

Comments on Session 1 of RSS meeting on Reproduction numbers

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This comment expands on the excellent presentation by Parag, Thompson and Donnelly on the differences between reproduction number R and epidemic growth rates r . As we also highlight in our paper presented two days later, in the vast majority of cases, R is effectively estimated from r through a convolution with the generation time distribution (whether directly or through a mechanistic model). Hence, compared to r , R has an extra layer of modelling assumptions (with all uncertainty, estimation issues and delays that follow), but provides a different piece of information. Beyond these differences, they both suffer from an equal array of issues related to both being an average over individuals, space, settings and time.

I therefore strongly disagree with Sir John Kingman's opinion that the concept should be buried before the next pandemic, in the sense that I do not see how, if a single number R cannot possibly summarise everything about the current epidemic trend, another single number r can solve the problem. It is still an average, with the same problems of having to decide what is averaged across.

However, I do believe the excessive focus on R_0 was highly unhelpful in early 2020. Unlike R_0 , the unconstrained growth rate (r_0) tell how fast cases will grow and, coupled with estimates of how long it takes to see the effect of interventions in the data, can provide crucial information about how long we have before breaching hospital capacity, and hence when to intervene. Early on in the pandemic, in the absence of data, generation time distributions from SARS-1 or MERS were used. In [1] we argued how dangerous it is then to quote R_0 estimates in isolation, as early estimates obtained from an r_0 of 0.1 day^{-1} (~ 7 -day doubling time, see references in [1]) and the longer generation times of SARS-1 or MERS may equally be obtained from a shorter generation time (clear signs of significant pre-symptomatic transmission were available) and a faster growth. This, in my opinion, contributed to obfuscating the fact that cases in Europe were growing twice as fast as the most influential early published studies assumed, even when estimates of R_0 did not change much (though I am convinced they were underestimates anyway). Later on, however, the problem becomes much less acute, because r is lower and the precise timing of interventions less relevant, and because the generation time distribution is better informed.

[1] Pellis, Lorenzo, et al. "Challenges in control of Covid-19: short doubling time and long delay to effect of interventions." *Philosophical Transactions of the Royal Society B* 376.1829 (2021): 20200264.