Endemic infectious states below the epidemic threshold and beyond herd immunity

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In the recent COVID-19 pandemic, we have witnessed a sequence of epidemic waves intertwined with anomalous fade-outs, characterized by periods of low but persistent epidemic prevalence. These long-lasting epidemic states complicate epidemic control because it becomes difficult to assess when control measures should be relaxed, as their lifting may result in new major outbreaks. Furthermore, this phenomenon challenges current modeling approaches, as classical epidemic models fail to explain its emergence. Inspired by this phenomenon, we propose a simple mechanism in [1] that is capable of reproducing several features observed in real data. Specifically, we introduce a modification of the Susceptible-Infected-Recovered (SIR) model within a meta-population framework, where a small inflow of infected individuals accounts for undetected internal or imported cases. By focusing on a regime where this external seeding is so small that it cannot be detected from the analysis of epidemic curves, we find that outbreaks of finite duration percolate over time, resulting in overall low but long-lasting epidemic states both below and above the epidemic threshold.

By employing a two-state description of the local dynamics, we can derive analytical predictions for the duration of outbreaks at global scales (Fig. 1-(a)). Our analysis reveals that outbreaks with extremely long durations, on the order of thousands of days as observed in Fig. 1-(a), can occur within an extended parameter range. This finding challenges the assumption that the total fade-out of the disease is guaranteed, even in cases of sub-critical spreading or when herd immunity is attained. We believe that the coarse-graining approach utilized to extract analytical information from the local dynamics holds further potential for exploring the intricate relationship between local and global dynamics inherent in any meta-population structure.

This work is specially pertinent as the current literature is struggling to find explanations to criticality signatures found in the COVID-19 spread (uninterrupted-yet-small prevalence, linear growth of the recoveries, high susceptibility to changes in mobility restrictions and social distancing, etc). Our model is capable of reproducing the persistence of the COVID-19 disease between waves in the census areas of England. We can also explain empirical features such as the exponential distribution of the time between outbreaks (Fig. 1-(b)), the linear growth of the recoveries and the near-critical values of the effective reproductive number. These results are remarkable given the simplicity of our assumptions and the lack of fine-tuning.

[1] Aguilar, J., Arregui García, B., Toral, R., Meloni, S., and Ramasco, J. J. . *Endemic infectious states below the epidemic threshold and beyond herd immunity*. Communications Physics. 6 (1), 187.
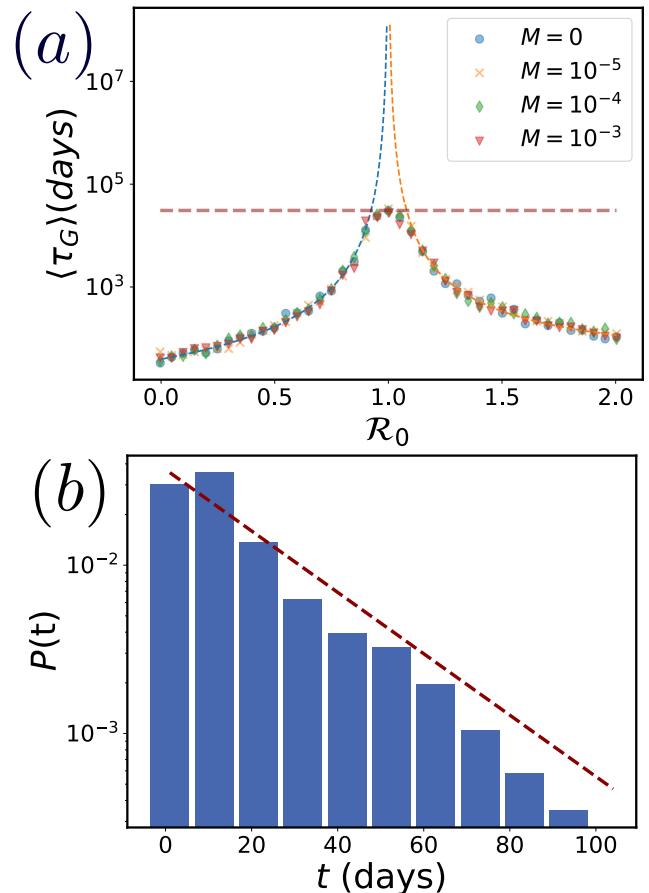
Fig. 1. In (a), dots show the duration of the first global outbreak averaged over 100 simulations for different values of the basic reproductive number $\mathcal{R}_0$ and mobility M. All simulations are stopped either at time $t_{\max} = 4 \times 10^4$ (days) (horizontal dotted line) or when the total prevalence reaches zero. Dashed curved lines show our analytical estimations. There is a region below and above the epidemic threshold for which the duration of epidemic outbreaks is much longer than the epidemic survival times in the classical SIR model. In (b), empirical distribution of times for which the regions in England have zero prevalence. As predicted by our theory, it is well-fitted by an exponential distribution. The value of the exponent of the best fit is 0.041(8), and can be used as a proxy for the rate at which infected individuals enter the region under study from outside per unit of time.