

Contribution to the discussion of the RSS meeting on R/local R/transmission by Sylvia Richardson, MRC Biostatistics Unit, University of Cambridge.

As explained in Parag et al and several other speakers in the meeting, the probability distribution of the generation time, i.e. the time between infection of a primary case and infection of secondary cases, is a crucial piece of epidemiological information for understanding the dynamics of any infectious disease, which is needed in much of the modelling work, e.g. for deriving R_t and for linking R_t to the growth rate.

In the case of SARS-CoV-2 where asymptomatic transmission can occur, the serial interval between the symptoms of a primary case and those of secondary cases, has commonly be used as a proxy for the generation time, but such a choice can lead to bias^{1,2} and be questionable as, for example, symptomatic cases might be more severe and have higher viral load. In the early phase of the epidemic, the main source of data for estimating serial interval has been line-listing of infector-infectee pairs from China, but representativeness and data quality will be influential on the distribution estimate, impinging its transferability to other populations³.

Given the importance of estimating the generation time for Covid-19, it is regrettable that too little attention has been paid to the challenging problem of designing data collection directly targeting the generation time in different strata. In the UK, planning intensive follow-up of contacts of representative samples of primary (symptomatic and asymptomatic) cases, captured by the already established randomised surveillance studies like ONS or REACT, would give valuable time stamped information on transmission pairs and allow estimation and tracking of the generation time distribution during the course of the pandemic. Monitoring the latter over time is important as it is likely to be affected by NPIs⁴ and other dynamic changes. Without ignoring the practical challenges, would the authors agree that investigating the feasibility of such follow up studies within a portfolio of surveillance tools would be beneficial?

¹Deng, Yuhao, et al. "Estimation of incubation period and generation time based on observed length-biased epidemic cohort with censoring for COVID-19 outbreak in China." *Biometrics* (2020).

²Britton, Tom, and Gianpaolo Scalia Tomba. "Estimation in emerging epidemics: Biases and remedies." *Journal of the Royal Society Interface* 16.150 (2019): 20180670.

³Griffin, John, et al. "Rapid review of available evidence on the serial interval and generation time of COVID-19." *BMJ open* 10.11 (2020): e040263.

⁴Ali, Sheikh Taslim, et al. "Serial interval of SARS-CoV-2 was shortened over time by nonpharmaceutical interventions." *Science* 369.6507 (2020): 1106-1109.