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Reply to comments on “Identifying mitigation strategies for COVID-19 superspreading on flights using models that account for passenger movement”

Mereness et al.’s comments on our paper [1] stem from an inadequate understanding of phenomenological infection modeling and stochastic methods. Further, they misinterpret our paper and other scientific literature. We address their main claims, which relate to (i) our mention of superspreading events on flights, (ii) validation, (iii) correlation of distance with infection risk, and (iv) airflow patterns in planes.

They cite three papers (1–3 of their references) as evidence to claim that “many” of the superspreading cases that we mentioned are likely to have occurred outside an aircraft. However, none of these references analyze or even cite, the two superspreading cases that we analyzed.

They fault our validation saying that we “cite their own previous studies as validation.” This misrepresents our work. We validated the model introduced in our paper against empirical observations from other scientific literature mentioned in Section 1.2.

They fault our infection model and its presentation. They mention that our infection model is a “handful of incomplete equations with no explanation of their connection.” Our infection model is presented in two equations. Equation (1) is the popular exponential model that gives infection risk as a function of dose. Equation (2) gives dose at time t as a function of distance to infective persons. We mention that it should be summed over all time steps to yield the total dose per person. Adding numbers and substituting the resulting dose into Equation (1) are simple, well-defined, steps.

They cite three papers (1, 2, and 4 of their references) as evidence to argue that the “correlation between distance and inhaled mass is a poor assumption in the aircraft cabin.” The last paper is in-press and unavailable to us. The other references actually contradict their claim. For example, Zee et al. (their reference 2, page 4) mention that “in aggregate, passengers seated closer to the index were exposed to more index expiratory material than those farther away.” Silcott et al. [2] (the original version of their first reference) shows a trend of higher exposure close to the index patient (e.g. on page 33). Accounting for droplets, omitted in these studies, would further emphasize the role of proximity.

We now consider their criticism that we did not include in-cabin airflow in our modeling. Mathematical modeling of complex interactions can broadly take two approaches, (i) phenomenological and (ii) mechanistic [3]. Phenomenological models extract information from real-world data to help capture complex causal relationships without requiring detailed mechanisms. Mechanistic models, on the other hand, use detailed specifications of the processes of the system. They have different tradeoffs [3], but are both widely used and accepted approaches in science.

A model using airflow patterns could be useful for mechanistic modeling provided enough empirical evidence to describe and parameterize the mechanistic formulation is available. We have used the phenomenological approach for the infection risk component of our

model, fitting parameters against the observed Guangzhou restaurant outbreak data and using it to model an extreme event on an aircraft. Such generalizations are common and there are numerous such instances in the literature, with generalizability being considered a positive feature for models. For example, data from pop-concerts was used for analyzing sporting events [4].

In fact, Mereness et al.’s observations would support the use of a phenomenological model rather than a mechanistic model as follows. They rightly point out that the number of virions to cause COVID-19 is not known and there is a high degree of in-host variability. Phenomenological models are particularly useful when such details are unknown because there is insufficient knowledge for mechanistic models to be accurate. This can be seen from the erroneous results in the study conducted by the aviation industry [2]. Using the approach advocated by Mereness et al., that study [2, page 33] concluded that “a minimum of 54 hours are required to produce an inflight infection.” However, genetic evidence (e.g. [5,6]) has conclusively shown in-flight infections for much shorter flights.

Some of the comments are due to the misunderstanding of stochastic modeling concepts. For example, they mention that the number of virions to cause infection is unknown. The dose threshold for infections is a characteristic of a deterministic dose-response model, not a stochastic one as we have used. They mention in-host variability to argue against using a dose-response model. While the deterministic model cannot account for the variation in susceptibility, stochastic models inherently account for this.

They point out that there are differences in empirical data (Fig 1 (a) and (b)) and probability maps (Fig 2 and 3). A stochastic infection model does not determine if a specific individual would be infected, unlike empirical data. Instead, it shows the probability of transmission for an individual at a given location. The cumulative probability for all travelers would give the expected number of infections. We compare this against the observed cumulative infections. Additionally, one can note trends, such as inclusion of pedestrian movement indicating an increased probability of infections at a distance from the index case, as observed in the London flight.

In the broad context, the goal of our paper is to identify and compare mitigation strategies that can prevent a large outbreak. It considers an extreme situation and shows that such risk can be mitigated using the now-established strategies of social distancing and masking. Our primary conclusion, that N95 masks or the equivalent can be very effective, is a widely accepted position in public health [7].

Author contributions

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