Using BBC Pandemic data to model the impact of isolation, testing, contact tracing and physical distancing on reducing transmission of COVID-19 in different settings

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Summary
- We used a model of secondary transmission stratified by setting (household, work, school, other) based on BBC Pandemic data from 40,585 UK participants, then simulated a range of different testing, isolation and tracing scenarios.
- Under the scenarios considered, which assumed optimistic but plausible parameter values, combined testing and tracing strategies reduced future infectiousness more than mass testing or self-isolation alone (50–70% vs 5–30%).
- Based on the current estimated level of symptomatic COVID-19 prevalence in the UK, most contact tracing strategies – if implemented immediately – could require over 1m individuals to be quarantined each day.
- If limits are placed on gatherings outside of home/school/work (e.g. maximum of 4 daily contacts in other settings), then partial manual contact tracing (i.e. familiar contacts only) could have a similar effect on transmission reduction as detailed full contact tracing.

Results

Table 1: 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 15% among household contacts and 6% among other contacts (i.e. overall R=2.8 in absence of control measures). Results under the assumption of some workplace restrictions remaining in place are shown in Table 3.

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	–	–	2.8	–
Self-isolation (SI)	Yes	No	–	–	2.2	20%
SI & HH quarantine	Yes	HH only	–	–	2.1	25%
SI, HH quarantine + work/school contact tracing	Yes	HH & work/ school	80% work/school; 50% other	–	1.3	52%
SI + manual CT of familiar contacts	Yes	All	80% work/school; 50% other	–	1.2	56%
SI + manual CT of familiar contacts + limit to 4 daily 'other' contacts	Yes	All	80% work/school; 50% other	–	1	64%
SI + manual contact tracing of all contacts	Yes	All	100%	–	0.8	69%
SI + app-based tracing	Yes	All	60%	–	1.7	38%
SI + app-based tracing + limit to 4 daily 'other' contacts	Yes	All	60%	–	1.4	48%
Mass weekly population testing	No	–	–	10%	2.6	4%

Table 2: Numbers of people isolated/quarantined per symptomatic case under different symptomatic prevalence assumptions. We assume quarantined contacts are independent (actual values may be lower due to correlation in risk in social contact networks) and current UK daily incidence is 100,000 symptomatic cases per day.

Scenario	Number of people quarantined per case	Newly quarantined per day (thousands) assuming current UK prevalence	Newly quarantined per day (thousands) assuming 50% current UK prevalence (i.e. ~2 weeks away)	Newly quarantined per day (thousands) assuming 10% current UK prevalence (i.e. ~1 month away)
Self-isolation (SI)	1	90	45	9
SI & HH quarantine	3.5	315	158	31.5
SI, HH quarantine + work/school contact tracing	33	2970	1490	297
SI + manual CT of familiar contacts	34	3060	1530	306
SI + manual CT of familiar contacts + limit to 4 daily 'other' contacts	31	2790	1400	279
SI + manual contact tracing of all contacts	47	4230	2120	423
SI + app-based tracing	16	1440	720	144
SI + app-based tracing + limit to 4 daily 'other' contacts	14	1260	630	126
Mass weekly population testing	1	90	45	9
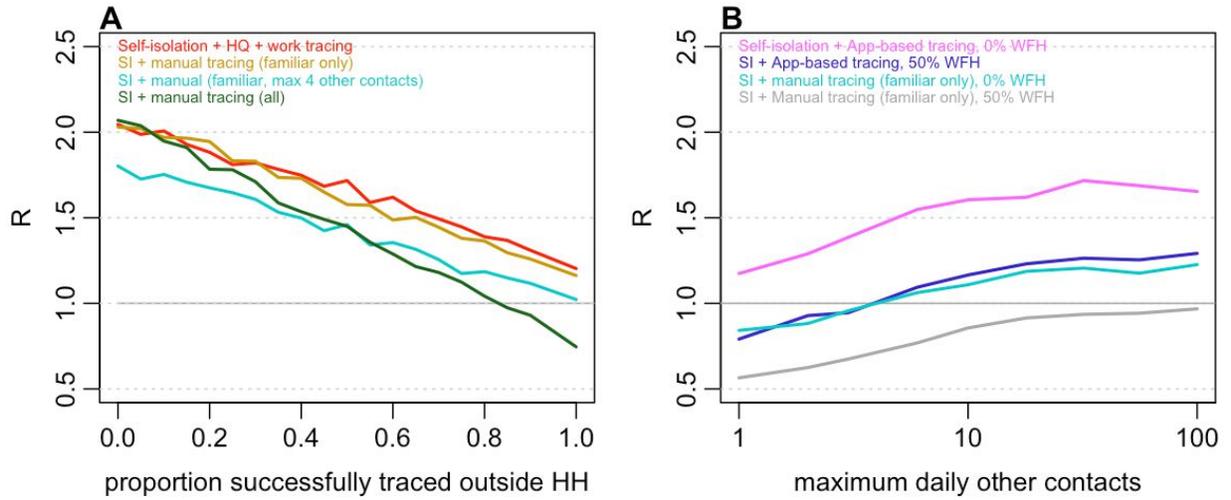
Figure 1: Impact of contact tracing effectiveness and physical distancing on reduction in reproduction number (baseline R=2.8). *A) Reduction in R under different strategies for different proportions of work/school/other contacts that are successfully traced. When no contacts outside the home are traced, the reduction is equivalent to self-isolation and household quarantine only. B) Effect of the maximum limit on 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%).*

Table 3: Mean reduction in effective reproduction number under different control measures when 50% of people have no work contacts. Results from simulated setting-specific secondary transmission, assuming secondary attack rate of 15% among household contacts and 6% among other contacts (i.e. overall R=2.8 in absence of control measures).

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	–	–	2.8	–
Self-isolation (SI)	Yes	No	–	–	1.7	38%
SI & HH quarantine	Yes	HH only	–	–	1.6	43%
SI, HH quarantine + work/school contact tracing	Yes	HH & work/ school	80% work/school; 50% other	–	1.1	60%
SI + manual CT of familiar contacts	Yes	All	80% work/school; 50% other	–	1.0	66%
SI + manual CT of familiar contacts + limit to 4 daily 'other' contacts	Yes	All	80% work/school; 50% other	–	0.7	74%
SI + manual contact tracing of all contacts	Yes	All	100%	–	0.7	75%
SI + app-based tracing	Yes	All	60%	–	1.4	52%
SI + app-based tracing + limit to 4 daily 'other' contacts	Yes	All	60%	–	1	63%
Mass weekly population testing	No	–	–	10%	2.1	26%

Methods

Simulation of individual-level contacts

We used data on 40,585 participants with recorded contacts in the BBC Pandemic dataset (Klepac et al, MedRxiv, 2020). 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 (similar to the approach described in Keeling et al, MedRxiv, 2020). In each simulation, we randomly specify a primary case as either under 18 or 18 and over, based on UK demography (21% under 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 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 (see 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).
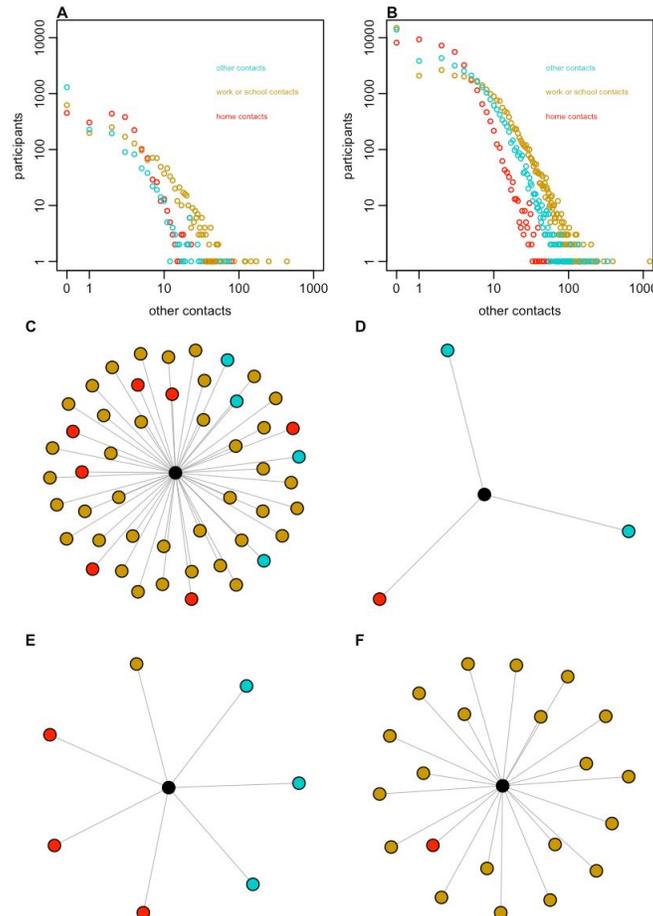
Figure 2: UK social contact patterns. *A) Distribution of daily contacts made at home, work/school and other settings by under 18s in the BBC study. C) Distribution of daily contacts by participants aged 18 and over. Panels C–F show examples of daily social contact patterns for three individuals in the model. Black point shows the individual reporting contacts, with social contacts coloured as in A–C.*

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.

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 = *(number of daily contacts) x (days infectious)* and $p_{inf} = SAR$ x *(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 = *(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(successfully traced)* x *P(individual adheres to quarantine)* . Hence the reduction in effective reproduction number resulting from control measures was equal to $R_{base} - R_{traced}$.
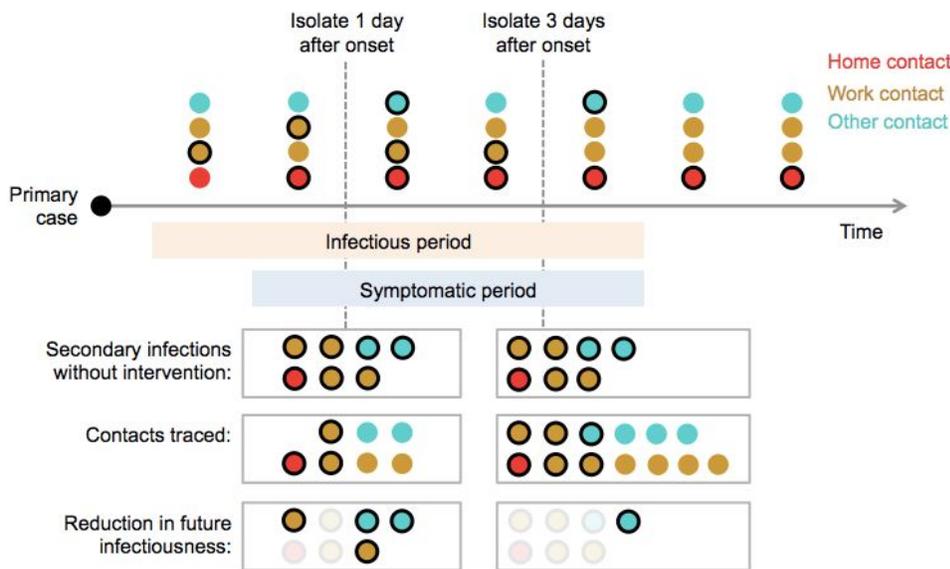
Figure 3: Effect of isolation and contact tracing on reducing future infectiousness. *Timeline shows symptomatic primary case with four daily contacts isolating 1 and 3 days after onset. We assume the household contact is the same person throughout, whereas other contacts are made independently. Had the primary case not been isolated, there would have been 7 secondary cases in this illustration. For isolation 1 day after onset, 7 contacts are traced, 3 of whom are infected; if all are traced and quaratined, overall the control measure results in a 3/7 reduction in effective reproduction number. For isolation 3 days after onset, 13 contacts are traced, 6 of whom are infected; if all are traced and quaratined, overall the control measure results in a 6/7 reduction in effective reproduction number.*

Scenarios

We considered several different scenarios, individually and in combination. These included: no control measures; mass testing of cases regardless of symptoms; self-isolation of symptomatic cases; household quarantine; work/school quarantine; manual tracing of familiar contacts (i.e. have been met before); manual tracing of familiar contacts and a limit on daily contacts made in 'other' settings; manual tracing of all contacts; app-based tracing with a given level of coverage influencing what proportion of people can potentially be traced; and a proportion of the adult population working from home. 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 sampled 10,000 individual-level sets of contact patterns for each scenario.

Risk of infection among household and close contacts

We reviewed contact tracing studies from multiple settings that stratified contacts within and outside household. 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. 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 (Liu et al, Lancet, 2020). In our main analysis, we therefore assume 15% HH SAR and 6% among all contacts, which generated a plausible value for the reproduction number.

Table 4: Secondary attack rates estimated from contact tracing studies.

Study	Country	SAR household	SAR close contacts	Contacts per case	Observed R
Bi et al	Shenzhen	12.9%	0.9%	3.0	0.24
Burke et al	USA	10.5%	0.0%	44.5	0.20
Luo et al	Guangzhou	10.1%	0.5%	14.3	0.34
Cheng et al	Taiwan	13.8%	1.5%	9.1	0.38
Yi et al	Ningbo	13.3%	5.1%	11.2	0.69

Assumed model parameters

Table 5: Parameter definitions and assumptions.

Parameter	Assumed value	Details & references
Individual-level epidemiology		
Reproduction number in absence of control measures	2.8	Follows from SAR assumptions. Consistent with range from CMMID & Imperial College dashboards.
Duration of infectiousness	5 days (for cases that will become symptomatic, 1st day is pre-symptoms)	Implies serial interval of 6.5 days (Bi et al, MedRxiv, 2020)
Relative infectiousness of asymptomatic cases	50%	Point estimate was 65% in Yi et al, (Chinese Journal of Epidemiology, 2020), 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	50%	Davies et al, MedRxiv, 2020; Russell et al, Eurosurveillance, 2020
Probability symptomatic individual will eventually self-isolate and be tested	90%	Assume virus only detectable during infectious period. 90% UK survey respondents said would likely comply with app request to self-isolate if rapid test available (Abeler et al, Oxford working paper, 2020)
Effective duration of infectiousness if self-isolate when symptomatic	P(1 days)=0; P(2 days)=0.05; P(3 days)=0.35; P(4 days)=0.4; P(5 days)=0.2.	Assume most likely to self-isolate on days 2–5 of infectious period (i.e. 1–4 days after onset). For 263 cases with known date of onset and confirmation in Singapore, of those who were confirmed within 4 days, 3% were confirmed on date of onset, 37% on second day, 40% on 3rd day, and 20% on 4th day. [https://github.com/beoutbreakprepared /nCoV2019]
Contact tracing		
Secondary attack rate among contacts in home	15%	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.
App-based tracing		
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 (2011 Census), so we assume 71% of population use smartphones. 75% of UK survey respondents said would probably or definitely download app (Abeler et al, Oxford working paper, 2020)
Mass testing		
Proportion of population that can be tested per week	10% (i.e. 4.2 million per week)	10,000 tests per million per day (i.e. 10x the highest number of daily tests performed anywhere in world so far: https://ourworldindata.org/covid-testing)