Reconstructing the secondary infection distribution of SARS-CoV-2 from heterogeneity in viral loads and social contacts

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SARS-CoV-2 has been shown to spread mainly through superspreading, with ~10% of individuals responsible for ~80% of onward transmission. We use an individual-based model to combine intra- and inter-host heterogeneity in viral loads during infection with person-to-person variation in numbers of daily contacts to estimate the secondary case distribution of SARS-CoV-2. We investigate the effect of different contact rates before and during the pandemic in the UK, the effect of symptomatic self-isolation, and the impact of testing with rapid antigen tests.

Introduction

- Transmission of SARS-CoV-2 is characterised by substantial variation in the number of secondary infections generated by an infected individual, i.e., "superspreading".
- This variability is believed to stem from variation in viral loads and social contacts between individuals and over the course of infection.
- Understanding the relative contribution of each to transmission may enable estimation of individual-level variation in the reproduction number with changes in social contacts during the SARS-CoV-2 pandemic, and the design of more finely-targeted control measures.

Methods

- Individual-based simulation model combining published data on wild-type viral load trajectories with daily social contacts reported via surveys before (BBC Pandemic, 2017-2018) and during (CoMix, 2020) the pandemic in the UK.
- Primary infectors were allocated a set of household contacts and daily out-of-household contacts.
- Infection of contacts was modelled as a stochastic process with probability of infection determined by primary case's infectious viral load on day of contact and duration of contact.
- Individuals assumed to self-isolate at home upon symptom onset or following a positive lateral flow antigen test taken every 3 days when asymptomatic, preventing non-household contact from that day forward.
- Mean, *R*, and degree of overdispersion, *k*, in reproduction number estimated by fitting Negative Binomial distribution to resulting secondary infection distribution.

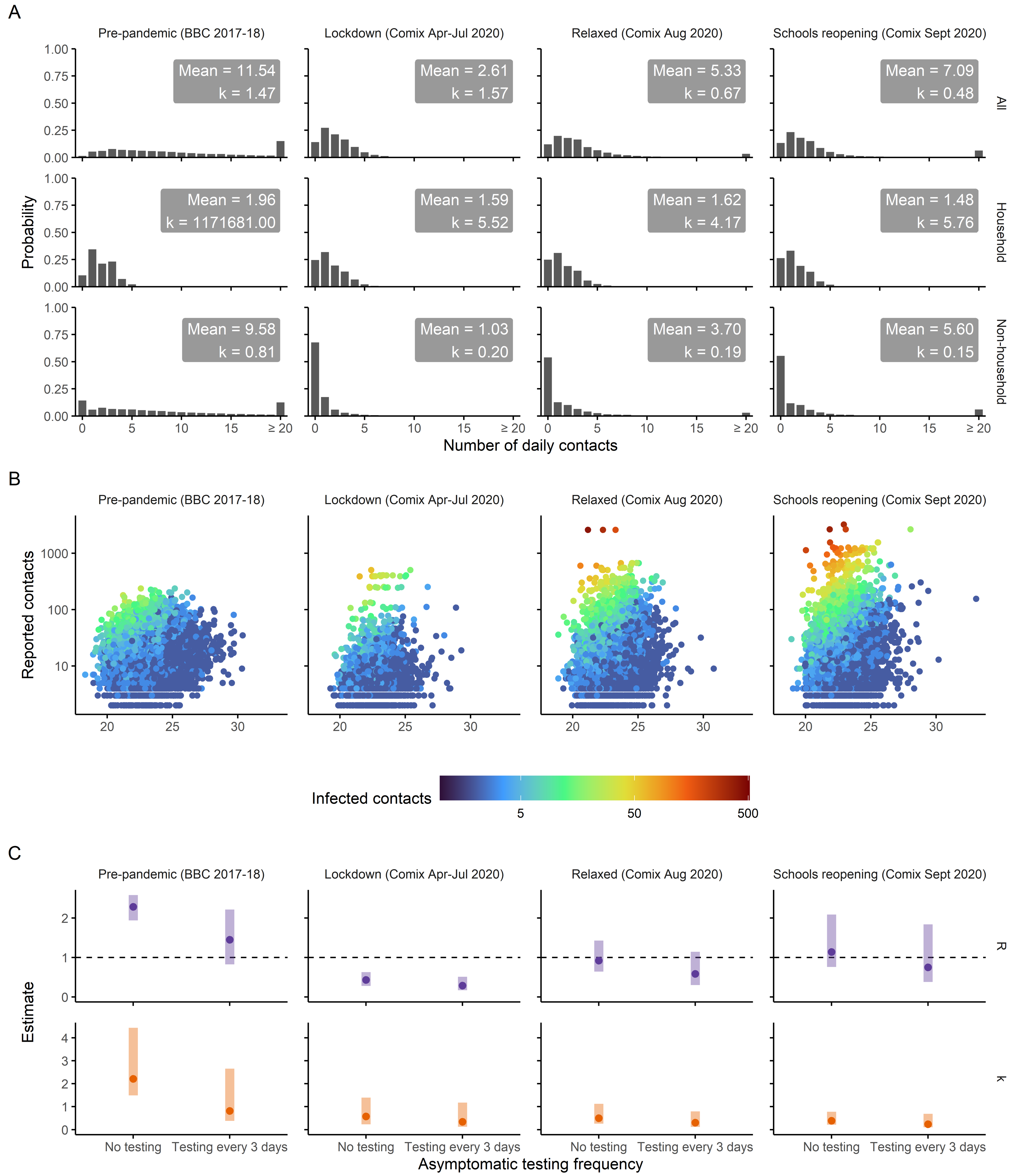

Figure: A) Distributions of all, household, and non-household contacts before (BBC Pandemic, 2017-2018) and during (CoMix, 2020) the SARS-CoV-2 pandemic in the UK. Pandemic contacts were assessed at 3 illustrative timepoints: Lockdown (April-July 2020); Relaxed restrictions (Aug 2020) and relaxed restrictions with schools open (Sept 2020). B) Simulated number of daily infections by individuals on given days (points) by number of reported contacts and viral load in Ct. C) Estimated reproduction number *R* and overdispersion *k* of the simulated secondary case distribution, with and without regular asymptomatic rapid testing every 3 days.

Findings

- Proportion of individuals reporting >20 contacts decreased from 14% pre-pandemic to 0.5% in the first lockdown, then increased to 3% after restrictions were relaxed and 6% when schools reopened.
- Estimated R_0 from model of 2.3 (95% UI: 1.9, 2.6) for pre-pandemic contact levels, and R_c (control reproduction number) of 0.4 (0.3, 0.6) in the first lockdown, 0.92 (0.6, 1.4) after restrictions were relaxed, and 1.1 (0.8, 2.1) when schools reopened, closely matching other estimates.
- High numbers of secondary infections were likely to occur when individuals had many contacts and a high viral load on a given day. For example when individuals had >100 reported contacts and a viral load higher than the average peak (<22.4 Ct) there was a 49% chance that >20 of those contacts would be infected.
- Rapid testing every 3 days has a greater relative impact when individuals have more contacts.

Conclusions

- SARS-CoV-2 superspreading can be reconstructed from a model of individual-level variation in viral load and daily contacts.
- Superspreading events occur when high viral loads coincide with high numbers of contacts, suggesting that testing prior to events may reduce their occurrence.
- Explicitly accounting for variation in both infectivity and contact rates may allow for targeted infection control measures with lower societal costs than blanket interventions.

Key references:

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