

Effectiveness of isolation, testing, contact tracing and physical distancing on reducing transmission of COVID-19 in different settings

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Summary

Methods:

- Using a model of individual-level transmission stratified by setting (household, work, school, other) based on BBC Pandemic data from 40,162 UK participants, we simulated the impact of a range of different testing, isolation, tracing and physical distancing scenarios (**Figures 1–2**).
- We estimated the reduction in effective reproduction number from strategies both individually and in combination, as well as estimating the number of cases and contacts that would need to be isolated and quarantined each day for a given levels of COVID-19 incidence.

Results:

- Under plausible but optimistic assumptions, we estimated that combined testing and tracing strategies reduced the effective reproduction number more than mass testing or self-isolation alone (50–70% vs 5–35%) (**Table 3**).
- If limits are placed on gatherings outside of home/school/work (e.g. maximum of 4 daily contacts in other settings or proportion of population working from home), then partial manual contact tracing (i.e. tracing of familiar contacts only) could have a similar effect on transmission reduction as detailed full contact tracing (**Table 3 and Figure 3**).
- In a scenario where there were 10,000 new symptomatic cases per day, we estimated most contact tracing strategies would require 130,000 to 430,000 individuals to be isolated or quarantined each day (**Table 4**).
- We estimated that if a high proportion of cases were symptomatic, self-isolation and contact tracing measures would lead to a greater relative reduction in transmission, whereas measures were less effective if the relative transmissibility of asymptomatic infections was higher (**Figure 4**).
- If there was no pre-symptomatic transmission, self-isolation and household quarantine would lead to a larger reduction in transmission. If cases took longer to self-isolate after becoming symptomatic (i.e. 3.4 days on average rather than 2.4 days), these measures were less effective (**Table 5**). Similar numbers of contacts needed to be quarantined in all scenarios.

Introduction

The novel SARS-CoV-2 coronavirus spread rapidly across multiple countries in early 2020 (1–3). A staple public health control measure for emerging directly-transmitted infections involves isolation of symptomatic cases as well as tracing, testing and quarantine of their contacts (2). The effectiveness of this measure in containing new outbreaks depends both on the transmission dynamics of the infection and the proportion of transmission that occurs without symptoms or prior to symptom onset (4). There is evidence that SARS-CoV-2 has a reproduction number of around 2–3 in the early stages of an outbreak (1,5) and many infections can occur without symptoms (6), which means isolation and contact tracing alone is unlikely to contain an outbreak unless a very high proportion of contacts are successfully traced (7).

Several countries have used combinations of non-pharmaceutical interventions to reduce SARS-CoV-2 transmission (3,8–10). As well as self-isolation of symptomatic individuals and tracing of their contacts, measures have included general physical distancing, remote working, community testing and cancellation of events. It has also been suggested that the effectiveness of contact tracing could be enhanced through app-based digital tracing (11). The effectiveness of contact tracing and resources required to implement successfully will depend on the social interactions within a population (12). Targeted interventions such as contact tracing also need to consider individual-level variation; if there is high individual-level variation in transmission, it can lead to superspreading events, and hence a large number of contacts that need to be traced in some instances (13). There are several examples of such events occurring for COVID-19, including meals, parties and other gatherings of close contacts (14,15).

We use social contact data from a large-scale UK study of over 40,000 participants (16,17) to explore a range of different control measures for SARS-CoV-2, including: self-isolation of symptomatic cases; household quarantine; manual tracing of familiar contacts (i.e. those that have been met before); manual tracing of all contacts; app-based tracing; mass testing regardless of symptoms; a limit on daily contacts made outside home, school and work; and a proportion of the adult population working from home. As well as estimating the reduction in transmission under different scenarios, we estimated how many primary cases and contacts would need to be quarantined per day at different levels of symptomatic case incidence.

Methods

Secondary attack rate data sources

To estimate the risk of transmission per contact in different settings, we collated contact tracing studies for COVID-19 from multiple settings that stratified contacts within and outside household (Table 1). Across studies, the estimated SAR within household was 10–15%, with a much smaller SAR outside household. However, all these studies were conducted in an ‘under control’ scenario (i.e. effective reproduction number $R < 1$) and some reported relatively few contacts, which may omit superspreading events. This suggests that SARS-CoV-2 may be driven by community transmission events as well as household contacts (15). In our main analysis, we therefore assume 20% HH SAR and 6% among all contacts, which led to an overall reproduction number of 2.7 in the model (described in next section) when no control measures were in place.

Transmission model

Our analysis is based on data on 40,162 UK participants with recorded social contacts in the BBC Pandemic dataset (16). Using these data, we simulated a large number of individual-level transmission events by repeatedly generating contact distributions for a primary case and randomly generating infections among these contacts. In each simulation, we randomly specify a primary case as either under 18 or 18 and over, based on UK demography, in which 21% of the population are under 18 (18). We then generate contacts by randomly sampling values from the marginal distributions of total contacts made in three different settings for their age group: at home; at work & school; and in ‘other’ settings (Figure 1). We used the marginal distributions rather than raw participant data to ensure non-identifiability and reproducibility in our publicly available model.

In the model, we assumed individuals had a certain probability of being symptomatic and getting tested if symptomatic, as well as an effective infectious period that depended on when/if they self-isolated following onset of symptoms (details in Table 2). During each day of the effective infectious period, individuals made contacts based on their recorded daily contacts, apart from contacts made within the home, which were fixed at the daily value over the entire infectious period. Once the individual-level contacts had been defined, we generated secondary infections at random based on assumed secondary attack rates among contacts, and estimated how many contacts would be successfully traced in each of these settings under different scenarios. We then calculated the reproduction number without tracing and subtracted the number of secondary cases that were effectively traced and hence removed from the potentially infectious pool to calculate the overall number of secondary cases that would contribute to future infectiousness (Figure 2).

For each contact setting, baseline secondary infections 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 $R_{isol} = B(R_{base}, p_{isol})$, where p_{isol} is the proportion of the infectious period not 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 $p_{trace} = P(\text{successfully traced}) \times P(\text{individual adheres to quarantine})$. Hence the reduction in effective reproduction number resulting from control measures was equal to $R_{base} - R_{traced}$.

Scenarios

We considered several different scenarios, individually and in combination. These included: no control measures; self-isolation of symptomatic cases; household quarantine; work/school quarantine; manual tracing of familiar contacts (i.e. have been met before); manual tracing of all contacts; app-based tracing with a given level of coverage influencing what proportion of people can potentially be traced; mass testing of cases regardless of symptoms; a limit on daily contacts made in ‘other’ settings; and a proportion of the adult population working from home.

We assumed individuals who were successfully isolated had no risk of onward transmission (even to household members). For app-based tracing to be successfully implemented in a given simulation, both the infectious individual and their contacts needed to have the app. In the scenario with mass testing of cases regardless of symptoms, we assumed infected individuals would be identified and immediately isolated at a random point during their 5 day infectious period. We assumed that infected individuals would not test positive if tested during the latent period. No other measures (e.g. self-isolation/quarantine) were in place for this scenario. We ran 10,000 simulations for each scenario.

Results

Under the control measures considered, we found that combined testing and tracing strategies reduced the effective reproduction number more than mass testing or self-isolation alone (Table 3). If only self-isolation of symptomatic cases was implemented in the model, it reduced transmission by around 18% on average. The addition of household quarantine to self-isolation resulted in an overall average reduction of 25%. In our simulations, self-isolation combined with manual contact tracing of all contacts reduced transmission by 66%; manual tracing of familiar contacts only (i.e. those that had been met before) was less effective, with only a 53% reduction in transmission. This was similar to contact tracing of school or work contacts only (52% reduction). We estimated that self-isolation combined with app-based tracing reduced transmission by around 40%, because both the primary case and contact would need to have the app to successfully quarantine an infected secondary case.

We estimated that if some level of physical distancing were maintained, it could supplement the reduction in transmission from contact tracing. For example, if daily contacts in other settings (i.e. outside the home, work and school) were limited to four people, our model suggested that manual tracing of familiar contacts only could lead to a 62% reduction in transmission, and app-based tracing a 47% reduction. We estimated that mass random testing of 10% of the population each week would reduce transmission by only 4%, because relatively few cases would be detected and many of those that were would have already spread infection to others.

We also considered the number of contacts that would need to be traced under different strategies. In a scenario where there were 100,000 new symptomatic cases per day, most contact tracing strategies would require over 1m individuals to be quarantined each day as a result (Table 4). If incidence was at a lower level of 10,000 new cases per day, there would be a corresponding ten-fold reduction in the number of daily contacts that needed to be quarantined. Although there was a similar reduction in transmission from manual testing of all contacts and manual testing of only familiar contacts with physical distancing in place for other settings (Table 3), the latter combination required fewer people to be quarantined each day (Table 4).

We found that the effectiveness of manual contact tracing strategies were highly dependent on how many contacts were successfully traced, with a high level of tracing required to ensure $R < 1$ in our baseline scenario (Figure 3A). If contact tracing were combined with a maximum limit to daily contacts made in other settings (e.g. by restricting events), we found that this limit would have to be relatively small (i.e. fewer than 15–20 contacts) before a discernible effect could be seen on R , and very small (i.e. fewer than

around 10 contacts) to ensure $R < 1$ for app-based tracing, even if 50% of adults also had no work contacts because remote working was in place (Figure 3B). We estimated that if only work contacts are restricted, a substantial proportion of the adult population would need to have zero work contacts to ensure $R < 1$ when combined with app-based tracing (Figure 3C). Under our baseline assumptions, we estimated that app-based tracing would require a high level of coverage to ensure $R < 1$ (Figure 3D), because both primary case and contacts would need the app; this is consistent with our finding that manual tracing would require a high proportion of contacts to be traced.

We also considered the impact of assumptions about proportion symptomatic and relative contribution of asymptomatic individuals to transmission. We estimated that if a high proportion of cases were symptomatic, self-isolation and contact tracing measures would lead to a greater relative reduction in transmission (Figure 4A); this is mostly because more primary cases would be detected. Control measures were slightly less effective if the relative transmissibility of asymptomatic infections was higher (Figure 4B), because it would mean more undetected transmission. However, because our baseline scenario assumed 70% of cases were symptomatic, the overall effect was less than it would be if the majority of cases were asymptomatic. We estimated that if there was no pre-symptomatic transmission, self-isolation and household quarantine would lead to a larger reduction in transmission (Table 5); correspondingly, if we assumed cases took longer to self-isolate after becoming symptomatic (i.e. 3.4 days on average rather than 2.4 days), these measures were less effective. However, the estimated overall reduction from self-isolation and manual contact tracing was similar across the three scenarios, because although more secondary infections occurred before isolation, a large proportion of them could be traced in the model.

Discussion

Using a model of setting-specific interactions, we estimated that strategies that combined testing and tracing reduced the effective reproduction number R more than mass testing or self-isolation alone. The effectiveness of these isolation and tracing strategies was further enhanced when combined with physical distancing measures, such as a reduction in work contacts among adults, or a limit to the number of contacts made outside home, school or work. Several countries have achieved a prolonged suppression of SARS-CoV-2 transmission using a combination of case isolation, contact tracing and physical distancing. In Hong Kong, isolation of cases and tracing of contacts was combined with other physical distancing measures, which resulted in an R near 1 throughout February and March 2020 (10). As well as early surveillance and containment measures (2), Singapore introduced additional ‘circuit breaker’ interventions to counter growing case numbers in April 2020 (19). In South Korea, testing and tracing has been combined with school closures and remote working (20,21)

In our analysis, we estimated that a large number of contacts would need to be traced and tested if incidence of symptomatic cases was high. This logistical constraint may influence how and when it is possible to transition from ensuring $R < 1$ through extensive physical distancing measures to reducing transmission predominantly through targeted isolation and tracing-based measures. Our estimate of 30–50 contacts being traced and tested per case in the manual tracing strategies we considered (Table 4) is consistent with the scale of testing being conducted per confirmed case in countries with a high estimated

proportion of cases reported as of mid-April 2020, such as Australia (64 tests per case) and South Korea (52 tests per case) (22,23). This suggests any planning for ongoing control based on isolation and tracing should account for the likely need to conduct at least 30–50 additional tests for each case detected.

Our analysis has several limitations. We focused on individual-level transmission between a primary case and their contacts, rather than considering higher degree network effects. If contacts were clustered (i.e. know each other), it could reduce the number of contacts that need to be traced over multiple generations of transmission. We also assumed that contacts made within the home are the same people daily, but contacts outside home are made independently each day. Repeated contacts would also reduce the number that need to be traced. However, our estimates are consistent with the upper bound of numbers traced in empirical studies (Table 1), as well as analysis of UK social interactions that accounts for higher degree contacts (12).

Because our data was not stratified beyond the four contact settings we considered (home, work, school, other), we could not consider further specific settings, e.g. mass gatherings. However, our finding that gatherings in other settings needed to be restricted to relatively small sizes before there was a noticeable impact on transmission is consistent with findings that groups between 10–50 people have a larger impact on SARS-CoV-2 dynamics than groups of more than 50 (24).

Our baseline assumptions were plausible but optimistic. In particular, we assume a delay of symptom onset to isolation of 2.4 days, and quarantine that was sufficiently fast to prevent any onwards transmission among successfully traced contacts. Based on viral shedding dynamics, this would imply tracing and quarantine within around two days of exposure (6). We also assumed that routine self-isolation would not increase household transmission. However, our conclusions about onwards transmission in the different control tracing scenarios would not be affected if some limited household transmission did occur, because we are assuming these individuals would be quarantined too. We also simulate contact patterns at random for each individual in our population, whereas in an outbreak, there is likely to be a correlation between degree and infection risk; individuals with multiple contacts may be more likely to acquire infection as well as transmit to others (25). If this were the case, and we assume the same secondary attack rates, the overall reduction may be lower than we have estimated; however, to keep the baseline reproduction number consistent, this correlation would have to be offset by a lower SAR among contacts.

Our results highlight the challenges involved in reducing SARS-CoV-2 transmission. Consistent with previous modelling studies (7,12) and observed outbreak dynamics globally, our analysis suggests that, depending on the overall effectiveness of testing, tracing, isolation and quarantine, a combination of self-isolation, contact tracing and moderate physical distancing may be required to ensure $R < 1$. Further, in a scenario where incidence is high, considerable numbers of individuals may need to be quarantined to achieve control using this approach.

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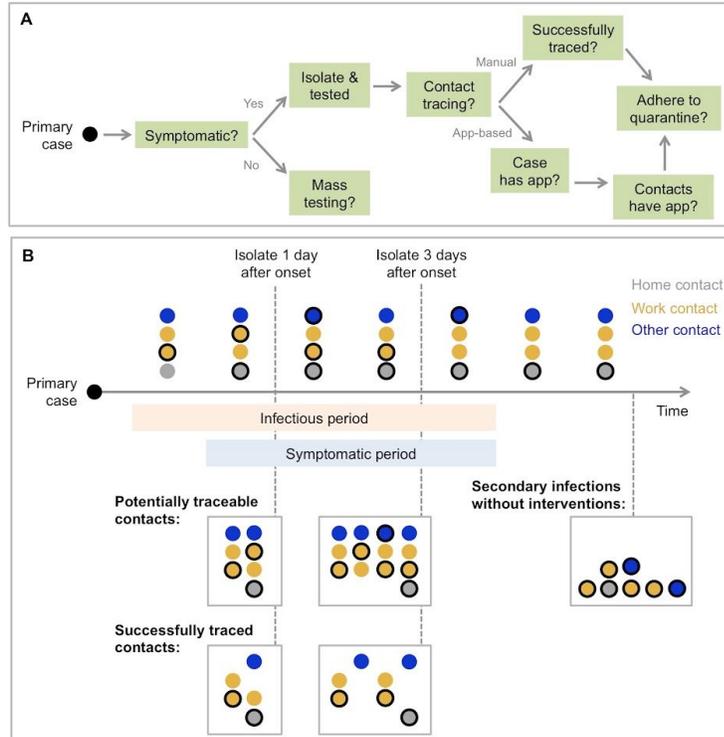


Figure 2: Effect of isolation and contact tracing on reducing transmission. *A) Factors that influence whether an individual is isolated and whether contacts are successfully traced in the model (parameters in Table 2). B) Implementation of contact tracing in the model. Timeline shows a primary case with four daily contacts self-isolating either 1 or 3 days after onset of symptoms. We assume the household contact is the same person throughout, whereas other contacts are made independently. Had the primary case not been isolated, there would have been 7 secondary cases in this illustration. For isolation 1 day after onset, 4 secondary infections are prevented immediately. Then 7 contacts are traced, 3 of whom are infected. In this example, two infected contacts pre-isolation are successfully traced and quarantined (i.e. one is missed), so overall the isolation-and-tracing control measure results in a $4+2 = 6$ reduction in effective reproduction number. For isolation 3 days after onset, 2 infections are prevented immediately. 13 contacts are potentially traceable, 5 of whom are infected. In the example, three infected contacts are successfully traced, so overall the control measure results in a $2+3 = 5$ reduction in effective reproduction number.*

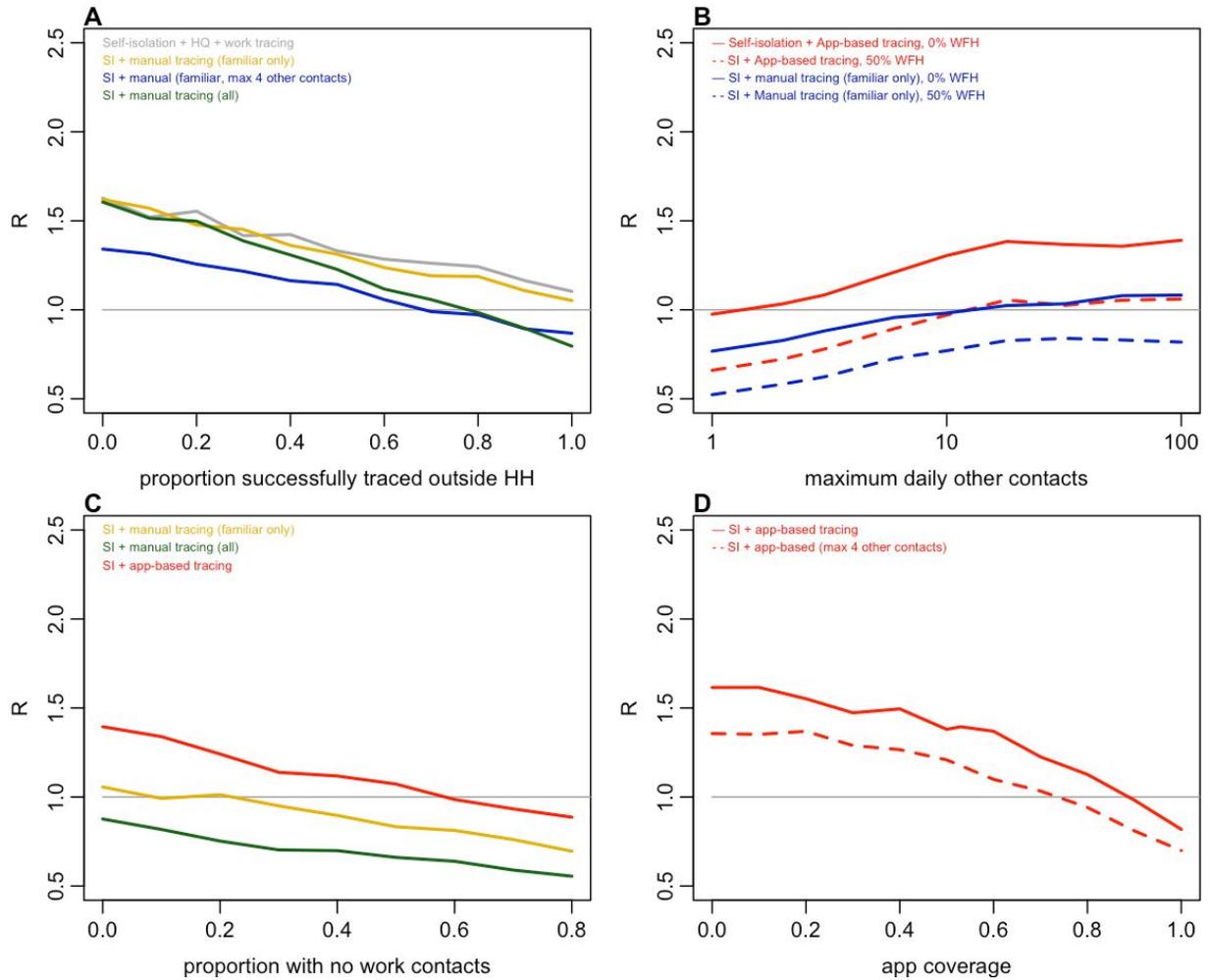


Figure 3: Impact of contact tracing effectiveness and physical distancing on reduction in reproduction number (baseline $R=2.7$). *A) Reduction in R under different strategies for different proportions of work/school/other contacts that are successfully traced. B) Effect of the maximum limit on the number of daily contacts in other settings and control tracing strategies on R , either when adults are working as normal, or when 50% have no work contacts (WFH=50%). C) Effect of proportion of population with no work contacts. D) Effect of app-based tracing under different assumptions about app coverage. In all panels, other parameters are as in Table 2.*

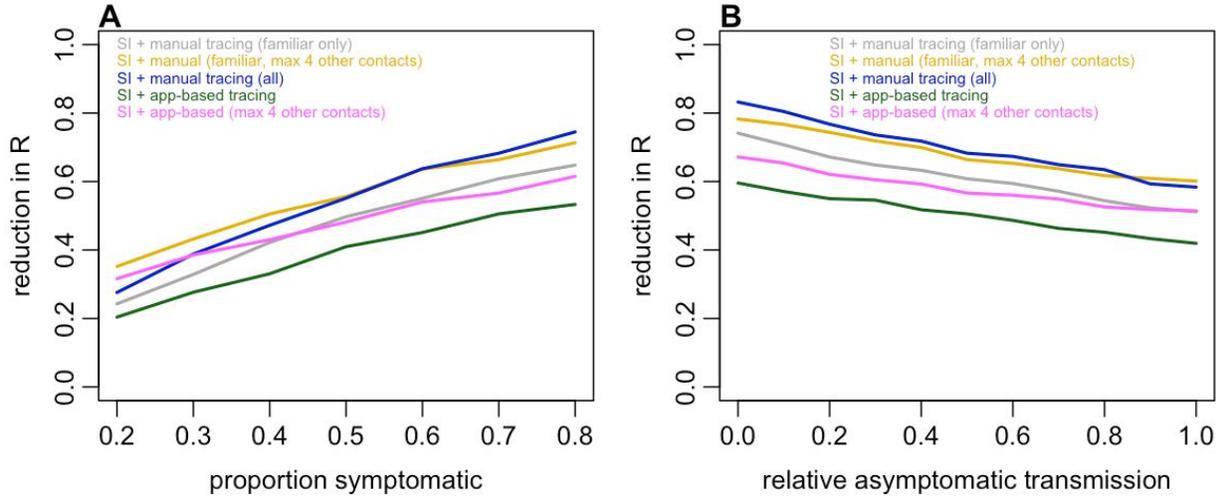


Figure 4: Impact of proportion of the population who are symptomatic and relative transmission from asymptomatic individuals on reduction in transmission. *A) Relative reduction in the reproduction number (i.e. ratio between baseline R and R under control measures) when different proportions of the population are symptomatic. B) Relative transmission reduction when asymptomatic individuals have different relative transmission risks compared to symptomatic individuals.*

Country	SAR among HH contacts	SAR among close contacts	Contacts per case	Observed R	Source
Shenzhen	12.9%	0.9%	3.0	0.24	(26)
USA	10.5%	0.0%	44.5	0.20	(27)
Guangzhou	10.1%	0.5%	14.3	0.34	(28)
Taiwan	13.8%	1.5%	9.1	0.38	(29)
Ningbo	13.3%	5.1%	11.2	0.69	(30)
Guangzhou	13.8%	7.1%	9.8	0.62	(31)

Table 1: Secondary attack rates estimated from contact tracing studies.

Parameter	Assumed value	Details & references
<i>Individual-level epidemiology</i>		
Reproduction number in absence of control measures	2.7	Follows from SAR assumptions. Consistent with meta-analysis of early studies (32).
Duration of infectiousness	5 days (for cases that will become symptomatic, 1st day is pre-symptomatic)	Given incubation period around 5 days (33), this assumption implies serial interval of around 6.5 days (26).
Relative infectiousness of asymptomatic cases	50%	Point estimate was 65% in (30), but secondary cases from asymptomatics were more likely to in turn be asymptomatic, suggesting lower contribution to transmission.
Proportion of cases that are eventually symptomatic	70%	Estimates for symptomatic proportion in non-targeted testing have typically ranged between 60–80% (3,34–36)
Probability symptomatic individual will eventually self-isolate and be tested	90%	We assume virus only detectable by PCR during the infectious period. 90% UK survey respondents said would likely comply with app request to self-isolate if rapid test available (37)
Effective duration of infectiousness if self-isolate when symptomatic	P(0 days)=0; P(1 days)=0.05; P(2 days)=0.25; (3 days)=0.25; P(4 days)=0.15; P(5 days)=0.3. This corresponds to a mean delay from onset to isolation of 2.4 days.	Assume most likely to self-isolate on days 2–5 of infectious period (i.e. 1–4 days after onset). For 269 cases with known date of onset and confirmation in Singapore, of those who were confirmed within 5 days, 2% were confirmed on date of onset, 26% on second day, 27% on 3rd day, 14% on 4th day and 31% on 5th day (38)
<i>Contact tracing</i>		
Secondary attack rate among contacts in home	10%	See ‘secondary attack rate’ section above

Secondary attack rate among other contacts	6%	See 'secondary attack rate' section above
Proportion of contacts that are familiar (i.e. have been met before)	100% at home 80% at work/school 51% in other settings	Based on BBC Pandemic data
Proportion of potentially traceable household contacts that are successfully traced	100%	Assumed
Proportion of potentially traceable workplace, school or 'other' contacts that are successfully traced	95%	Assumed
Probability traced contacts adhere to quarantine	90%	Proportion of traced contacts that are successfully removed from the potentially infectious group. Same justification as 'Probability symptomatic individual will eventually self-isolate and be tested' parameter above.
<i>App-based tracing</i>		
Proportion of population that would have app	53% (= 71% x 75%)	85% of age 16+ in UK are smartphone users (Ofcom, 2019). 16% of UK are under 10 or over 80 (18), so we assume 71% of population use smartphones. 75% of UK survey respondents said would probably or definitely download app (37)
<i>Mass testing</i>		
Proportion of population that are tested per week	5% (i.e. 460,000 tests per day for UK)	0.7% of population tested per day, i.e. equal to the highest number of daily per capita tests performed anywhere in world as of mid-April 2020 (Iceland, 7 per 1000) (22)

Table 2: Parameter definitions and assumptions.

Scenario	Self-isolation	Contact tracing	% non-HH contacts that are potentially traceable	% population tested each week	Effective reproduction number	Effective reduction in transmission
No control	No	No	–	–	2.7	–
Self-isolation (SI)	Yes	No	–	–	1.7	37%
SI & HH quarantine	Yes	HH only	–	–	1.6	41%
SI, HH quarantine + work/school contact tracing	Yes	HH & work/school	80% work/school; 50% other	–	1.1	58%
SI + manual CT of familiar contacts	Yes	All	80% work/school; 50% other	–	1.1	61%
SI + manual CT of familiar contacts + limit to 4 daily ‘other’ contacts	Yes	All	80% work/school; 50% other	–	0.87	68%
SI + manual contact tracing of all contacts	Yes	All	100%	–	0.85	68%
SI + app-based tracing	Yes	All	53%	–	1.4	49%
SI + app-based tracing + limit to 4 daily ‘other’ contacts	Yes	All	53%	–	1.1	57%
Mass weekly population testing	No	–	–	5%	2.7	3%

Table 3: Mean reduction in effective reproduction number under different control measures (i.e. the relative reduction from quarantining infectious individuals that would have gone undetected

with no intervention). Results from simulated setting-specific secondary transmission, assuming secondary attack rate of 20% among household contacts and 6% among other contacts (i.e. overall $R=2.7$ in absence of control measures). Results under the assumption of some workplace restrictions remaining in place are shown in Table 4.

Scenario	Number of people quarantined per case	Newly quarantined per day (thousands) assuming 100k new symptomatic cases per day.	Newly quarantined per day (thousands) assuming 25k new symptomatic cases per day.	Newly quarantined per day (thousands) assuming 10k new symptomatic cases per day.
Self-isolation (SI)	1	90	45	9
SI & HH quarantine	3.5	315	158	31.5
SI, HH quarantine + work/school contact tracing	31	2790	1400	279
SI + manual CT of familiar contacts	35	3150	1580	315
SI + manual CT of familiar contacts + limit to 4 daily 'other' contacts	28	2520	1260	252
SI + manual contact tracing of all contacts	48	4320	2160	432
SI + app-based tracing	15	1350	675	135
SI + app-based tracing + limit to 4 daily 'other' contacts	14	1260	630	126
Mass weekly population testing	1	90	45	9

Table 4: Numbers of people isolated/quarantined per symptomatic case under different assumptions about new symptomatic cases per day. We assume quarantined contacts are independent.

Scenario	Baseline assumptions		No pre-symptomatic transmission		Longer delay to self-isolation if symptomatic	
	Reduction	I/Q	Reduction	I/Q	Reduction	I/Q
Self-isolation (SI)	37%	1	51%	1	21%	1
SI & HH quarantine	41%	3.4	55%	3.4	28%	3.5
SI, HH quarantine + work/school contact tracing	58%	32	64%	31	53%	31
SI + manual CT of familiar contacts	61%	34	68%	34	56%	34
SI + manual CT of familiar contacts + limit to 4 daily 'other' contacts	68%	31	72%	30	63%	30
SI + manual contact tracing of all contacts	68%	46	70%	48	67%	46
SI + app-based tracing	49%	16	59%	16	41%	16
SI + app-based tracing + limit to 4 daily 'other' contacts	57%	14	65%	14	49%	14

Table 5: Reduction in transmission and number isolated or quarantined per symptomatic case under different assumptions about pre-symptomatic period and delay to self-isolation. A) No pre-infectious period, i.e. distribution of time to isolation is as follows: P(0 days)=0.05; P(1 days)=0.25; P(2 days)=0.25; (3 days)=0.15; P(4 days)=0.3; P(5 days)=0. B) Longer delay to isolation: P(0 days)=0; P(1 days)=0; P(2 days)=0.05; (3 days)=0.25; P(4 days)=0.25; P(5 days)=0.45.