Discussion of the papers by Mishra et al (2021) and Teh et al. (2021)

I congratulate both teams for these welcome contributions on modelling the COVID19 pandemic. To produce results of such quality within exacting timescales is a genuine achievement.

Both studies infer a time-varying reproduction number R_t from summary data constructing hierarchical Bayesian frameworks embodying R_t as an intrinsic parameter. Observations arise as noisy, time-shifted, representations of an autoregressive infection process with weights specified by generation-time probabilities and moderated by R_t. With a common root in Flaxman et al. (2020), the papers differ in their treatment of temporal effects and spatial coupling (with Teh et al. (2021) adopting an explicitly spatio-temporal Gaussian process for $\log R_t$ while Mishra et al. (2021) use a random walk prior), in their use of data, and in certain underlying assumptions.

Neither study, in the prior for R_t, incorporates foreseeable effects such as step changes following interventions, the impact of improved testing on track-and-trace measures, or the expected decline in R_t due to susceptible depletion. Incidentally, the presentation of the infection model in Mishra et al. (2021) seems confusing, with R_t between equations (1) and (2) changing from an instantaneous reproduction number to a 'raw' reproduction number, subsequently re-scaled by the susceptible proportion before reporting. The papers' general approach is arguably the 'image analyst's take' on epidemic modelling, where the objective is to recover a 'true' R_t from a noisy image, with prior distributions providing regularisation rather than capturing mechanistic thinking.

This approach differs from that often taken by modellers of plant or animal pathogens, who aim to estimate parameters controlling distinct aspects of the transmission process, such as contact rates and spatial kernel functions, and then to extrapolate 'mechanistic' understanding to other settings. The quantity R_t, where this can be defined, is a by-product of the transmission process and putative surveillance and control strategies, rather than an intrinsic parameter. It is common in such fields to present results, not in terms of R_t, but rather using predictive distributions of practically important outcomes (e.g. Parry et al. (2014)). This latter approach is only feasible thanks to the well understood nature of the host population and the richness of available data. For modellers of COVID19 the host population's mixing structure is complex, reflected in the model used by Ferguson et al. (2020) that informed the UK's early response. Moreover, available data typically include coarse-scale summaries of detected cases, hospitalisations and deaths, with biases and uncertainties from reporting processes. With the need to support real-time decision making, it is understandable that these studies have adopted the approach taken.

Some questions and sensitivities nevertheless merit further exploration. Both papers employ highly dispersed distributions in infection and observation models. As the prior for the dispersal parameters places increasing weight on high dispersal, might we expect the data to become less informative regarding R_t, with implications for uncertainty in forecast outcomes? Similarly, since step-changes in R_t are not explicitly accommodated by the prior then, should the imputed R_t exhibit rapid changes, must these be explained by the volatility terms in the Gaussian process or random-walk prior, again with implications for uncertainty in forecasting? Can we incorporate more mechanistic thinking

to mitigate such potential sensitivities - for example using priors based on mean-reverting univariate or multivariate auto-regressive processes for $\log R_t$, where the mean may change according a jump process?

Further questions relate to model assessment. Mishra et al. (2021) compare posterior median predictions with observed case numbers and, given that the plots of Figure 5 utilise a logarithmic scale, find considerable disparity. Teh et al. (2021) *inter alia* investigate their methods' ability to recover the true R_t, when data are generated from their model. Are the methods capable, for example, of recovering 'ground truths generated using more detailed simulation models (*cf* Firestone et al. (2019))? For example, when analogous data are simulated for a *structured* population with reproduction matrix $\mathbf{R}_t$, can the imputed R_t imputed successfully track the maximal eigenvalue of the true $\mathbf{R}_t$, or may it underestimate this quantity given that the distribution of infections over groups may not match the corresponding eigenvector? A comparison with simpler smoothing methods would also be welcome.

The papers highlight an important challenge in statistical modelling of pandemics - that of statistical inference for more complex mechanistic models that can potentially inform the design of targeted control strategies. This demands that the richness of available data is better matched to the complexity of models; achieving such a matching is a major challenge in itself. The authors of these papers have made effective use of available data and their modelling is an important step towards understanding the impact of spatial interactions. It will be interesting to explore whether their framework extends to other heterogeneities, such as those arising from age structure, whose importance has been highlighted in other studies (e.g. Lau et al., 2020).

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References

Parry, M., Gibson, G.J. Parnell, S., Gottwald, T.R., Irey, M. S., Gast, T. C. & Gilligan C. A. (2014) Bayesian inference for an emerging arboreal epidemic in the presence of control, *Proc. Nat. Acad. Sci.*, **111** 6258-6262;

Firestone, S. M., Hayama, Y., Bradhurst, R., Yamamoto, T., Tsutsui T & Stevenson, M. A. (2019) Reconstructing foot-and-mouth disease outbreaks: a methods comparison of transmission network models, *Scientific Reports* **9**, Article number: 4809.

Ferguson, N. M. et al. (2020) Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand, MRC Centre for Global Infectious Disease Analysis, Report 9. DOI: 10.25561/77482

Flaxman, S., Mishra, S., Gandy, A. et al.(2020) Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe *Nature*, **584**, 257–261

Lau, M. S. Y., Grenfell, B., Thomas, M., Bryan, M., Nelson, K., & Lopman, B. (2020) Characterizing superspreading events and age-specific infectiousness of SARS-CoV-2 transmission in Georgia, USA, *Proc. Nat. Acad. Sci.*, **117** 22430-22435. DOI:10.1073/pnas.2011802117