# Appendix: Effectiveness of isolation, testing, contact tracing and physical distancing on reducing transmission of SARS-CoV-2 in different settings: a mathematical modelling study

*Adam J. Kucharski PhD*[1*], *Petra Klepac PhD*[1,2], *Andrew J. K. Conlan PhD*[3], *Stephen M. Kissler PhD* [4], *Maria Tang MMath*[2], *Hannah Fry PhD* [5], *Julia R. Gog PhD* [2], *W. John Edmunds PhD* [1], *CMMID COVID-19 working group*

[1]*Centre for Mathematical Modelling of Infectious Diseases, London School of Hygiene & Tropical Medicine*
[2]*Department of Applied Mathematics and Theoretical Physics, University of Cambridge*
[3]*Department of Veterinary Medicine, University of Cambridge*
[4]*Department of Immunology and Infectious Diseases, Harvard T.H. Chan School of Public Health*
[5]*Centre for Advanced Spatial Analysis, University College London*

## Model description

In each simulation, for each of the four contact settings, the number of baseline secondary infections per primary case under no control measures were drawn from a binomial distribution $R_{base} = B(N_c, p_{inf})$, where $N_c = (\text{number of daily contacts}) \times (\text{days infectious})$ and $p_{inf} = SAR \times (\text{relative infectiousness})$, where relative infectiousness = $1$ if an individual is (pre-)symptomatic and 50% if asymptomatic. We then generated secondary infections accounting for reduction in $R_{isol} = B(R_{base}, 1-p_{isol})$, where $p_{isol}$ is the proportion of the infectious period spent in isolation. In the household setting, we assume $N_c = (\text{number of daily contacts})$ because the household contacts will be repeated each day. The number of infected contacts successfully traced were in turn drawn from a binomial distribution $R_{traced} = B(R_{isol}, p_{trace})$, where $p_{trace} = P(\text{successfully traced}) \times P(\text{individual adheres fully to quarantine})$. For each contact, we generated a time of infection uniformly from the period during which the index case was infectious and not isolated. We assumed manually traced contacts were quarantined within two days of index case being isolated, and app-based contacts immediately. If contacts were quarantined after becoming infectious (i.e. more than 4 days after infection), then we scaled their contribution to $R_{traced}$ based on the proportion of their infectious period they spent out of quarantine. For example, if a contact spent 3/5 days of their infectious period within quarantine, then only 60% of onwards transmission was averted. The overall reduction in transmission resulting from control measures was therefore equal to $R_{control} = R_{base} - R_{traced}$. The overall effective reproduction number $R_{eff}$ under different control scenarios was equal to the mean of $R_{control}$ across all simulations. Full model code is available from: https://github.com/adamkucharski/2020-cov-tracing

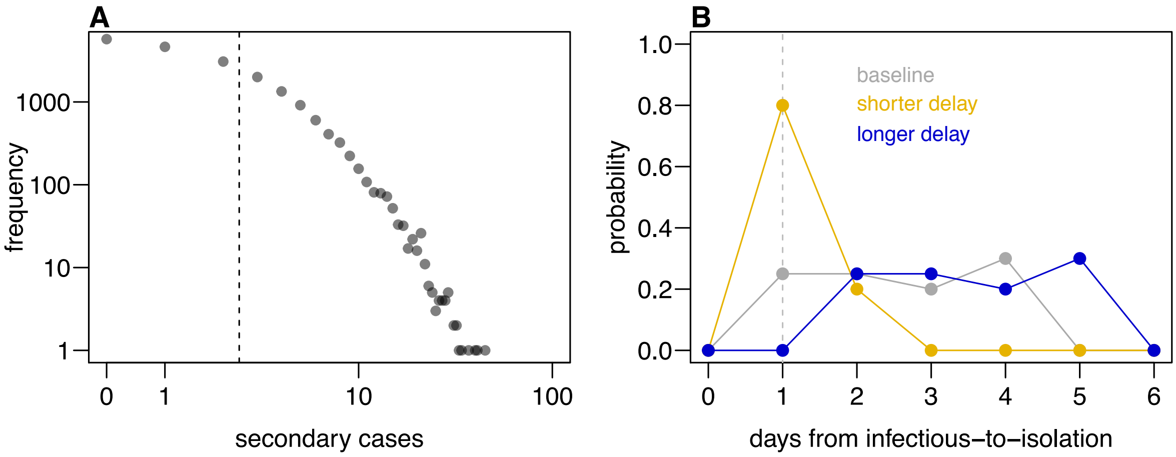

***Figure S1: Model assumptions about transmission and infectiousness.*** *A) Individual-level distribution of secondary transmission in baseline scenario. Dashed line shows mean (i.e.* $R_{eff}$*). B) Distribution scenarios for delay from infectious-to-isolation. We assume the pre-symptomatic period lasts one day; dashed line shows time of onset of symptoms in these scenarios.*

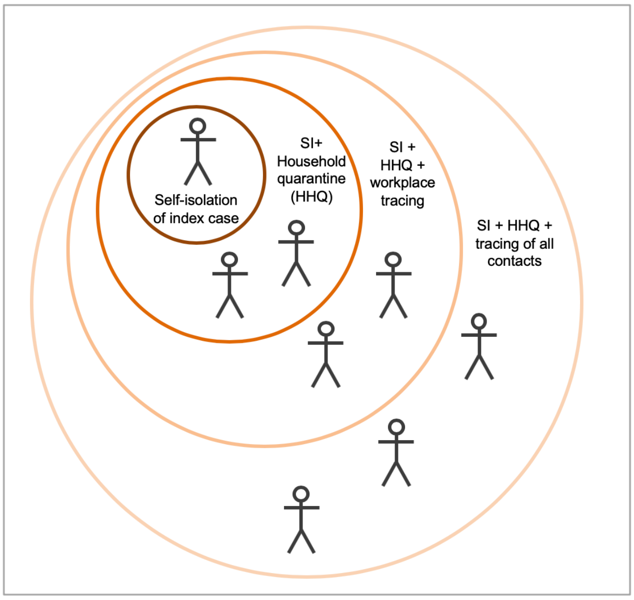

***Figure S2: Schematic of different contact tracing assumptions.*** *Upon onset of symptoms, the index case may isolate; the household may then be quarantined and contacts may then be traced at school/work or also in other settings (i.e. tracing of all contacts).*

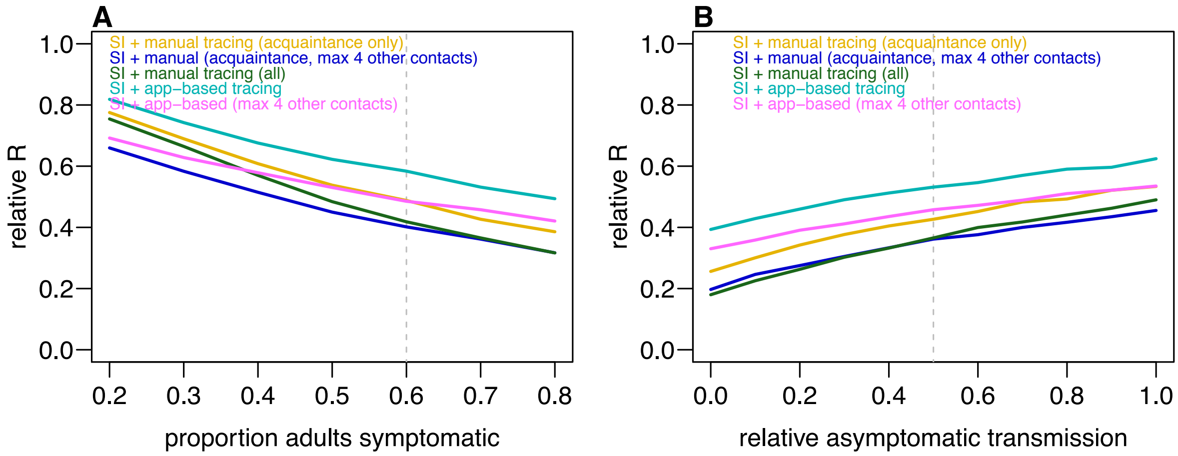

***Figure S3: Impact of proportion of the adult population who are symptomatic and relative transmission from asymptomatic individuals on reduction in transmission.*** *A) Relative reduction in the reproduction number (i.e. ratio between baseline R and R under control measures) when different proportions of the adult population are symptomatic. We assume that the proportion of children that are symptomatic is scaled according to our baseline assumption, i.e. the proportion is equal to 25/60 multiplied by the adult proportion. B) Relative transmission reduction when asymptomatic individuals have different relative transmission risks compared to symptomatic individuals. Dashed lines show baseline assumption.*

| Scenario | Baseline assumptions | | HH SAR=20%, other contact SAR=7% | | HH SAR=40%, other contact SAR=5% | |
|---|---|---|---|---|---|---|
| | Reduction | Quar. | Reduction | Quar. | Reduction | Quar. |
| Self-isolation within home (SI) | 29% | 0 (0-0) | 30% | 0 (0-0) | 24% | 0 (0-0) |
| Self-isolation outside home | 35% | 0 (0-0) | 34% | 0 (0-0) | 33% | 0 (0-0) |
| SI & HH quarantine (HHQ) | 37% | 2 (0-4) | 37% | 2 (0-4) | 41% | 2 (0-4) |
| SI + HHQ + work/school contact tracing (CT) | 53% | 13 (1-110) | 53% | 13 (1-110) | 55% | 13 (1-110) |
| SI + HHQ + manual CT of acquaintances | 57% | 22 (1-120) | 58% | 22 (1-120) | 57% | 21 (1-120) |
| SI + HHQ + manual contact tracing of all contacts | 64% | 29 (1-140) | 64% | 29 (1-140) | 62% | 29 (1-140) |
| SI + HHQ + app-based tracing | 47% | 4 (1-69) | 47% | 4 (1-71) | 49% | 4 (1-70) |
| SI + HHQ + manual CT of acquaintances + app-based tracing | 61% | 25 (1-130) | 61% | 25 (1-130) | 60% | 25 (1-130) |
| SI + HHQ + manual CT of acquaintances + limit to 4 daily ‘other’ contacts | 64% | 17 (1-110) | 64% | 17 (1-100) | 63% | 17 (1-100) |
| SI + HHQ + manual CT of acquaintances + app-based tracing + limit to 4 daily ‘other’ contacts | 66% | 21 (1-110) | 67% | 21 (1-110) | 64% | 21 (1-110) |

**Table S1: Reduction in transmission and number of contacts quarantined per symptomatic case under different assumptions about secondary attack rate (SAR) among contacts made within and outside households.** Median and 90% prediction interval shown for contacts quarantined. HH SAR=20% and other contact SAR=7% corresponded to baseline $R_{eff}$=2.9; HH SAR=40% and other contact SAR=5% corresponded to baseline $R_{eff}$=2.7.

| **Scenario** | **Baseline assumptions** | | **Shorter delay to self-isolation** | | **Longer delay to self-isolation** | |
|---|---|---|---|---|---|---|
| | Reduction | Quar. | Reduction | Quar. | Reduction | Quar. |
| Self-isolation within home (SI) | 29% | 0 (0-0) | 47% | 0 (0-0) | 18% | 0 (0-0) |
| Self-isolation outside home | 35% | 0 (0-0) | 53% | 0 (0-0) | 20% | 0 (0-0) |
| SI & HH quarantine (HHQ) | 37% | 2 (0-4) | 54% | 2 (0-4) | 25% | 2 (0-4) |
| SI + HHQ + work/school contact tracing (CT) | 53% | 13 (1-110) | 62% | 13 (1-110) | 47% | 13 (1-110) |
| SI + HHQ + manual CT of acquaintances | 57% | 22 (1-120) | 63% | 21 (1-120) | 51% | 21 (1-110) |
| SI + HHQ + manual contact tracing of all contacts | 64% | 29 (1-140) | 67% | 29 (1-140) | 59% | 29 (1-140) |
| SI + HHQ + app-based tracing | 47% | 4 (1-69) | 58% | 4 (1-69) | 38% | 4 (1-70) |
| SI + HHQ + manual CT of acquaintances + app-based tracing | 61% | 25 (1-130) | 65% | 25 (1-130) | 56% | 25 (1-130) |
| SI + HHQ + manual CT of acquaintances + limit to 4 daily ‘other’ contacts | 64% | 17 (1-110) | 69% | 17 (1-100) | 60% | 17 (1-110) |
| SI + HHQ + manual CT of acquaintances + app-based tracing + limit to 4 daily ‘other’ contacts | 66% | 21 (1-110) | 70% | 21 (1-110) | 63% | 21 (1-110) |

**Table S2: Reduction in transmission and number of contacts quarantined per symptomatic case under different assumptions about pre-symptomatic period and delay to self-isolation.** Assumptions about the distributions of delays shown in Figure S1. Median and 90% prediction interval shown for contacts quarantined.