Congratulations to the authors of the contributions to this Special Topic Meeting. In the UK, the SARS-CoV-2 epidemic has been characterised by a high degree of spatial and temporal heterogeneity: some regions (notably the North West) have experienced persistently high incidence compared to others, and large fluctuations in social mixing have been caused partly by mandatory social distancing measures. Such heterogeneity requires sophisticated epidemiological intelligence to detect spatiotemporal fluctuations early, thus providing valuable evidence to inform effective decisions on local disease control measures.

The two papers presenting methods for estimating local effective reproduction numbers, R_{it}, are based on the renewal equation method applied to UK Local Authority Districts (LADs) (Teh *et al.* and Mishra *et al.*). The stochastic process nature of these approaches is required at this level, where the continuous-state-space assumption of ODE approximations fail and discrete-space models become the only option. Teh *et al.* has the distinct advantage of accounting for the spatial relation between LADs, making use of LAD-LAD human mobility data, and spatial correlation of R_{it}. Since R_{it} is the expected number of infections "created" by an infected individual in LAD i at time t, it is a measure of risk posed by an individual *to the rest of the population*, and not just the population within the LAD. Thus they avoid underestimating R_{it} (up the accuracy of their mobility data) by not ignoring the effect of an infected individual outside their own LAD. Spatial correlation of R_{it} has the further advantage of pooling information from neighbouring LADs, allowing estimates for low-incidence LADs to be informed via spatial proximity. In the low-incidence SARS-CoV-2 endgame, spatial modelling of cases will become central to prevalence estimation in a heterogeneous surveillance landscape.

The main limitation of the above approaches, highlighted by Parag *et al.*, is *a priori* estimation of the generation interval, which itself may vary spatiotemporally. The solution lies in directly fitting spatially-explicit epidemic models to incidence data, with the advantage of providing a flexible framework to incorporate spatio-temporal information at all scales. Two decades of research in Bayesian methods has enabled this, providing not only R_{it}estimates, but hazard ratios for individual-level covariates and the ability to model spatio-temporal variation in transition rates [1, 2, 3]. Nevertheless, applying these methods at scale is challenging and will require ongoing collaboration between statisticians, epidemiologists and computer scientists to realise an agile software solution which can be applied rapidly in response to disease outbreaks.

References

[1] G.J. Gibson and E. Renshaw. Estimating parameters in stochastic compartmental models using markov chain methods. *IMA J. Math. Appl. Med. Biol.*, 15:19–40, 1998.

[2] Matthew Parry, Gavin J. Gibson, Stephen Parnell, Tim R. Gottwald, Michael S. Irey, Timothy C. Gast, and Christopher A. Gilligan. Bayesian inference for an emerging arboreal epidemic in the presence of control. *Proc Natl Acad Sci U S A*, 111(17):6258–6262, Apr 2014.

[3] Lloyd A. C. Chapman, Simon E. F. Spencer, Timothy M. Pollington, Chris P. Jewell, Dinesh Mondal, Jorge Alvar, T. Déirdre Hollingsworth, Mary M. Cameron, Caryn Bern, and Graham F. Medley. Inferring transmission trees to guide targeting of interventions against visceral leishmaniasis and post–kala-azar dermal leishmaniasis. *Proceedings of the National Academy of Sciences*, 117(41):25742–25750, 2020. ISSN 0027-8424. doi: 10.1073/pnas.2002731117. URL `https://www.pnas.org/content/117/41/25742`.