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when a serotype strain becomes more antigenically similar to other serotypes than its own.<sup>3</sup> The force of the invading strain can result in a selective sweep, reducing viral diversity with a subsequent drop in cases. Chen and colleagues added spatial random effects to account for the introduction of new dengue serotypes, and population immunity was labelled annual anomaly in the model. However, we would like to suggest to the authors that the greatest dengue year on record in 2019, in terms of incidence, be treated as unique in that it was probably fuelled by viral evolutionary events resulting in genotype replacements and might falsely augment the differential dengue virus burden between a higher-than-usual 6-year mean dengue incidence (inclusive of 2019) versus the comparison year of 2020. From an academic standpoint, we would be curious to see how the model would perform if the outlier year of 2019 were removed.

We appreciate the authors' timely contribution to understand the multifaceted disease ecology of dengue coupled with human movement data in the context of COVID-19.

We declare no competing interests.

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- 1 Chen Y, Li N, Lourenço J, et al. Measuring the effects of COVID-19-related disruption on dengue transmission in southeast Asia and Latin America: a statistical modelling study. *Lancet Infect Dis* 2022; **22**: 657–67.
- 2 Yek C, Nam VS, Leang R, et al. The pandemic experience in southeast Asia: interface between SARS-CoV-2, malaria, and dengue. *Front Trop Dis* 2021; **2**: 46.
- 3 Katzelnick LC, Coello Escoto A, Huang AT, et al. Antigenic evolution of dengue viruses over 20 years. *Science* 2021; **374**: 999–1004.

### Authors' reply

Christina Yek and colleagues raise two additional considerations when interpreting our recent findings that COVID-19 interventions reduced dengue incidence in 2020.<sup>1</sup> First, whether administrative delays might be an additional, unconsidered dimension to under-reporting and, second, whether the inclusion of abnormal data from 2019 might bias our predictions of cases averted.

Disruption-induced administrative delays in reporting are plausible and would have led to fewer dengue cases being reported in 2020. To minimise this, we restricted our analysis to January–December, 2020, despite more recent data being available from 2021. Searches for data were last updated on Feb 2, 2022, and no delay-related changes were identified compared with the original searches from Feb 23, 2021. If administrative delays did occur in 2020, they were probably quickly rectified before early 2021. Furthermore, our case fatality-based under-reporting analysis would probably have detected under-reporting due to administrative delays if they had occurred. Many countries with dengue endemics (eg, Sri Lanka) have separate reporting procedures for suspected dengue deaths that involve distinct, rapid reporting channels that are regularly audited.<sup>2</sup> Delays in reporting dengue cases but not deaths would result in higher case fatality rates, which we did not detect for any country.

We also agree that 2019 was an abnormally high incidence year for dengue and this would have resulted in below average incidence in 2020, similar to previous post-outbreak years (eg, 2017 in Brazil), even in the absence of COVID-19 interventions. These post-outbreak reductions are probably due to a combination of viral (eg, genotype replacement, as suggested), mosquito (eg, successful vector control), and host (eg, rising immunity to circulating viruses) factors that might differ between

outbreaks but have a consistent effect of suppression.<sup>3,4</sup> The annual anomaly term in our model estimates this expected post-outbreak reduction. Although 2019 was an unprecedented year for dengue globally, many countries have had similar outbreaks previously (see the appendix [p 31] in our Article<sup>1</sup>), allowing annual anomaly effects to be appropriately estimated. Inclusion of this term decreases predicted cases in 2020 and, thus, cases averted by COVID-19 interventions. Therefore, removing 2019 dengue data from the historical model-fitting dataset, as suggested, marginally increases our estimate of dengue cases averted by COVID-19 interventions but also substantially increases prediction uncertainty (0.76 million [95% credible interval 0.00–2.23] vs 0.72 million [0.12–1.47]). We therefore believe the original estimates we presented<sup>1</sup> offer the best overall estimate of the protective effects of COVID-19 interventions against dengue.

We declare no competing interests.

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- 1 Chen Y, Li N, Lourenço J, et al. Measuring the effects of COVID-19-related disruption on dengue transmission in southeast Asia and Latin America: a statistical modelling study. *Lancet Infect Dis* 2022; **22**: 657–67.
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