

An imperfect tool: COVID-19 ‘test & trace’
success relies on minimising the impact of false
negatives and continuation of physical
distancing.

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1

Abstract

2 The increasingly evident role of asymptomatic and pre-symptomatic trans-
3 mission means testing is central to COVID-19 control, but test sensitivity
4 estimates are low (around 65%). We extend an existing branching pro-
5 cess contact tracing model, adding diagnostic testing and refining parameter
6 estimates. Poor test sensitivity potentially reduces the efficacy of contact
7 tracing, due to false-negative results impacting quarantine. We show that,
8 counter-intuitively, faster testing could also reduce operational test sensitiv-
9 ity, exacerbating this effect. If sensitivity-based risks are mitigated, we find
10 that contact tracing can facilitate control, but small changes in the popula-
11 tion reproduction number (1.3 to 1.5) could impact contact tracing feasibility.

12 Main

13 In December 2019, SARS-CoV-2, a novel coronavirus strain, was detected
14 in Hubei Province, China [1]. By 31st January 2020 the first UK cases of
15 COVID-19, the disease caused by SARS-CoV-2, were confirmed [2]. Ini-
16 tial modelling studies indicated that fast and effective contact tracing could
17 contain the UK outbreak in most settings [3, 4]. However, by 20th March
18 there were almost 4,000 confirmed cases nationwide [5], at which point the
19 UK Government halted national contact tracing and scaled up physical dis-
20 tancing measures, including the closure of schools and social venues, ex-
21 tending to heightened restrictions on non-essential travel, outdoor activities
22 and between-household social mixing [6]. Similar patterns occurred in other
23 countries [7, 8].

24 By early May 2020 these measures were estimated to have reduced the
25 effective reproduction number, R , from 2.6 to 0.62 [9, 10] and so from 12th–
26 13th May in England some limitations on outdoor exercise were lifted and
27 workers encouraged to return to work if they could maintain physical dis-
28 tancing [11].

29 Capacity for diagnostic testing in the UK, as in other countries, has been
30 escalated over recent months, with capacity reaching over 300,000 tests a day
31 by the end of June (<https://coronavirus.data.gov.uk/testing>). Cur-
32 rently, testing of asymptomatic individuals is limited to staff and patients
33 in NHS and social care facilities [12], but on the 28th of May the UK Gov-
34 ernment rolled out the initial stages of their ‘Test & Trace’ contact tracing
35 programme to the general population, which aims to follow chains of trans-
36 mission and use isolation to prevent onward spread. Since the beginning of
37 ‘Test & Trace’ over 3 million people were tested by the end of July, just under
38 50,000 of which were positive [13].

39 Crucially, the current strategy only tests symptomatic contacts and noti-
40 fies individuals that they no longer need to isolate following a negative test,
41 which comes back in 24 or 48 hours depending on type of test [13]. However,
42 there are critical limitations to the diagnostic test, with poor sensitivity (cur-
43 rent estimates imply close to 65% [14, 15]), especially in community-based
44 settings, leading to high false negative rates which are exacerbated by high
45 variability in symptom severity [15]. Infectious individuals who test falsely
46 negative may prematurely resume their normal activities, contributing to
47 ongoing chains of transmission: reliance on testing of contacts will always
48 reduce the effectiveness of contact tracing, potentially substantially [16].

49 Imperfect adherence and the innate difficulties in identifying contacts will
50 pose challenges for ‘Test & Trace’, particularly in crowded urban settings [17].
51 Therefore, evaluating both the limitations of contact tracing and how to
52 maximise its effectiveness could be crucial in preventing an exponential rise in
53 cases, which might see contact tracing capacity rapidly exceeded and stricter
54 physical distancing measures required [18].

55 As our knowledge of the transmission dynamics of SARS-CoV-2 grows,
56 extending Hellewell et al.’s [3] UK-focused contact tracing study with new
57 insights could inform this ‘Test & Trace’ strategy. The key conclusion of the
58 initial study was that highly effective contact tracing would be sufficient to
59 control an initial outbreak of COVID-19 in the UK, however substantial new
60 evidence supports much higher pre- and asymptomatic transmission rates
61 than had initially been considered [19, 20, 21]. The focus on rapid testing
62 in the UK contact tracing programme also requires a detailed assessment of
63 the associated trade-offs through mechanistic modelling of the testing pro-
64 cess. Up-to-date modelling studies are therefore needed to investigate the
65 feasibility of contact tracing and the conditions under which it is effective.

66 We use improved incubation period and serial interval estimates [22, 23,
67 24], consider imperfect self-reporting and tracing rates and simulate the use
68 of diagnostic tests for both detection and tracing of asymptomatic infection
69 chains. We also simulate decision-making regarding quarantine procedures
70 for traced individuals and explore the trade-offs introduced by poor test sen-
71 sitivity, particularly when negative test results are used to advise individuals
72 to cease self-isolation.

73 **Results**

74 **Testing**

75 By comparing the time individuals are tested after exposure in the model
76 to temporal estimates of PCR test sensitivity [15] we see that an average of
77 65% sensitivity is a relatively realistic expectation if testing is conducted 2 or
78 more days post-isolation (Figure 1a). Test sensitivity is expected to peak at
79 just over 75% 8 days post-exposure, but the majority of testing in the model
80 occurs between 4 and 7 days post-exposure, where sensitivity estimates have
81 more variance.

82 In the case of a 2 day testing delay, 29.3% of cases are tested before 5 days
83 post-exposure, at which point sensitivity estimates are around 62%, and only

84 10.2% of cases are tested before 4 days post-exposure. The time-weighted
85 average of expected test sensitivity for all cases tested in the model with a 2
86 day delay is 68.0%. For a 4 day test delay, less than 1% of cases are tested
87 before day 5 post-exposure, but just under 10% are tested after day 14, when
88 test sensitivity drops to 61%.

89 However, in the case of immediate testing, 65% sensitivity could be a
90 substantial over-estimate, with 64.5% of cases being tested before 5 days
91 post-exposure and 48.9% before 4 days, meaning the test could be less than
92 33% sensitive for around half of all cases tested.

93 Even if test sensitivity was constant, the timing of testing and quarantine
94 duration has an impact on the risk of a large outbreak (at least 2,000 cases)
95 and can undermine the positive impact of testing within a contact tracing
96 programme. The probability of a large outbreak occurring is greater with
97 an assumed test sensitivity of 65% compared to scenarios where no testing
98 was carried out at all if testing is rapid and results in an immediate return
99 to normal behaviour (Figure 1b, upper left panel). This result was observed
100 across all contact tracing coverage rates. The deleterious effect of releasing
101 false negative cases is mitigated by using a precautionary seven-day quaran-
102 tine period, which reduced the risk of a large outbreak 11.7% to 3.9% for
103 $R_S = 1.3$ with 60% contact tracing (Figure 1b).

104 A two day delay in carrying out the tests also led to a decrease in the
105 probability of a large outbreak, from 11.7% to 6.3% for R_S of 1.3. Combining
106 the two-day delay in testing and the seven-day precautionary quarantine
107 reduced the risk of a large outbreak further, from 11.7% to 3.4% for $R_S =$
108 1.3 and 60% contact tracing.

109 In the case of instant testing and an immediate end to quarantine if the
110 test is negative, there was a comparatively small benefit from scaling up
111 of contact tracing coverage from 0% to 100%, implying that much of the
112 potential positive impact of contact tracing could be lost if such an approach
113 were taken.

114 Whilst a test with 65% sensitivity and no minimum quarantine period
115 can reduce the benefits of contact tracing, if a test were to be 95% sensitive,
116 this would improve the outcome compared to no testing in all scenarios.
117 However, with a two-day test delay and seven-day precautionary quarantine
118 a 65% sensitive test is almost as effective in reducing transmission as a 95%
119 sensitive test due to this strategy ensuring quarantine of all cases during peak
120 transmission periods irrespective of test result.

121 Case detection

122 Even with perfect contact tracing and employing good diagnostic practices
123 (100% of contacts traced in 24 hours and a minimum quarantine period of
124 7 days), a large proportion of cases are likely to go unobserved (Figure 2).
125 High levels of symptomatic self-reporting to the tracing programme and im-
126 proved test sensitivity can increase case detection: 95% sensitivity and 100%
127 self-reporting gives an increase from 30.5% to 73.9% compared to 65% sensi-
128 tivity and 50% self-reporting (both for $R_S = 1.3$). However, this still results
129 in 26.1% of cases being missed, hence detecting every case is essentially in-
130 feasible.

131 Super-spreading events

132 Every missed case is a potential new chain of transmission and, given the high
133 heterogeneity in the secondary case distribution, characterised by dispersion
134 parameter k , there is a substantial risk of super-spreading events. Consid-
135 ering a scenario with poor adherence to self-reporting guidelines and where
136 one missed case leads to a cluster of either 5 or 100 new cases, we assume
137 observation of the outbreak only occurs when the first case is hospitalised,
138 after which contact tracing may be initiated (Figure 3a and b).

139 For a cluster of 5 new cases the median total unobserved outbreak size
140 before the first case is hospitalised is 13 cases for $R_S = 1.3$ and 16 cases for
141 $R_S = 1.5$, which translates to 8.0% and 36.9% probability of a large outbreak
142 respectively if 60% contact tracing can be implemented (Figure 3c). For a
143 cluster of 100 new cases the median is 219 for $R_S = 1.3$ and 238 for $R_S = 1.5$,
144 translating to 36.3% and 84.9% probability of a large outbreak with 60%
145 contact tracing. This emphasises the importance of maintaining physical
146 distancing measures that restrict the attendance of indoor social gatherings
147 to avoid super-spreading events which could rapidly escalate.

148 Additional observations

149 More generally, the probability of a large outbreak given the current outbreak
150 size (Figure 3c) could be used to assess at what point during an epidemic
151 contact tracing would be unable to control transmission, as well as to inform
152 targets for coverage and speed. In our model both the time taken to trace
153 contacts and the proportion of contacts traced had effects on the risk of a
154 large outbreak, although increasing tracing speed may have the counter-effect

155 of reducing average test sensitivity due to impact on test timing with respect
156 to exposure.

157 We also found that higher contact tracing coverage results in a lower
158 overall number of individuals which are traced, tested and quarantined, due
159 to the lower outbreak size. This means that achieving greater efficacy in
160 tracing will ultimately require fewer resources. However, these resources are
161 likely to be needed in a more condensed period of time.

162 **Conclusions**

163 Our results show that with a test sensitivity of 65%, fast testing which rec-
164ommends infected but false-negative individuals to cease quarantine could be
165 counter-productive, undermining contact tracing efforts, and may be worse
166 than not testing. However the impact of low test sensitivity could be miti-
167gated by applying a minimum quarantine period to all traced contacts and
168 using positive tests to prompt further contact tracing. This would allow
169 negative individuals to leave quarantine comparatively early, but not imme-
170diately upon receipt of test result. Simply slowing down the decision-making
171 process, so any false negative tests occur later in the infectious period, will
172 also reduce the amount of transmission caused by premature cessation of
173 quarantine and potentially increase likelihood of a more accurate test re-
174sult [15]. Control policies in some countries are being designed to account
175 for the high proportion of false negative individuals: for instance Greece
176 requires negative-testing international arrivals to self-quarantine for seven
177 days [25]; in Singapore two negative tests 24 hours apart are required to
178 release from quarantine [26].

179 We show that even a test with low (65%) sensitivity can improve contact
180 tracing outcomes if the impact of false negative cases can be limited by
181 employing appropriate precautionary measures. This effect is seen because
182 testing can bridge asymptomatic links in transmission chains that would
183 otherwise have been missed, although there is some uncertainty surrounding
184 the infectiousness of asymptomatic individuals [23]. Nonetheless, this benefit
185 is only possible, provided testing is applied to all contacts, not just those
186 displaying symptoms as was the initial UK policy.

187 Testing asymptomatic contacts would require more testing and resources,
188 as well as potentially testing individuals earlier in their infectious period,
189 before symptom onset. Earlier testing increases the impact of immediate
190 quarantine cessation for false negative cases, so this would require a minimum

191 quarantine period. Despite these considerations, if very good contact tracing
192 can be implemented from the beginning of the outbreak then fewer total
193 resources will be required because of a smaller final outbreak size, meaning
194 the key factor for feasibility will be time-limited resource access.

195 We demonstrated that small increases in the reproduction number un-
196 der physical distancing measures, R_S , has a large impact on the feasibility
197 of contact tracing. We only consider values of R_S up to 1.5, which is still
198 substantially lower than estimates of R_0 in the absence of any interventions
199 ($R_0 \approx 2.7$ [27]), but may be achievable with partial interventions. Our esti-
200 mates of R_S reflect a decrease in social contacts of almost 50% but even 60%
201 coverage and a one day trace time is insufficient to negate the risk of a large
202 outbreak. This reiterates that physical distancing is still critical, even with
203 highly effective contact tracing, and that contact tracing will likely be insuf-
204 ficient to allow a complete return to normal life without additional measures,
205 such as an effective vaccine.

206 In addition to general physical distancing, the risk posed by a single large
207 super-spreading event means that relaxing restrictions on large gatherings,
208 particularly indoors, could lead to a rise in case numbers, especially in com-
209 munities where self-reporting rates are expected to be poor. Even with very
210 low $R_S = 1.1$, a local cluster of 100 unobserved cases could approximately
211 double in size before being detected.

212 However, we found that the risk of a large outbreak ($\geq 2,000$ cases) was
213 relatively low for $R_S = 1.1$ no matter what the contact tracing and testing
214 strategy. What is of note to national governments who are exiting extreme
215 social distancing is that a dramatic change in the dynamics occurs in the
216 small absolute increase of R_S to 1.3. At $R_S = 1.1$ with a poorly resourced
217 or ineffective contact tracing system the probability of a large outbreak is
218 roughly 1%. However when $R_S \geq 1.3$ then an ineffective contact tracing
219 system becomes noticeable, at which stage it is too late to act.

220 A number of our assumptions may cause our results to appear unduly
221 optimistic. For example, we model a scenario with very low initial case num-
222 bers and assume that tracing can be initiated before test results are received,
223 and that contacts of up to 3 days pre-onset are traced. This means there
224 is potentially an increased requirement for maintaining physical distancing
225 measures, even if contact tracing is deployed at high coverage nationwide.

226 We also consider the test to have a fixed sensitivity over the course of
227 infection, whereas previous studies show that testing too early or late after
228 exposure can dramatically increase false negative rates [15]. However, these

229 temporal estimates ignore variation in the incubation period, assuming a
230 fixed onset time of 5 days. Additionally, high between-person variance has
231 been observed in the natural history of infection [23]. It is therefore unclear
232 what is driving these temporal changes in sensitivity or whether this temporal
233 profile makes sense on an individual basis.

234 Furthermore there were worrying trends in adherence to movement re-
235 strictions towards the end of “lockdown”, suggesting that recommended quar-
236 antine through the ‘Test & Trace’ programme may also be affected; an un-
237 published study of 90,000 adults across the UK in the two weeks up to 25th
238 May found that lockdown adherence may have dropped to 50% [28]. Our as-
239 sumption of 90% untraced symptomatic individuals self-isolating is therefore
240 at the upper end of realistic, although symptomatic individuals will perhaps
241 be more cautious or less mobile due to the burden of symptoms. However,
242 this could also have repercussions on assuming that contact-traced individu-
243 als will self-isolate when asked to do so, particularly if asymptomatic.

244 Modelling studies in other countries have proposed combinations of con-
245 tact tracing and population-level mitigation strategies [29] and a recent UK
246 study puts R_S in the range of 1–1.6 for a combination of school closures,
247 50% reduction in social contacts and elderly shielding [10]. This covers the
248 range of values considered in this study and demonstrates the potential level
249 of physical distancing together with high-coverage contact tracing to keep
250 the effective reproduction number below one.

251 We also assume the Negative Binomial dispersion, k , of secondary cases,
252 does not vary with R_S due to different social distancing measures. This
253 relationship is poorly characterised, but it is believed that social distancing
254 may increase k , leading to decreased heterogeneity in number of contacts,
255 potentially making outbreak control harder, although this effect is expected
256 to be at least cancelled out by the reduction in the mean [30]. Furthermore
257 it is also possible that less heterogeneity in contacts may make tracing of
258 individual contacts more feasible, allowing for a higher coverage.

259 Contact tracing improvements include *secondary contact tracing* as seen
260 in Vietnam, i.e. tracing the contacts of contacts of known cases, to get ahead
261 of the chain of transmission [31]. The use of a digital tracing app across
262 the UK if combined with manual tracing could boost tracing coverage [32]
263 and interactive dashboards are being rolled out across a number of countries
264 to inform modelling efforts and raise public awareness [33]. Backwards con-
265 tact tracing, whilst highly labour intensive, could also fill vital gaps where
266 transmission links have been missed [34]. As experience in contact tracing

267 develops, it will also likely be possible to give contacts a prior probability of
268 infection (based on the duration and contact setting for example) and com-
269 bine this with the test results to give a more accurate measure by which to
270 determine isolation requirements.

271 Overall, we conclude that contact tracing could bring substantial benefits
272 to controlling and preventing outbreaks, with tracing coverage and speed
273 playing an important role, as well as testing. However, any ‘test & trace’
274 strategy must carefully consider the limitation of poor test sensitivity, as well
275 as the additional tracing information obtained from testing asymptomatic
276 individuals. Poorly sensitive tests are inappropriate for ruling out a diagnosis,
277 and infectious individuals immediately halting quarantine following a false
278 negative result could have dangerous implications. In line with previous
279 studies [8], we have demonstrated that contact tracing alone is highly unlikely
280 to prevent large outbreaks unless used in combination with evidence-based
281 physical distancing measures, including restrictions on large gatherings.

282 **Methods**

283 In this extension of a previous COVID-19 branching process model [3], the
284 number of potential secondary cases generated by an index case is drawn
285 from a Negative Binomial. The exposure time for each case, relative to in-
286 fector onset, is drawn from a shifted Gamma distribution that allows for
287 pre-symptomatic transmission and is left-truncated to ensure secondary case
288 exposure time is after the primary case exposure time. Secondary cases are
289 averted if the primary case is classified as ‘quarantined’ at the time of infec-
290 tion, assuming within household segregation is possible. The probability of
291 quarantine depends on whether the primary case was traced, any test result,
292 and adherence to self-isolation recommendations (Figure 4). Each simulation
293 was seeded with five infected individuals that are initially undetected by the
294 contact tracing system.

295 **Secondary case distribution**

296 A standard Negative Binomial assumption was used to represent hetero-
297 geneity in onward transmission due to factors such as individual contact
298 patterns or infectiousness, with the mean relating to the *effective repro-*
299 *duction number under physical distancing* R_S which takes a value of 1.1,
300 1.3 or 1.5 with a constant dispersion parameter $k = 0.16$, as used in the

301 original analysis [30, 3]. The estimates of k for SARS-COV-2 are wide-
302 ranging, from $k = 0.1$ (*range* : 0.05 – 0.2) for pre-lockdown UK [34] to
303 $k = 0.25$ (*range* : 0.13 – 0.88) for Tianjin, China during lockdown mea-
304 sures [35]. Due to the variation in the literature we have not updated this
305 parameter as 0.16 lies within these ranges and it is not yet possible to derive
306 accurate national estimates of k for post-lockdown scenarios. Here a smaller
307 k represents greater heterogeneity in transmission and results in the majority
308 of index cases leading to no secondary infections, while a small proportion of
309 individuals infect a large number of secondary cases. All parameter estimates
310 and references can be found in Table 1.

311 **Generation interval**

312 The incubation period (time from exposure to symptoms) is assumed to fol-
313 low a Lognormal distribution with mean 1.43 and standard deviation 0.66
314 on the log scale [22]. Each new case is then infected at an exposure time
315 drawn from a Gamma-distributed infectivity profile (shape = 17.77, rate =
316 1.39 day^{-1} , shift = 12.98 days) relative to their infector’s symptom onset.
317 If this time is before the infector’s exposure then this value is rejected and
318 re-sampled to prevent negative generation intervals. This Gamma distribu-
319 tion has been fitted under these sampling assumptions to serial interval data
320 published by He et al. [23] using the `fitdistr` package in R and our resulting
321 distributions qualitatively match those presented in the original paper (Fig-
322 ure 5). The exposure time is then compared to the isolation times of the
323 infector and cases are averted if the infector is in isolation when the infection
324 event would have happened. For non-averted cases, symptom onset times are
325 then drawn from the Lognormal incubation period distribution and the prob-
326 ability of a case remaining asymptomatic throughout their infected period is
327 fixed at 40% [19, 20].

328 **Contact tracing**

329 New cases are identified either through tracing contacts of known cases or
330 symptomatic individuals self-reporting to the system, which we model as a
331 two-stage process. Firstly, if an individual is symptomatic (i.e. has a fever
332 and/or dry persistent cough) but untraced we assume that a combination of
333 reduced social activity due to illness, and awareness of COVID-19 preven-
334 tion measures, results in a 90% chance of self-isolation one day after symptom

335 onset. Secondly, individuals who self-isolate in this way then have a proba-
336 bility of contacting the tracing programme and reporting their symptoms as
337 a potential case, which can be varied in the model.

338 The assumption of 90% self-isolation relies on high levels of public aware-
339 ness and draws on evidence from COVID-19 studies in the United States
340 and Israel that suggest 87.3% to 94% of individuals may isolate if they had
341 COVID-19 symptoms [36, 37]. These figures are supported by a US-based
342 2013 study that reports 72% of respondents would stay at home if they had
343 flu-like symptoms, provisional on access to sick pay [38], without the ad-
344 ditional factor of social responsibility introduced by pandemic awareness.
345 However, it is important to note that this figure may still be optimistic, with
346 one study reporting 62.2% of Japanese citizens surveyed went to work within
347 seven days of onset of symptoms [39] and another that 75.1% of individuals
348 living in a UK households with COVID-19 symptoms admit to leaving the
349 house in the last 24 hours [40].

350 Contact tracing is initiated where an existing case has been identified
351 and isolated. The contacts of that individual are then traced with 40%–
352 100% coverage. If a contact is successfully traced they will always isolate.
353 The time taken to trace and isolate a contact is either one day or drawn from
354 a Uniform distribution of 1–4 days. In the absence of testing, traced contacts
355 are assumed to isolate until non-infectious—approximately 14 days [23]. Any
356 contacts that show symptoms or test positive will have their contacts traced;
357 this continues until no further cases result in transmission chain extinction.

358 **Testing**

359 In simulations that include testing, we assume test sensitivities of 65% or
360 95% with the lower value representing true sensitivity observed in healthcare
361 settings [14, 15] and the higher value being closer to measurements in con-
362 trolled conditions [41] and also to demonstrate utility of an alternative testing
363 protocol with higher sensitivity. Due to the nature of the branching process
364 model, only infected individuals are modelled so the impact of test specificity
365 cannot be assessed under these methods, although the implications would be
366 related to programme feasibility rather than efficacy. Current specificity es-
367 timates are believed to be reasonably high in comparison [42, 16, 43], with
368 some estimates of close to 100%, but false positive tests could lead to unnec-
369 essary negative socioeconomic impact under any scheme requiring quarantine
370 of healthy individuals.

371 When testing is included in the model, all individuals that either self-
372 report to the contact tracing system (individual A in Figure 4), or are traced
373 contacts (B & D in Figure 4), are tested. From the moment a contact self-
374 reports or is traced, either a zero- or two-day delay is simulated before the
375 test result is returned, chosen to be representative of UK programme tar-
376 gets. If a positive test is returned, the individual’s contacts are traced. If a
377 negative test is returned, two different scenarios are explored; either a) im-
378 mediate departure from quarantine, or b) the individual is asked to complete
379 a precautionary quarantine period (e.g. 7 days from beginning of isolation).
380 Any contacts of a negative-testing case that were successfully identified prior
381 to receiving the test result are still isolated and tested.

382 **No active case detection**

383 A scenario in which there is no active case detection in the community is
384 considered whereby the only detected cases are those who are hospitalised.
385 This is simulated by reducing the case reporting proportion to 6%, reflect-
386 ing the hospitalisation rate in the UK [44]. Time from symptom onset to
387 hospitalisation is drawn from an Exponential distribution with mean 5.954
388 days (fitted to data published alongside a modelling study [44]). We then
389 defined the undetected outbreak size as the number of cases that were ex-
390 posed prior to the first hospitalisation, given an initial seeding of 5 index
391 cases at $t = 0$. We also consider a scenario of 100 index cases to represent a
392 mass super-spreading event, such as the large outbreaks seen in meat-packing
393 plants across Europe [45] or an instance in the SARS outbreak where a flight
394 attendant is thought to have infected more than 100 individuals [46].

395 **Simulation process**

396 Results presented are the combined output of 5,000 simulations for each
397 parameter combination, or scenario, considered. These results are used to
398 derive the probability of a large outbreak given a range of conditions. A
399 *large outbreak* is considered to be 2,000 cases and each simulation is run
400 for a maximum of 300 days. The threshold of 2,000 cases was chosen by
401 running simulations with a maximum of 5,000 cases and noting which of the
402 simulated epidemics that went extinct; 99% of extinction events occurred
403 before reaching 2,000 cases. The model was written in R and the code is
404 publicly available in an online GitHub repository (<https://github.com/>

405 `timcdlucas/ringbp`).

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Parameter	Values	Refs
Number of initial cases	5, 100	range
Effective reproduction number under physical distancing, R_S	1.1, 1.3, 1.5	range
Dispersion of R_S , k	0.16	[30, 3]
Proportion asymptomatic	40%	[19, 20]
Delay: onset to isolation	1 day	
Incubation period (Lognormal)	mean log: 1.43	[22, 23]
Incubation period (Lognormal)	sd log: 0.66	[22, 23]
Infection time (Gamma)	shape: 17.77	[23]
Infection time (Gamma)	rate: 1.39 day ⁻¹	[23]
Infection time shift	-13.0 days	[23]
Untraced self-isolation prob.	90%	[36, 37, 38]
Self-reporting probability	0.5–1.0	range
Contact tracing coverage	0–100%	range
Min time to trace contacts	1 day	
Max time to trace contacts	1–4 days	range
Test sensitivity	65%, 95%	[15, 14, 41]
Delay: isolate to test result	0–2 days	range
Isolation duration if -ve test	0–7 days	range
Proportion cases hospitalised	6%	[44]
Onset to hospitalisation (Exp)	mean: 5.95 days	[44]

Table 1: Model parameters values/ranges. Parameters taken from the literature are fixed and for other parameters a range of values are explored.

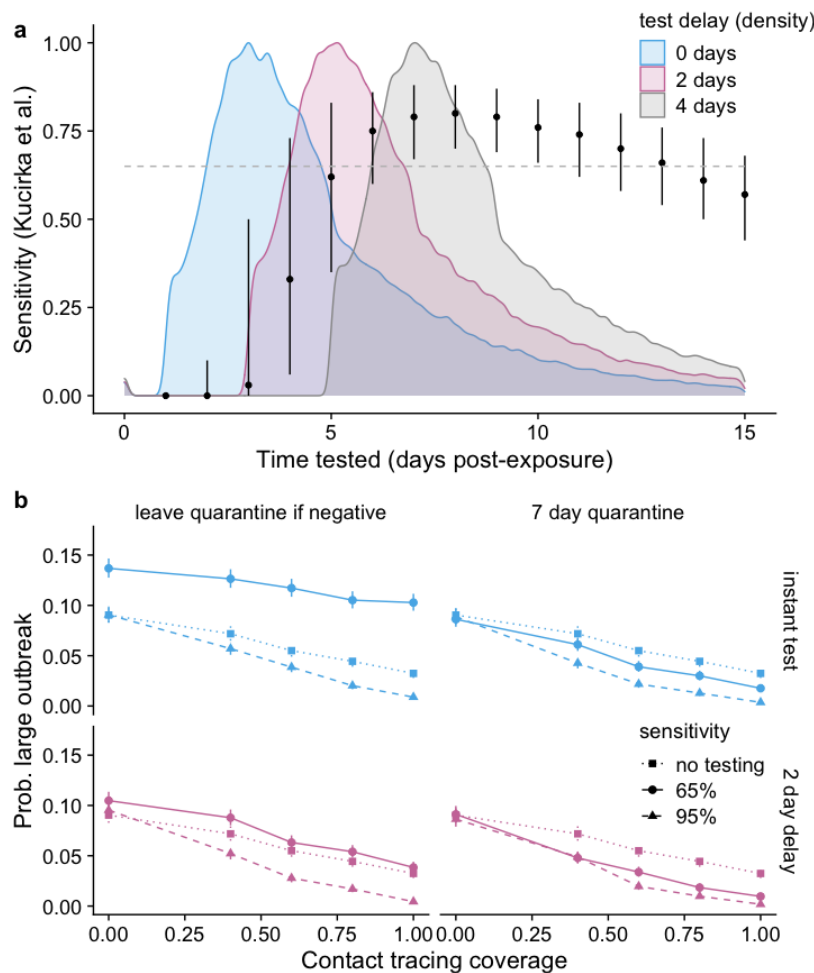


Figure 1: **Test sensitivity and mitigation.** **a)** Normalised density distributions of time cases are tested in our model, measured in days post-exposure, for an immediate test upon identification (blue), a 2 day delay to testing (pink) and a 4 day delay (grey) for $R_S = 1.3$. Black data points are temporal sensitivity estimates from Kuchirka et al. [15]. Grey dashed line represents 65% sensitivity (as assumed in the model). **b)** Comparing effectiveness of test-and-release of negative-testing cases (left-hand panels) with a minimum seven-day quarantine period (right-hand panels). Assuming 65% sensitivity; 50% self-reporting; 1 day trace delay. Error bars: 95% confidence intervals from simulation output variation.

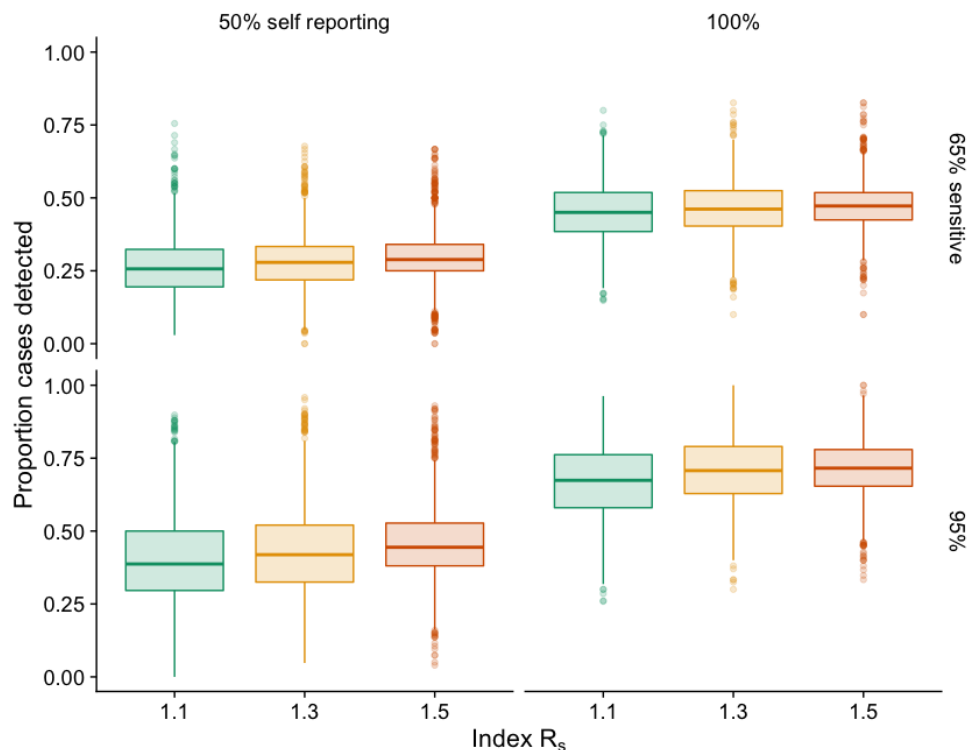


Figure 2: **Case detection.** Proportion of cases detected for varying self-reporting of symptomatic cases (50% and 100%) and diagnostic test sensitivity (65% and 95%). Effective reproduction number under physical distancing: $R_S = 1.1, 1.3$ and 1.5 . Box boundaries represent lower (25%), median (50%) and upper (75%) quartiles; whiskers represent the full range of values, excluding outliers, which are marked individually.

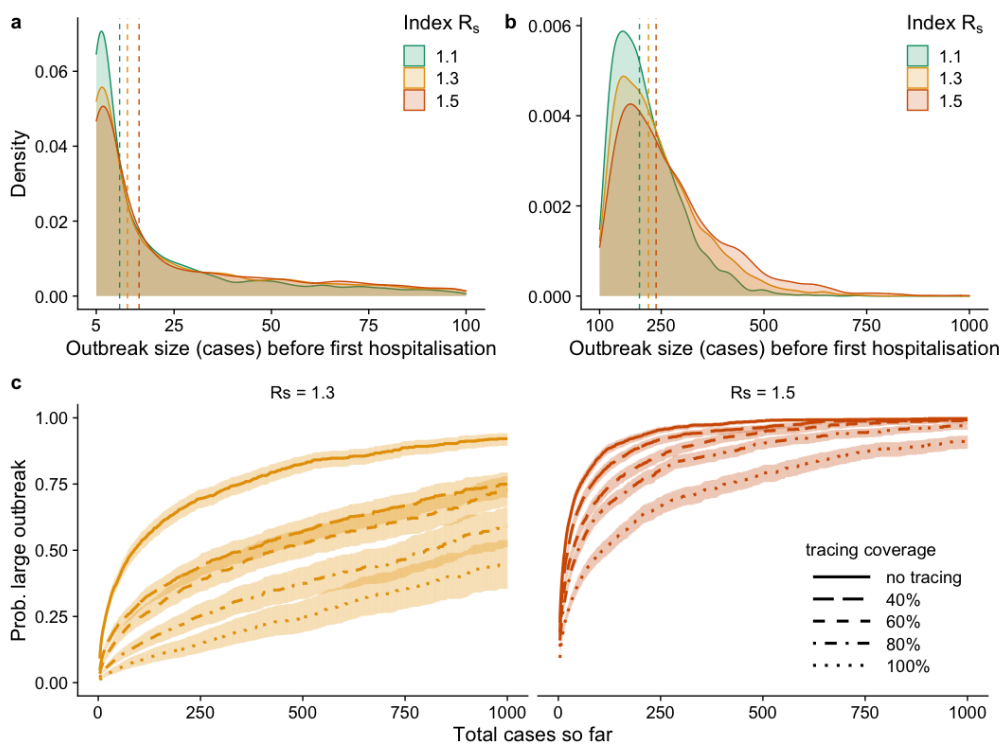


Figure 3: **Super-spreading scenarios.** **a)** Total cases occurring before first hospitalisation in a population with no active tracing or case detection from one super-spreading event (5 new cases). **b)** Same as a) but with 100 new cases. Vertical dashed lines represent median values. **c)** Probability of outbreak by total number of cases so far. Sensitivity = 65%, self-reporting proportion = 50%, individuals testing negative are isolated for a minimum of 7 days, time to test from isolation = 2 days. Error windows: 95% confidence intervals calculated from simulation output variation.

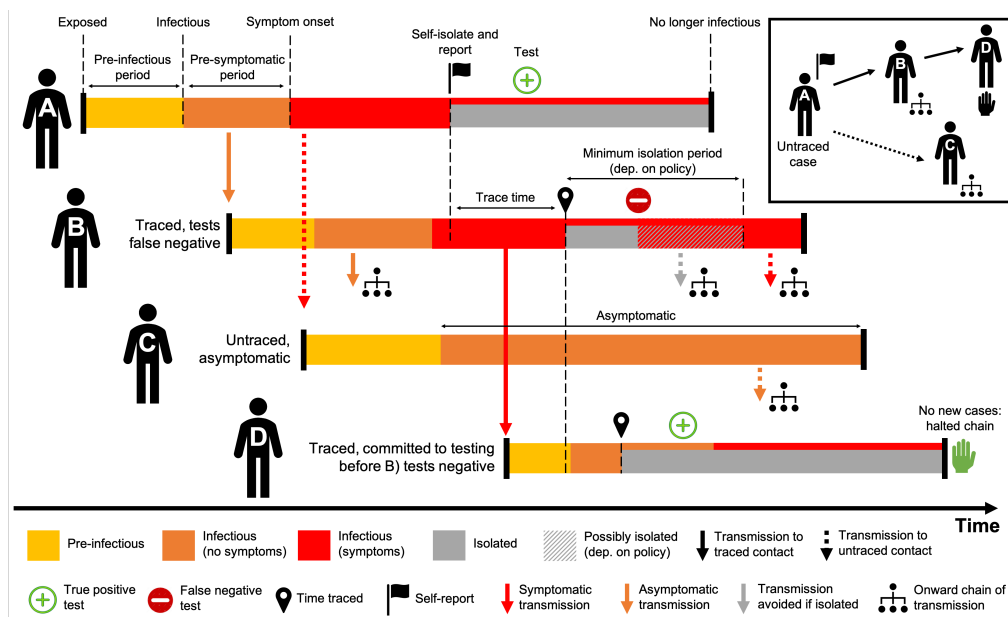


Figure 4: **Contact tracing schematic.** Overview of the contact tracing process implemented in our model. **Person A** isolates and self-reports to the contact tracing programme with some delay after symptom onset, by which time they have infected Persons B and C. When Person A self-reports contact tracing is initiated. They are then tested with positive result and remain isolated for their infectious period. **Person B** was infected by A prior to their symptom onset and is detected by tracing after some delay, after infecting Person D. After isolating they are tested, with a false negative result. This leads to B either a) stopping isolation immediately or b) finishing a minimum 7 day isolation period. Both may allow new onward transmission. **Person C** was infected by A but not traced as a contact. Person C does not develop symptoms but is infectious, leading to missed transmission. **Person D** was traced and tested before the false negative test was returned for Person B. The test for D returns positive, meaning that D remains isolated, halting this chain of transmission.

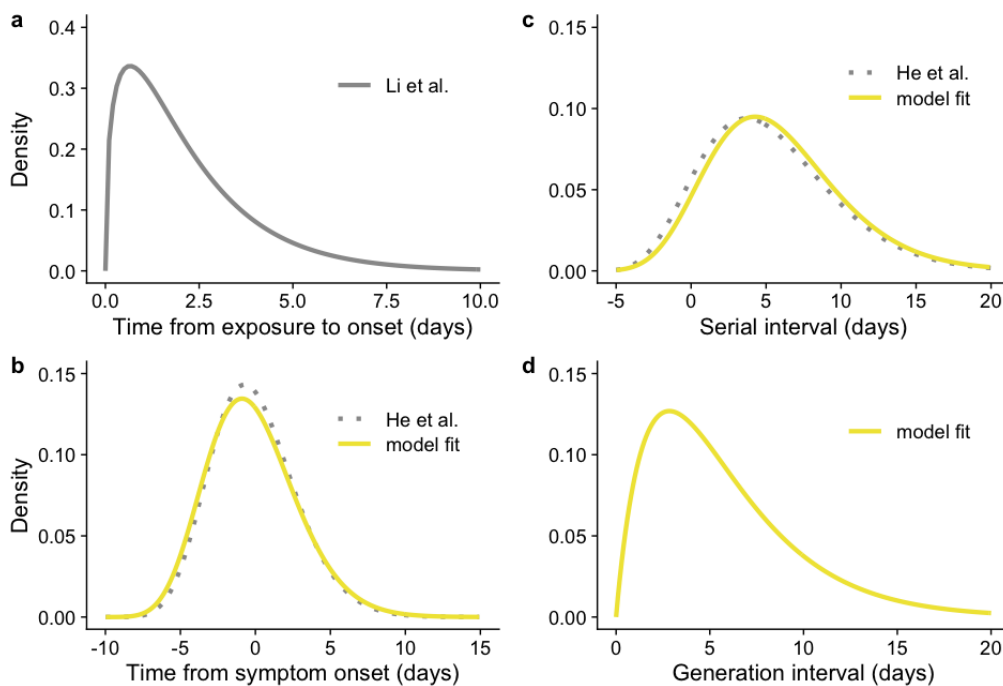


Figure 5: **Parameters' distributions.** Distributions for **a)** incubation period (exposure time to symptom onset) from Li et al. [22]; **b)** transmission profile relative to symptom onset, fitted to data and compared to He et al. [23]; **c)** serial interval, fitted and compared to He et al. [23]; and **d)** generation interval, combined distribution from a) and b) with re-sampling to prevent negative serial intervals, as described in the main text.

