Response to RSS discussion
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First, as Lessler and Metcalf summarise, we show how early selection and depletion of individuals with high contact rates biases naive estimates of transmission upwards, and thus overestimates both the peak of the outbreak and the impact of interventions. With regard to the latter, we highlight that in particular the predicted impact of relaxing or stopping interventions can also be highly sensitive to assumptions about heterogeneity. In that sense, we agree with Pellis that the excessive focus on R_0 has been unhelpful. We further agree with O'Neill that, in general, short-term predictions are more robust to model specification. However, the issue we illustrate (not capturing enough heterogeneity in the model) may actually lead to the wrong short-term predictions!

Although discussants' comments regarding spatial and temporal variation in R and growth rates (Diggle, Dagpunar) are not directly related to our study, this variation may be partially driven by the selection of high-risk individuals and communities. To better capture temporal heterogeneity in transmission related to weekdays vs. weekends and day and night (O'Neill), we have in the meanwhile developed a spatially and demographically explicit model of the Netherlands that directly captures these aspects.

We agree on the importance of capturing age in models (Kingman), as this will at least partially capture the selection/use of high-risk sub-populations. However, we highlight that age will never capture all heterogeneity, and that individuals within the same age bracket may still vary a lot based on their health-related behaviour. This means that more sophisticated models are still likely to underestimate heterogeneity to some extent, which means that these models may not always adequately capture the selection and depletion of high-risk individuals.

Finally, both Richardson and Riley suggest that more and better data collection is needed on transmission pairs. We fully support this notion, especially as this would also help inform mechanistic modelling choices about the level of heterogeneity in individual contribution to transmission.