk of an April/May surge despite rapid scale-up of vaccination. Currently, sustained mask use in the US is one important brake on the surge; if mask use starts to drop then we may see increasing death numbers in the US through until May. In Europe, cases and deaths are increasing despite extensive social distancing mandates, slowly increasing vaccination rates, and reduced mobility. These steady increases, particularly in Central and Eastern Europe, are expected to peak in late April due to tighter lockdowns and rising vaccination. Many countries in the Middle East appear to be following the same pattern as in Europe, with likely a B.1.1.7-driven epidemic. The rapid increases in Turkey are particularly concerning. The last area of major increases is South Asia. Bangladesh, Pakistan, and many states in India have rapid increases in cases and deaths. Given much lower sequencing rates, it is harder to be sure which variant is accounting for this increase. Rising cases in settings where seroprevalence data suggest more than 60% have been infected suggest that the surge may be related to an escape variant. Daily infections in our reference and worse scenarios are expected to remain between 3.5 million to 6 million through until July 1.

Current situation

- Daily reported cases in the last week increased by 14% to reach 523,400 per day on average compared to 459,800 the week before (Figure 1).
- Daily deaths in the last week increased by 7% to reach 11,100 per day on average compared to 10,400 the week before (Figure 2). This makes COVID-19 the number 3 cause of death globally this week (Table 1).
- The daily death rate is greater than 4 per million in 33 countries; most of these countries are in South America or Europe (Figure 3).
- We estimated that 12% of people globally have been infected as of March 29 (Figure 4).

- Effective R, computed using cases, hospitalizations, and deaths, is greater than 1 in countries in North America, South America, sub-Saharan Africa, Europe, the Middle East, and South Asia (Figure 5).
- The infection detection rate is below 25% (Figure 6).
- Based on available sequencing data and a variant spread model, we estimate the distribution of three variants of concern (Figure 7). B.1.1.7 is widely circulating in Europe, the Middle East, and North America. B.1.351 is widely distributed in Southern and Central sub-Saharan Africa. P1 is becoming the dominant variant in much of South America.

Trends in drivers of transmission

- Mobility last week was 18% lower than the pre-COVID-19 baseline (Figure 9). Mobility was near baseline (within 10%) in 49 countries. Mobility was lower than 30% of baseline in 47 countries.
- As of March 29, we estimated that 63% of people always wore a mask when leaving their home (Figure 11). Mask use was lower than 50% in 45 countries.
- There were 126 diagnostic tests per 100,000 people on March 29 (Figure 13).
- Globally, 71.1% of people say they would accept or would probably accept a vaccine for COVID-19. The fraction of the population who are open to receiving a COVID-19 vaccine ranges from 36% in Cameroon to 94% in Campeche (Figure 16).
- In our current reference scenario, we expect that 2.9 billion will be vaccinated by July 1 (Figure 17).

Projections

- In our **reference scenario**, which represents what we think is most likely to happen, our model projects 4,402,000 cumulative deaths on July 1, 2021. This represents 1,140,000 additional deaths from March 29 to July 1 (Figure 18). Daily deaths are expected to peak in late April and then decline but remain over 7,500 a day on July 1 (Figure 19).
- If **universal mask coverage (95%)** were attained in the next week, our model projects 255,000 fewer cumulative deaths compared to the reference scenario on July 1, 2021 (Figure 18).
- Under our **worse scenario**, which incorporates slightly faster declines in mask use and increases in mobility, our model projects 4,663,000 cumulative deaths on July 1, 2021 (Figure 18). This represents 261,000 more deaths than in the reference scenario. Daily deaths remain over 12,500 on July 1 in this scenario.
- By July 1, we project that 284,000 lives will be saved by the projected vaccine rollout. This does not include lives saved through vaccination that has already occurred.

- Daily infections differ markedly between the reference and worse scenarios. Daily infections are expected to steadily increase in the worse scenario, reaching 6 million per day by July 1. In the reference scenario, we expect daily infections to stay stable around 4 million until late May and then decline to 3.5 million by July 1.

Model updates

In previous weeks, we captured the relationship between past transmission intensity and variant spread by including invasion rates for both the non-escape (B.1.1.7) and escape (B.1.351 and P.1) variants as covariates in our regression model, alongside other predictors like mask usage and mobility data. This week we have removed the variants from our regression model and incorporated them mechanistically into our fit of transmission intensity to past infections. The mechanistic model allows us to track infections due to the increased transmission intensity of the escape variants from infections due to natural- and vaccine-immunity breakthrough.

Limited evidence from the Novavax and AstraZeneca placebo arms suggests cross-variant immunity between escape variants and ancestral variants is between 0 and 30%. The spread of B.1.351 in South Africa and P.1 in Amazonas, Brazil, provides further data on the implied level of cross-variant immunity and increased transmissibility of these escape variants. To capture the uncertainty around both cross-variant immunity and escape variant transmissibility, we explored over 1,100 combinations of cross-variant immunity from natural infection, increased transmission intensity of the non-escape variants, and increased transmission of the escape variants, and selected a joint distribution of these three parameters that best matches the invasion rates of B.1.351 in South Africa and P.1 in Amazonas, Brazil.

We sampled the transmission intensity increase of B.1.1.7 relative to ancestral-type SARS-CoV-2 uniformly from a 30% increase to a 50% increase. The proportion of people previously infected with ancestral-type virus who are immune to the escape variants is sampled uniformly between 0.0 and 0.6. Finally, the transmission intensity increase of the escape variants relative to the increase in transmission intensity of B.1.1.7 is sampled from a normal distribution centered at 0.5 with a standard deviation of 0.13. This encodes our assumptions about how B.1.1.7 and the escape variants will compete as they show up in the same location. In absolute terms, this puts the transmission intensity of the escape variants in the range of 5%–16% when cross-variant immunity is 0.0 and 16%–28% when cross-variant immunity is 0.6. Our results this week incorporate this range of uncertainty in these critical parameters governing the impact of the escape variants.

In general, to determine the timing of initial invasion of a variant of concern (VOC) into a new location, we consider multiple data sources. For the US in particular, we use both the GISAID database and CDC data on confirmed and suspected VOC cases. In the presence of limited data, we use either a cutoff of five VOC sequences in the GISAID database or 25 suspected or confirmed VOC cases in the CDC database to indicate that local transmission is ongoing. One example of this is our identification of local transmission of P.1 in Florida due to the 42 suspected or confirmed VOC cases reported to the CDC database. However, as we gain more data, we take a more data-driven approach by fitting a model to the fraction of all GISAID sequences in a location that are a particular VOC. This data is taken as the gold standard, and the results of this model can override the simpler decision based on thresholds of sequences or cases. A practical application of this approach is the removal of B.1.351 local transmission from the US. There are more than five B.1.351 sequences in the GISAID database as well as more than 25 confirmed or suspected B.1.351 cases in the CDC database for a number of states in the US. However, the fraction of all sequences in the GISAID database that are B.1.351 has decreased in these states over time and is currently at 0% in all but North Carolina. This indicates that while B.1.351 infections have been detected in these states, we do not yet have strong evidence that these infections have led to the rapid invasion we have seen by VOCs in other settings. Of course, as new data are acquired, this situation will be re-evaluated on a state-by-state basis.

Current situation

Figure 1. Reported daily COVID-19 cases

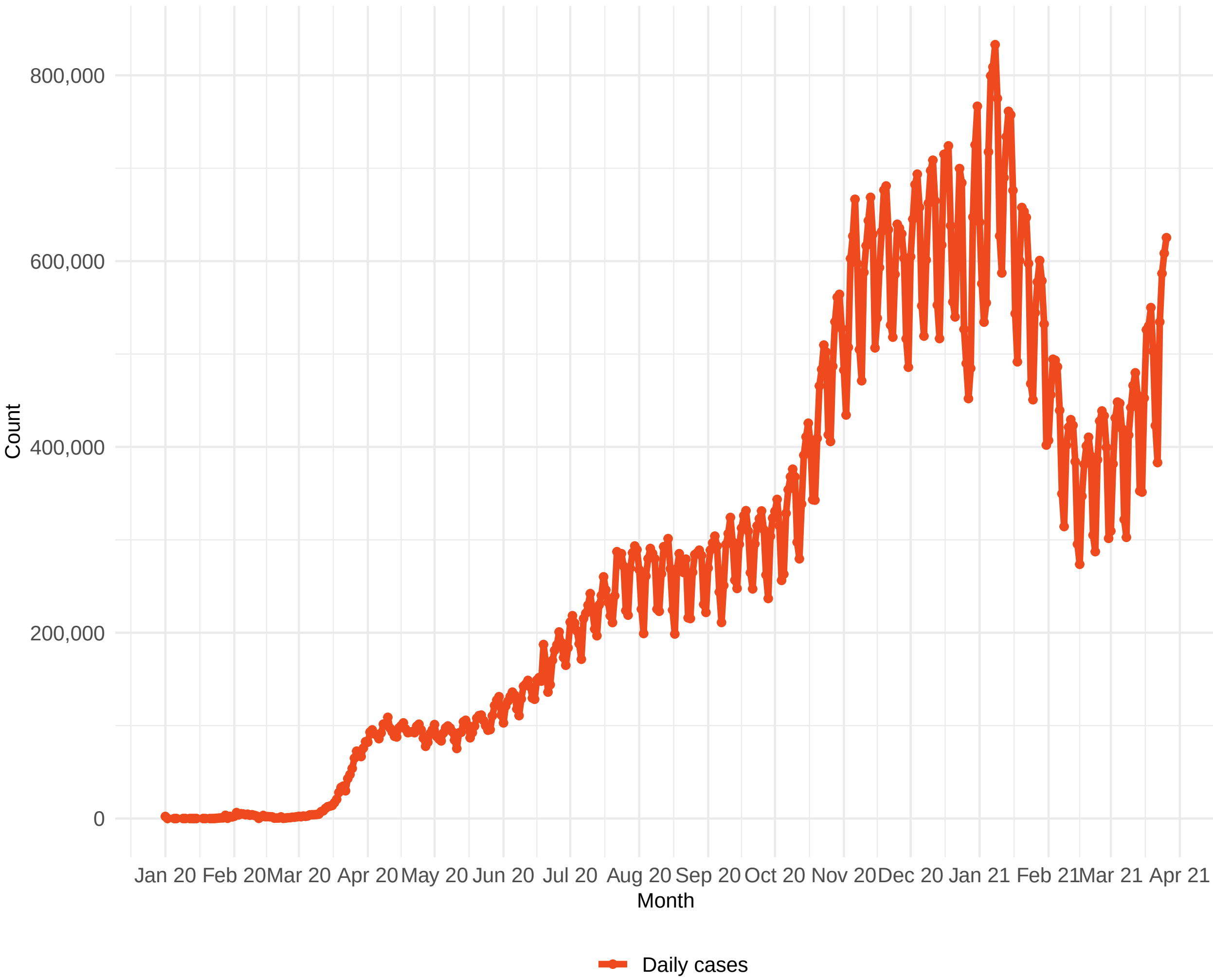


Table 1. Ranking of COVID-19 among the leading causes of mortality this week, assuming uniform deaths of non-COVID causes throughout the year

Cause name	Weekly deaths	Ranking
Ischemic heart disease	175,727	1
Stroke	126,014	2
COVID-19	77,663	3
Chronic obstructive pulmonary disease	63,089	4
Lower respiratory infections	47,946	5
Tracheal, bronchus, and lung cancer	39,282	6
Neonatal disorders	36,201	7
Alzheimer's disease and other dementias	31,217	8
Diabetes mellitus	29,830	9
Diarrheal diseases	29,509	10

Figure 2. Reported daily COVID-19 deaths and smoothed trend estimate.

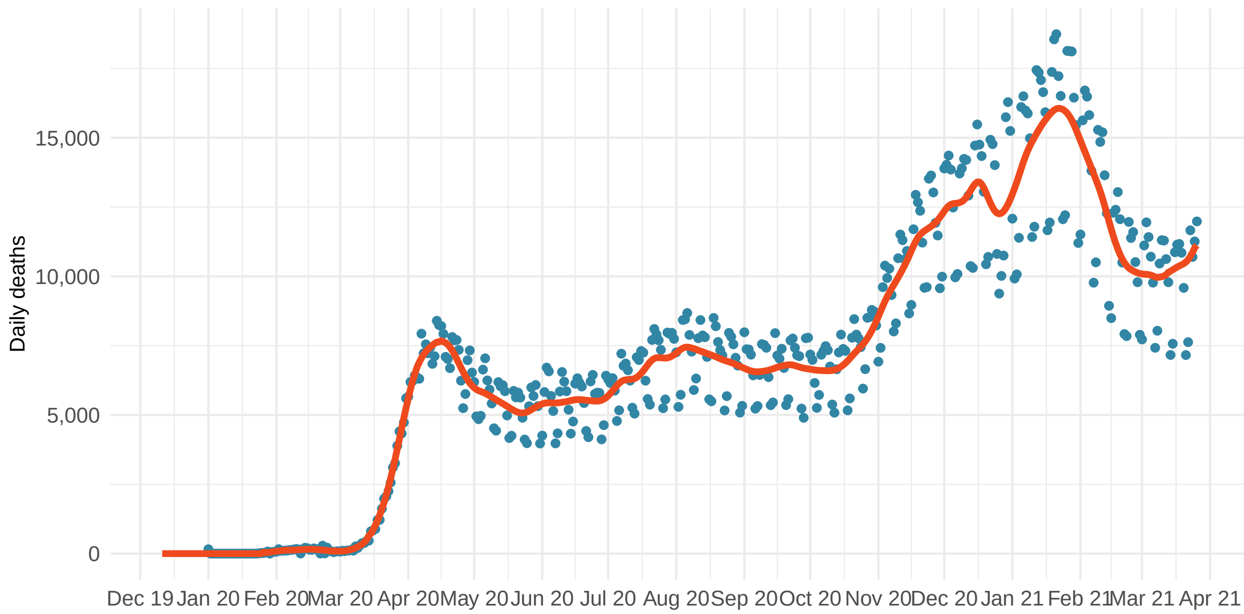


Figure 3. Daily COVID-19 death rate per 1 million on March 29, 2021

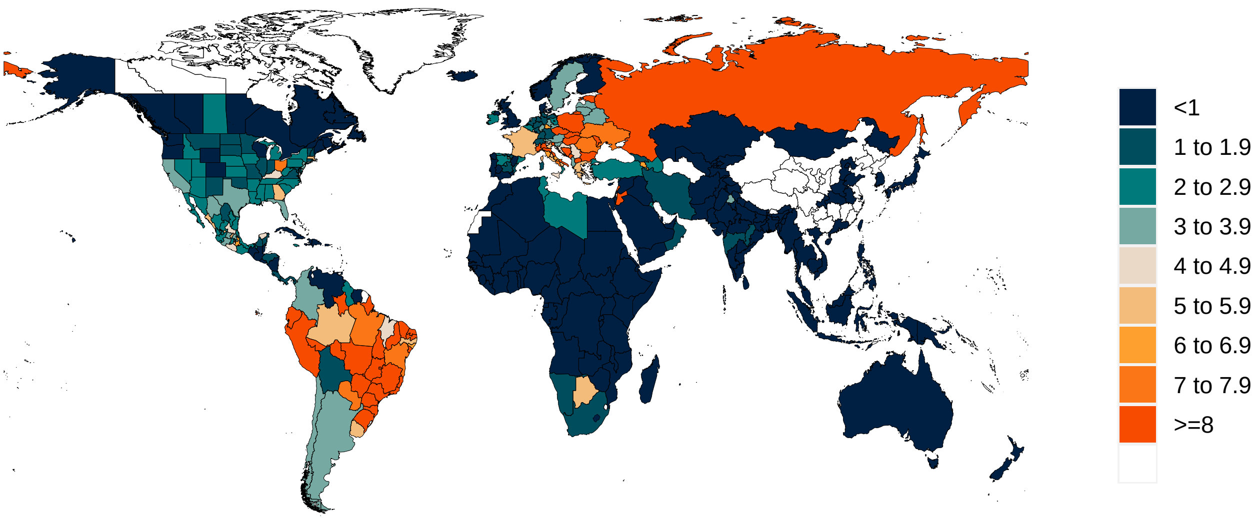


Figure 4. Estimated percent infected with COVID-19 on March 29, 2021

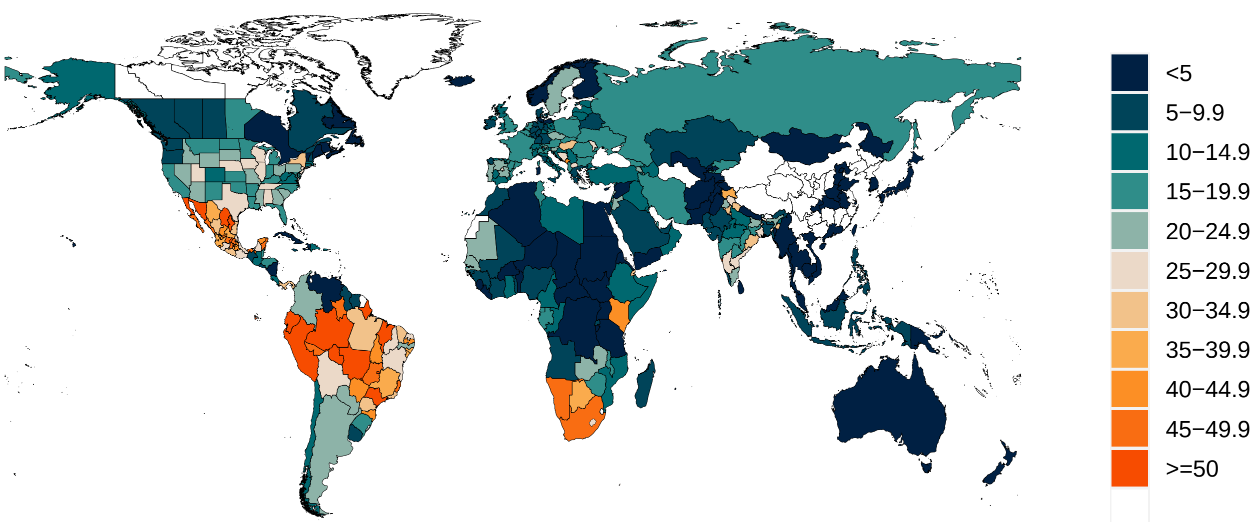


Figure 5. Mean effective R on March 18, 2021. The estimate of effective R is based on the combined analysis of deaths, case reporting and hospitalizations where available. Current reported cases reflect infections 11-13 days prior so estimates of effective R can only be made for the recent past. Effective R less than 1 means that transmission should decline all other things being held the same.

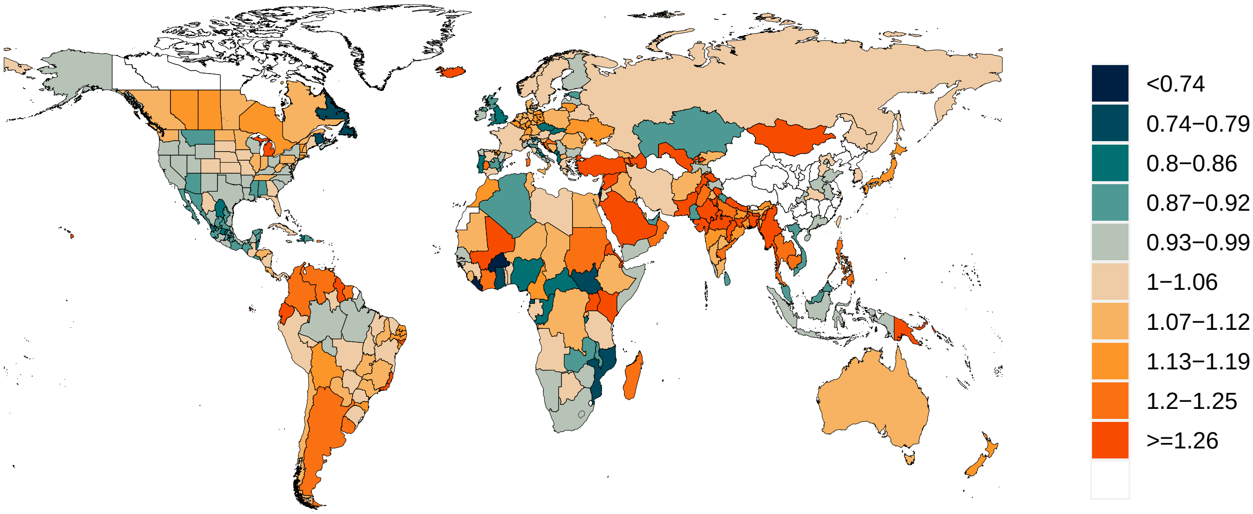
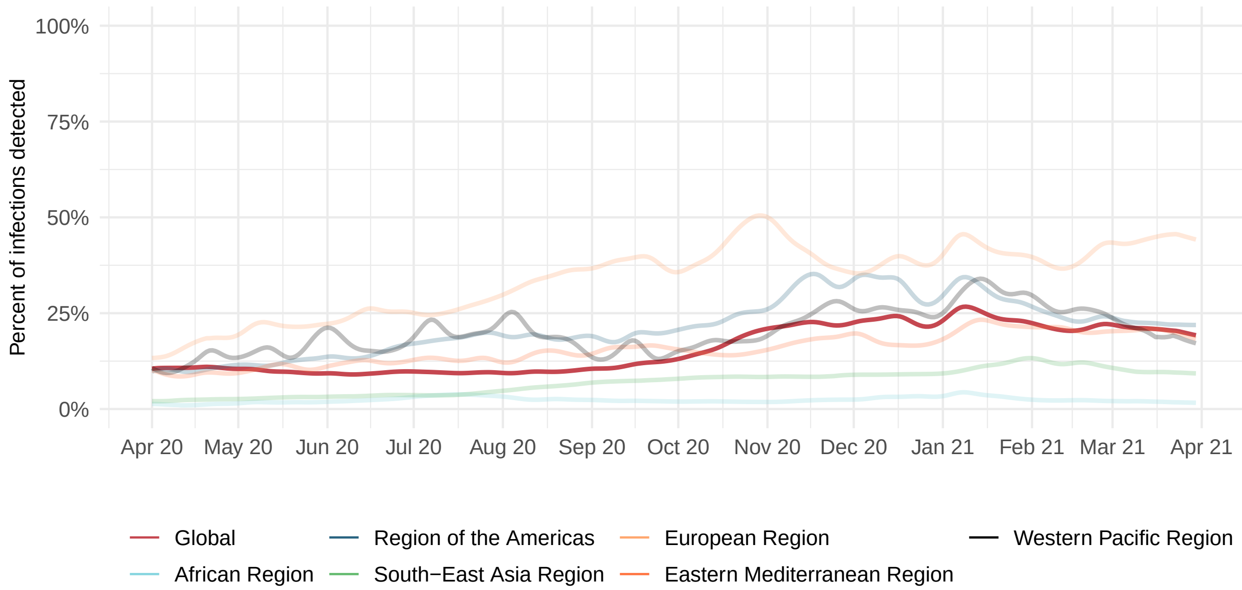


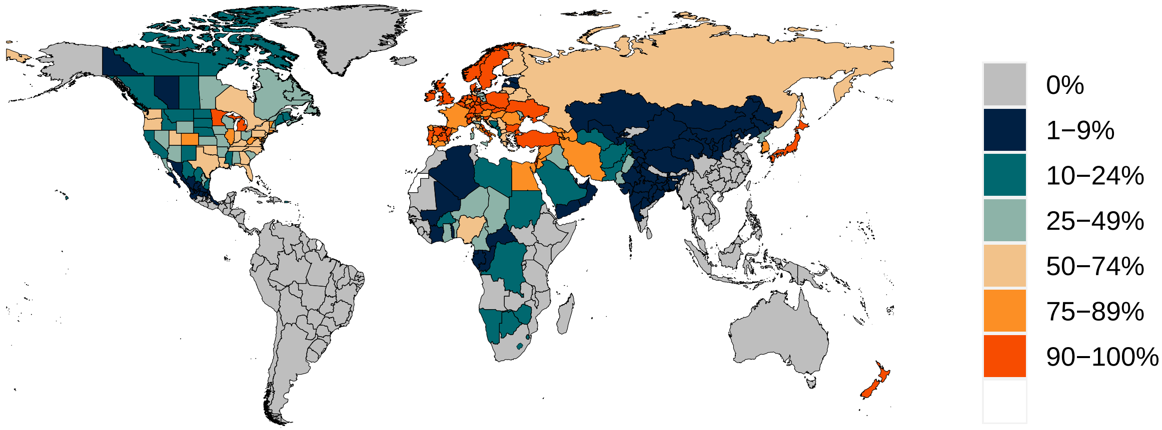
Figure 6. Percent of COVID-19 infections detected. This is estimated as the ratio of reported daily COVID-19 cases to estimated daily COVID-19 infections based on the SEIR disease transmission model.



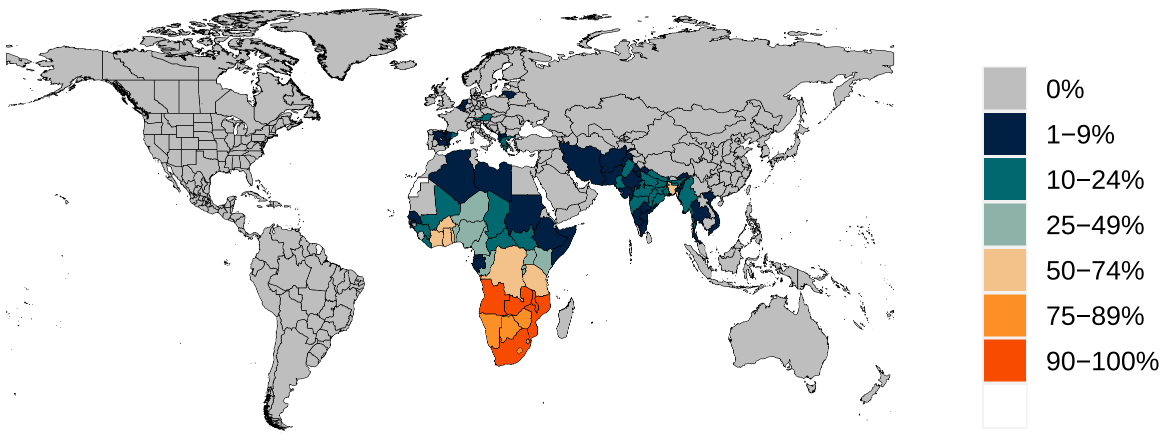
*Due to measurement errors in cases and testing rates, the infection to detection rate (IDR) can exceed 100% at particular points in time.

Figure 7. Percent of circulating SARS-CoV-2 for 3 primary variants on March 29, 2021.

A. Percent B.1.1.7 variant

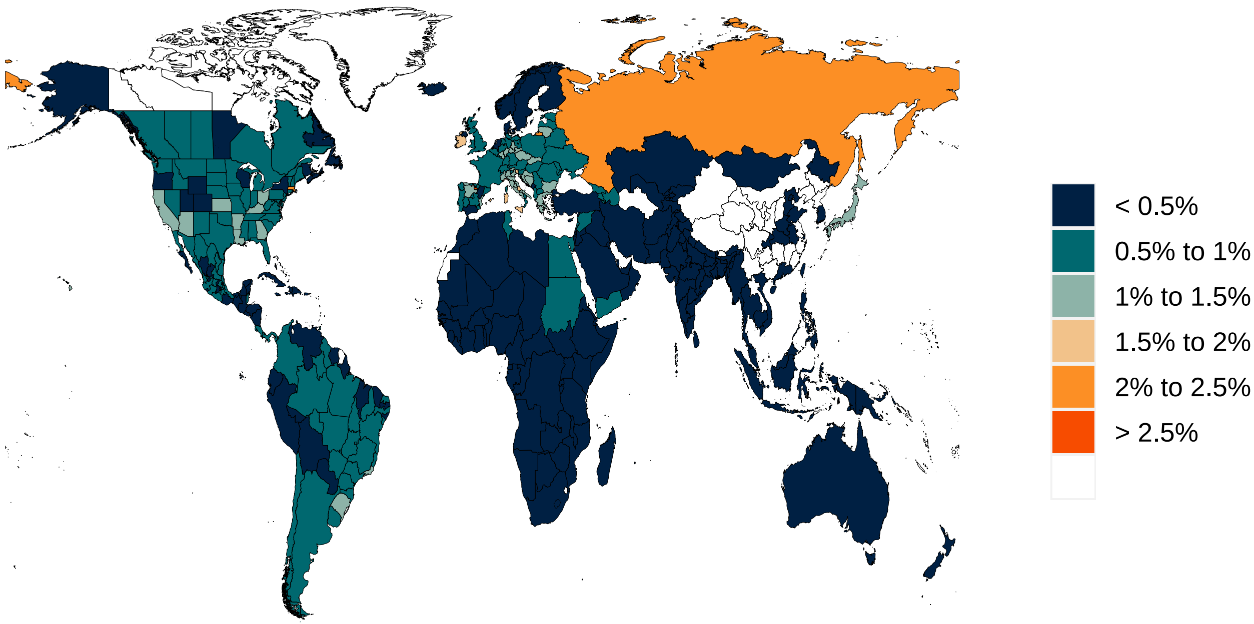


B. Percent B.1.351 variant



C. Percent P1 variant

Figure 8. Infection fatality ratio on March 29, 2021. This is estimated as the ratio of COVID-19 deaths to infections based on the SEIR disease transmission model.



Critical drivers

Figure 9. Trend in mobility as measured through smartphone app use compared to January 2020 baseline

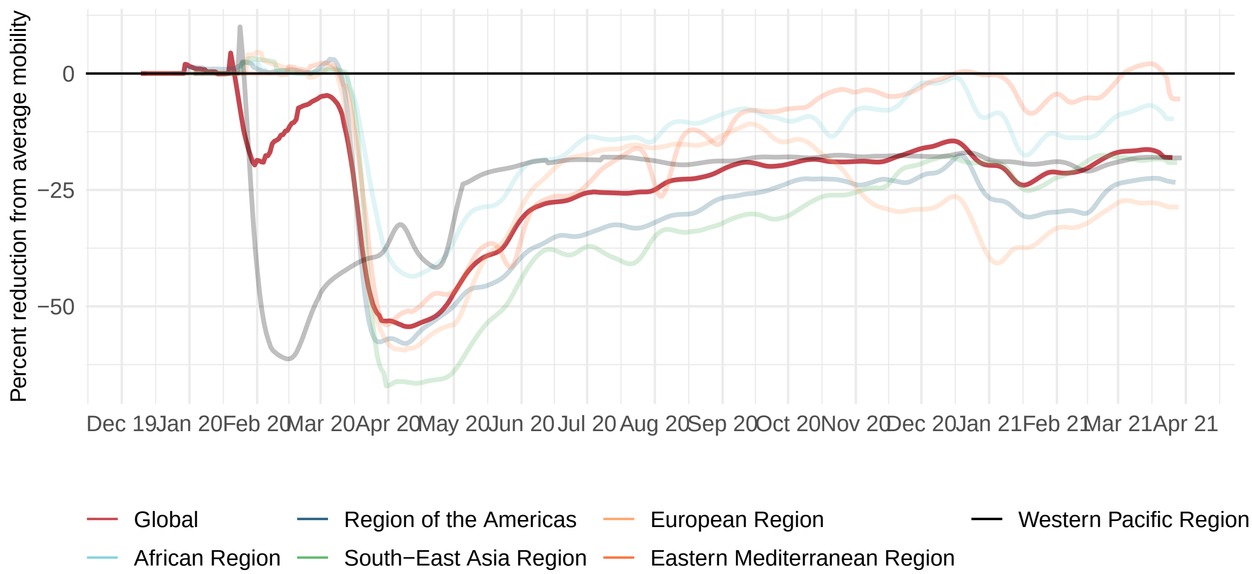


Figure 10. Mobility level as measured through smartphone app use compared to January 2020 baseline (percent) on March 29, 2021

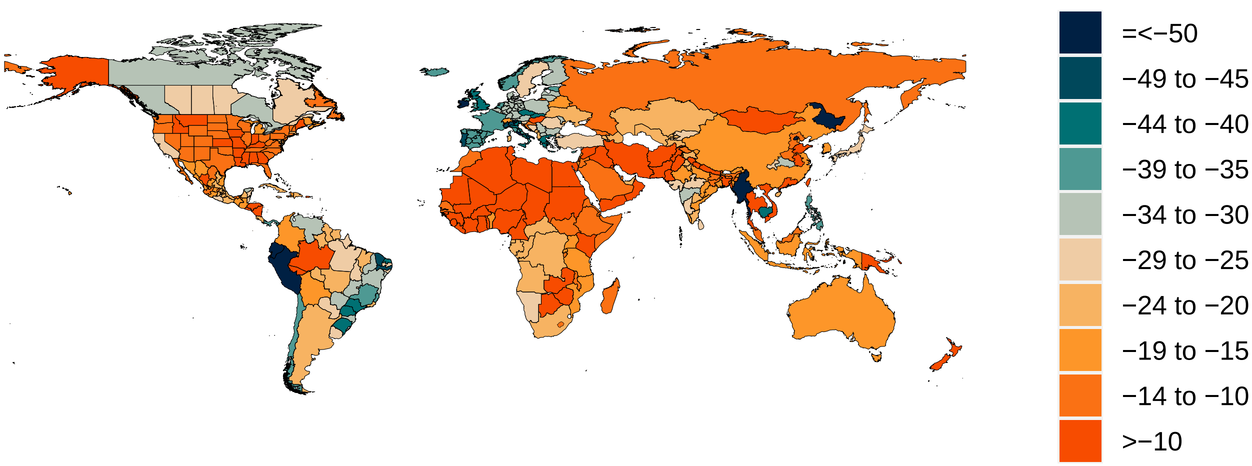


Figure 11. Trend in the proportion of the population reporting always wearing a mask when leaving home

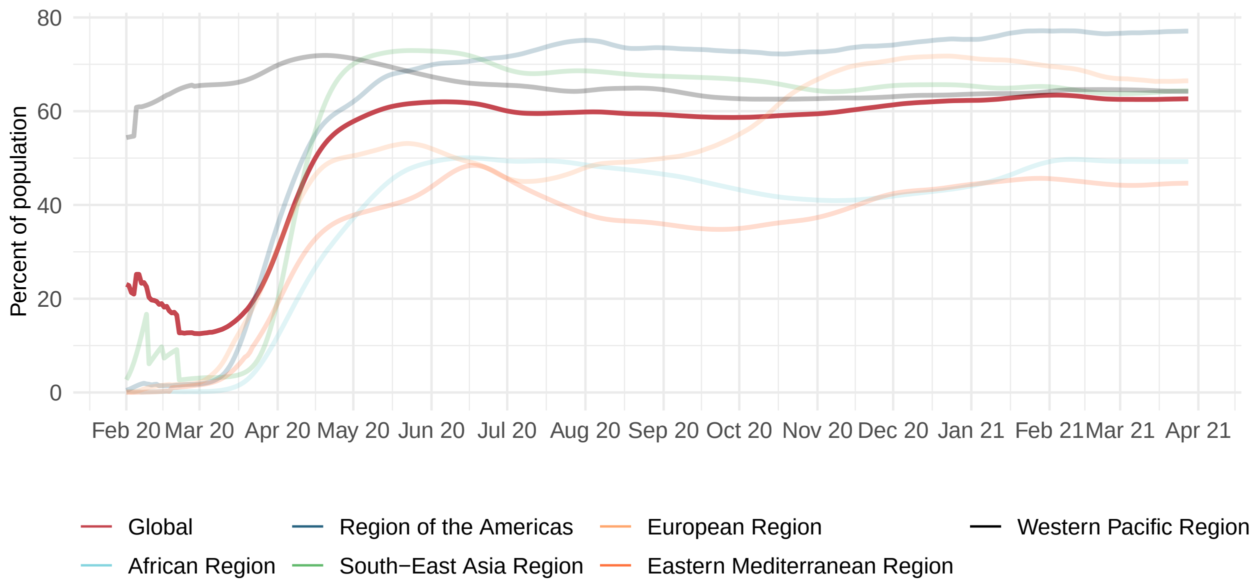


Figure 12. Proportion of the population reporting always wearing a mask when leaving home on March 29, 2021

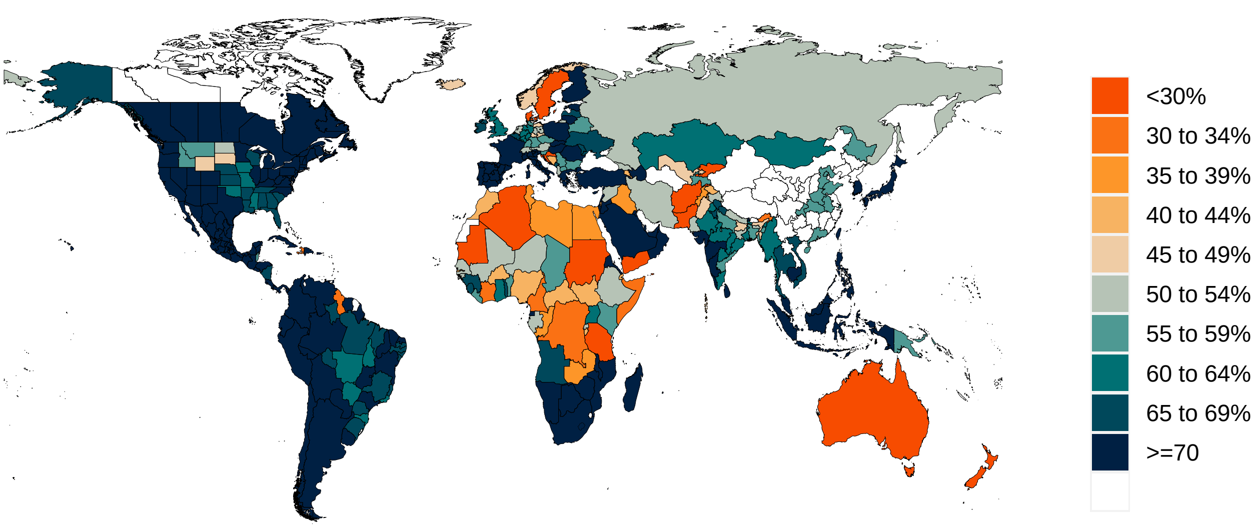


Figure 13. Trend in COVID-19 diagnostic tests per 100,000 people

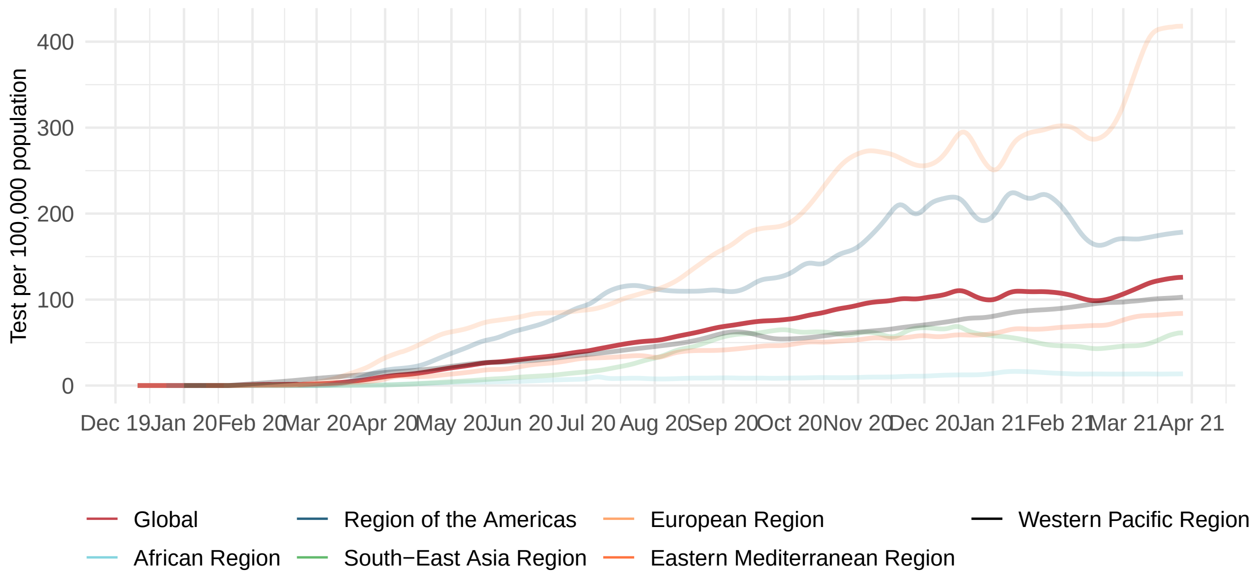


Figure 14. COVID-19 diagnostic tests per 100,000 people on March 26, 2021

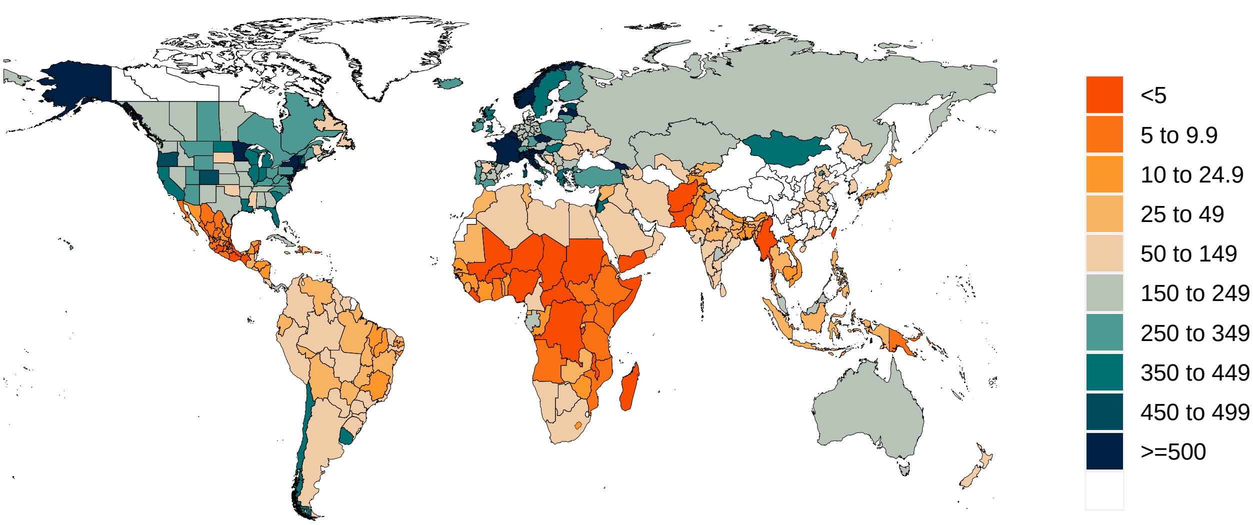


Figure 15. Increase in the risk of death due to pneumonia on February 1 2020 compared to August 1 2020

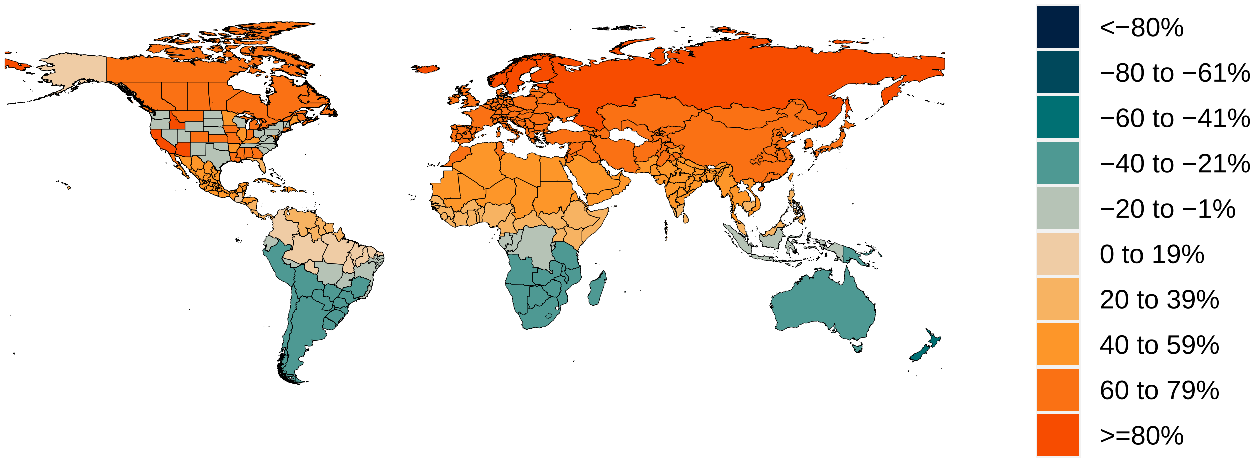


Table 3. The SEIR model uses variant-specific estimates of vaccine efficacy at preventing symptomatic disease and at preventing infection. We use data from clinical trials directly, where available, and make estimates otherwise. More information can be found on our website (http://www.healthdata.org/node/8584).

Vaccine	Efficacy at preventing disease: D614G & B.1.1.7	Efficacy at preventing infection: D614G & B.1.1.7	Efficacy at preventing disease: B.1.351 & P.1	Efficacy at preventing infection: B.1.351 & P.1
AstraZeneca	75%	52%	10%	7%
CanSinoBio	66%	57%	50%	44%
CoronaVac	50%	43%	38%	33%
Johnson & Johnson	72%	72%	64%	56%
Moderna	94%	85%	72%	62%
Novavax	89%	77%	49%	43%
Pfizer/BioNTech	95%	86%	72%	63%
Sinopharm	73%	63%	56%	48%
Sputnik V	92%	80%	70%	61%
Other mRNA vaccines	95%	83%	72%	63%
All other vaccines	75%	65%	57%	50%

Figure 16. This figure shows the estimated proportion of the adult (18+) population that is open to receiving a COVID-19 vaccine based on Facebook survey responses (yes and yes, probably).

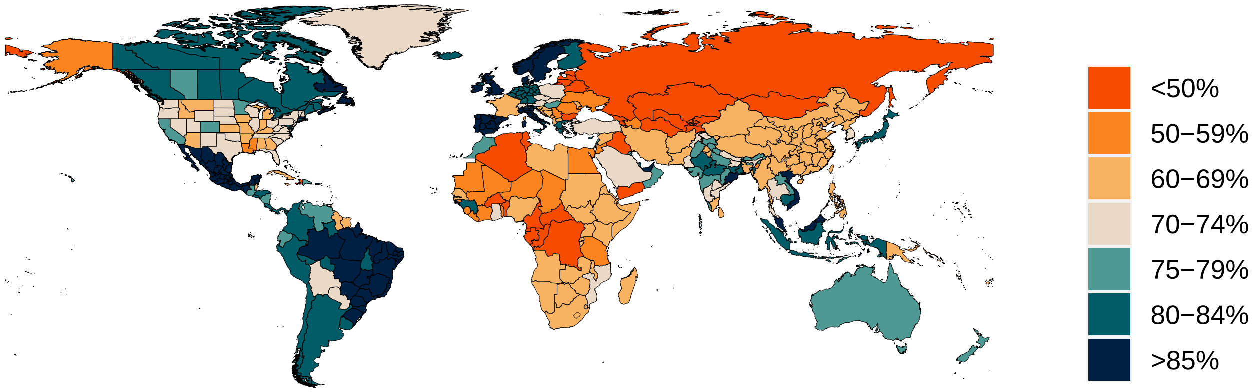
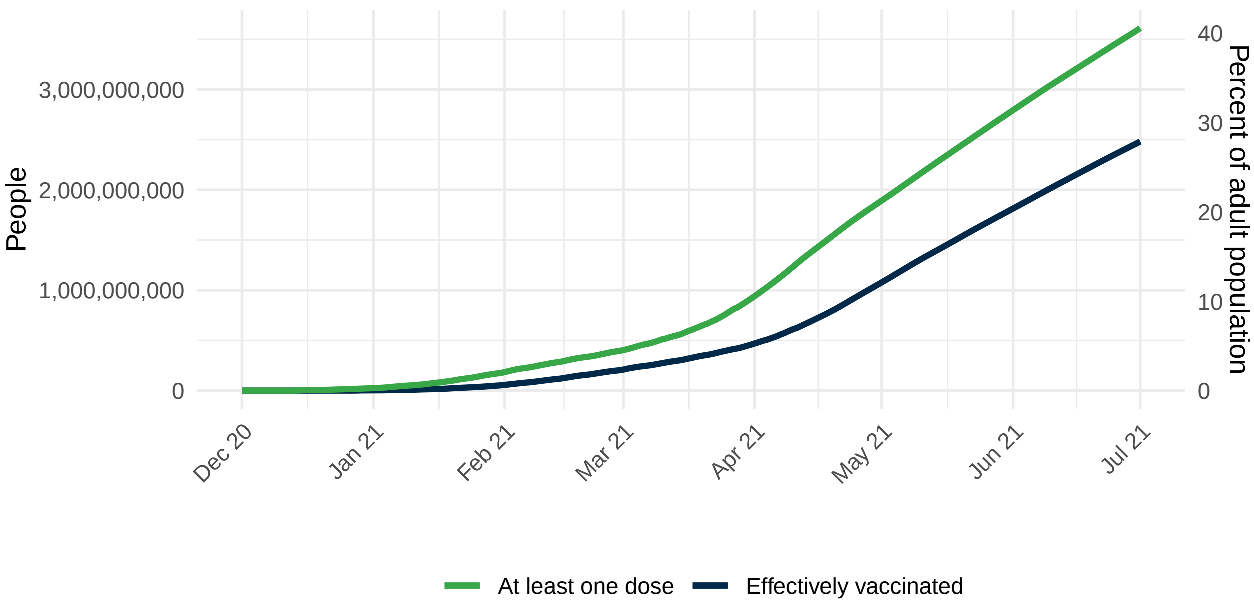


Figure 17. The number of people who receive any vaccine and those who are effectively vaccinated and protected against disease, accounting for efficacy, loss to follow up for two-dose vaccines, partial immunity after one dose, and immunity after two doses.



Projections and scenarios

We produce three scenarios when projecting COVID-19. The **reference scenario** is our forecast of what we think is most likely to happen:

- Vaccines are distributed at the expected pace.
- Governments adapt their response by re-imposing social distancing mandates for 6 weeks whenever daily deaths reach 8 per million, unless a location has already spent at least 7 of the last 14 days with daily deaths above this rate and not yet re-imposed social distancing mandates. In this case, the scenario assumes that mandates are re-imposed when daily deaths reach 15 per million.
- Variants B.1.1.7 (first identified in the UK), B.1.351 (first identified in South Africa), and P1 (first identified in Brazil) continue to spread from locations with (a) more than 5 sequenced variants, and (b) reports of community transmission, to adjacent locations following the speed of variant scale-up observed in the regions of the UK.
- In one-quarter of those vaccinated, mobility increases toward pre-COVID-19 levels.
- People who receive vaccines stop wearing masks three months after they have been fully vaccinated.

The **worse scenario** modifies the reference scenario assumptions in three ways:

- First, it assumes that variants B.1.351 or P1 begin to spread within 3 weeks in adjacent locations that do not already have B.1.351 or P1 community transmission.
- Second, it assumes that all those vaccinated increase their mobility toward pre-COVID-19 levels.
- Third, it assumes that people who receive vaccines stop wearing masks one month after they have been fully vaccinated.

The **universal masks scenario** makes all the same assumptions as the reference scenario but also assumes 95% of the population wear masks in public in every location.

Figure 18. Cumulative COVID-19 deaths until July 01, 2021 for three scenarios.

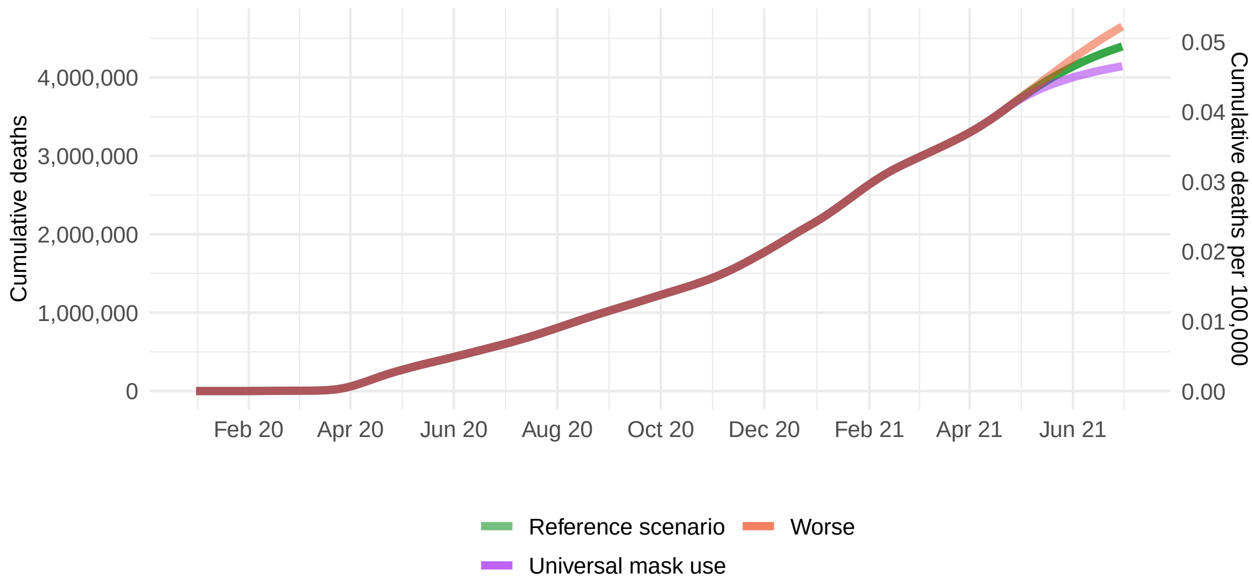


Figure 19. Daily COVID-19 deaths until July 01, 2021 for three scenarios,

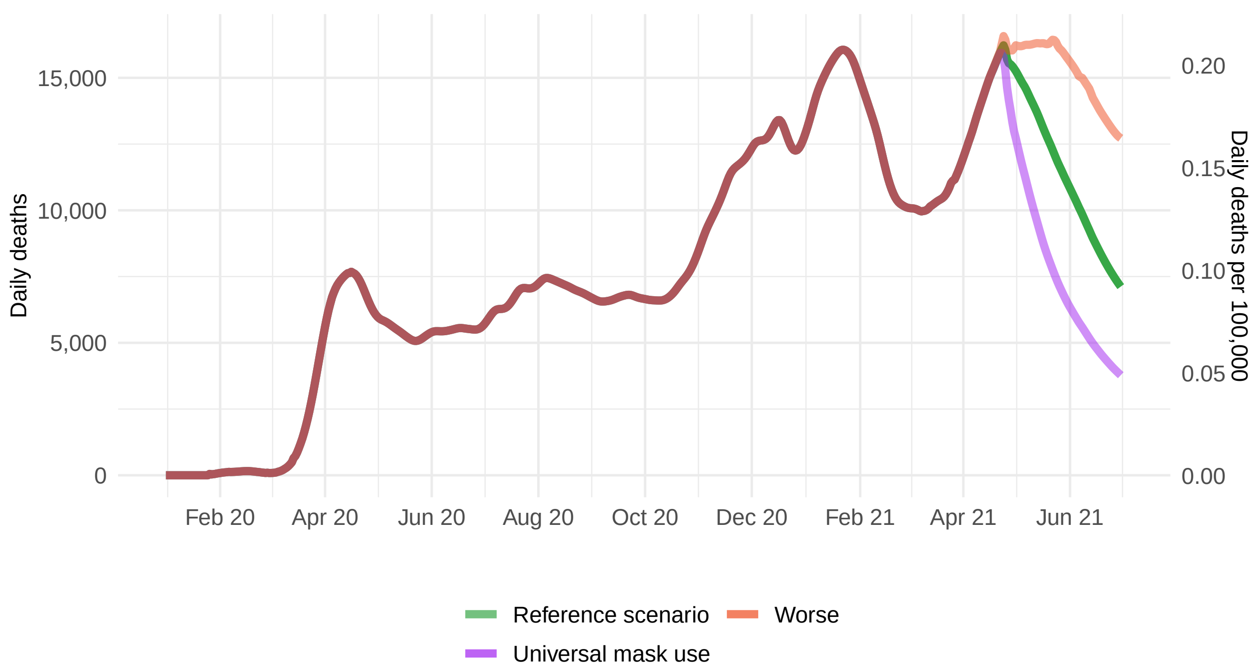
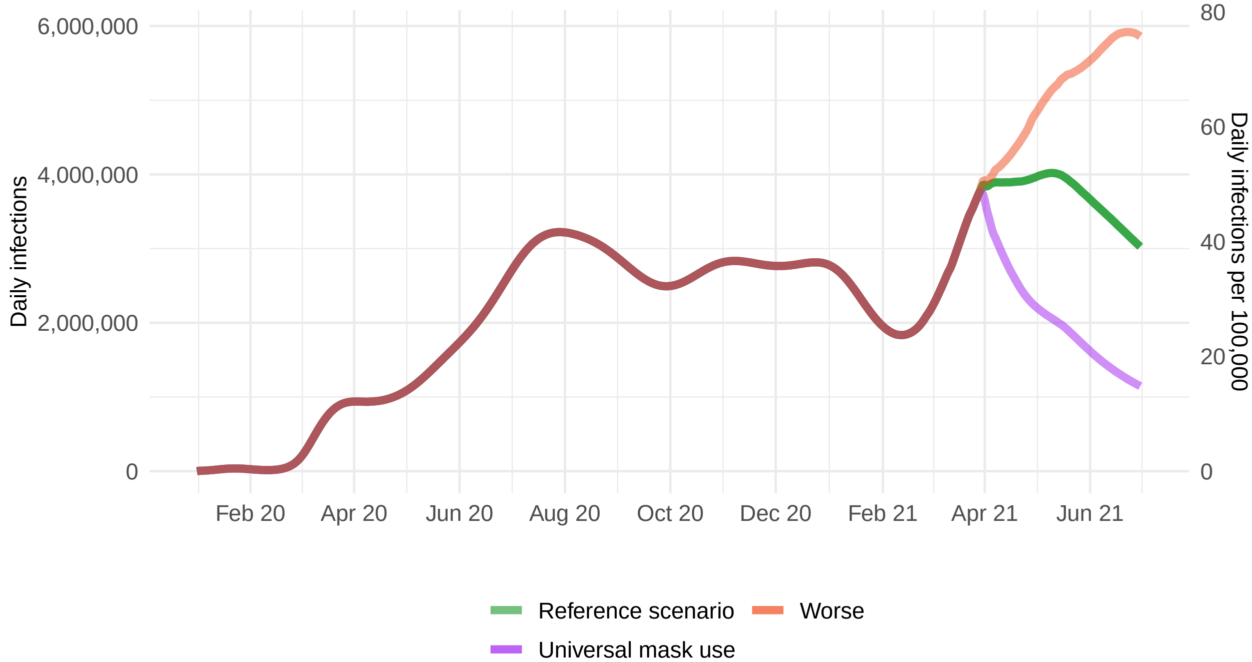


Figure 20. Daily COVID-19 infections until July 01, 2021 for three scenarios.



More information

Data sources:

Mask use data sources include Premise; Facebook Global Symptom Survey (This research is based on survey results from University of Maryland Social Data Science Center) and the Facebook United States Symptom Survey (in collaboration with Carnegie Mellon University); Kaiser Family Foundation; YouGov COVID-19 Behaviour Tracker survey.

Vaccine hesitancy data are from the COVID-19 Beliefs, Behaviors, and Norms Study, a survey conducted on Facebook by the Massachusetts Institute of Technology (https://covidsurvey.mit.edu/).

Vaccine hesitancy data are from the Facebook Global Symptom Survey (This research is based on survey results from University of Maryland Social Data Science Center), the Facebook United States Symptom Survey (in collaboration with Carnegie Mellon University), and from the Facebook COVID-19 Beliefs, Behaviors, and Norms Study conducted by the Massachusetts Institute of Technology.

Genetic sequence and metadata are primarily from the GISAID Initiative. Further details available on the COVID-19 model FAQ page.

A note of thanks:

We wish to warmly acknowledge the support of these and others who have made our COVID-19 estimation efforts possible.

More information:

For all COVID-19 resources at IHME, visit http://www.healthdata.org/covid.

Questions? Requests? Feedback? Please contact us at https://www.healthdata.org/covid/contact-us.