Supplementary Information

Contents

1 Model definition

Our analyses are based on a model first developed for ring vaccination for smallpox [1], and which we adapted to describe the spread of COVID-19 with isolation and contact tracing [2]. The model describes transmission with a discrete time branching process, and keeps track of numbers of latent and infectious individuals, numbers of diagnosed cases, and numbers of isolated infected individuals. The model distinguishes between close contacts (e.g. in the household) and casual contacts.

We use the following notation:

- $E_{t,\tau}$ is the number of persons infected at time $t-\tau$, who are still latently infected (i.e. infected but not yet infectious) at time t.
- $I_{t,\tau}$ is the number of persons who became infectious at time $t-\tau$, who are still infectious and not isolated at time t.
- $Q_{t,\tau}$ is the number of persons who because infectious at time $t-\tau$, who are in isolation at time t.
- D_E is the maximum duration of the latent period. The default value is 3 days.
- D_I is the duration of the infectious period (including persons in isolation). The default value is 10 days. See below for details.

The time dynamics of the model are implemented as a set of difference equations with a time step of 1 day. We did not use time dependent simulations in this paper, therefore we will not describe the time dependent model further here. Some results for the time dependent evolution of an outbreak are given in [2].

2 Parameters

2.1 Infection related parameters

The probability of moving from the latent to the infectious state per day τ of the latent period is defined as

$$P_I(\tau) = (0.5, 0.7, 1.0), \qquad \tau = 1, ..., D_E \ .$$

The probability of transmission upon contact on day τ of the infectious period $P_T(\tau)$ was modelled with a discretized Weibull distribution with parameters estimated from published data. Similarily, the probability of developing symptoms on day τ of the infectious period $P_S(\tau)$ was modelled with a discretized Weibull distribution with parameters estimated from published data ([3, 4]), with the additional assumption that 20% of infected persons never develop symptoms. For details of the estimation procedure, see section 4.1.

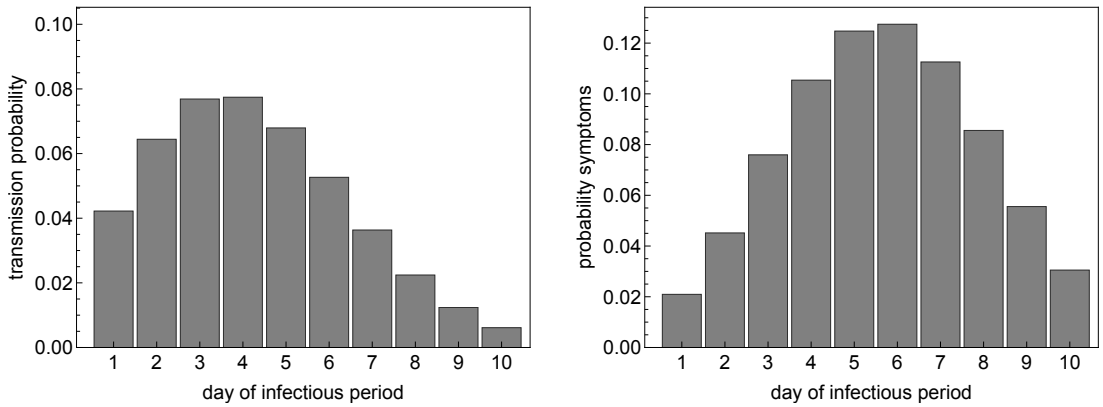


Figure S1. The transmission probability and probability of developing symptoms per day of the infectious period.

2.2 Contact distributions

We distinguish between close contacts (e.g. in the household), and casual contacts. For close contacts we assume that the number of contacts per day follows a Poisson distribution with mean μ_1. For casual contacts, we assume that the number of contacts per day is distributed according to a negative binomial distribution with parameters n and p. We denote the mean of this distribution by μ_2. We chose these parameters such that the total mean daily contact number $\mu_1 + \mu_2$ and its standard deviation are approximately equal to the daily number of contacts (13.85) and standard deviation (10.54) reported for the Netherlands in the Polymod study [5]. With contact reduction the daily number of contacts was reduced to around 5 per day, which is slightly more than reported by [6] for the period of the lockdown.

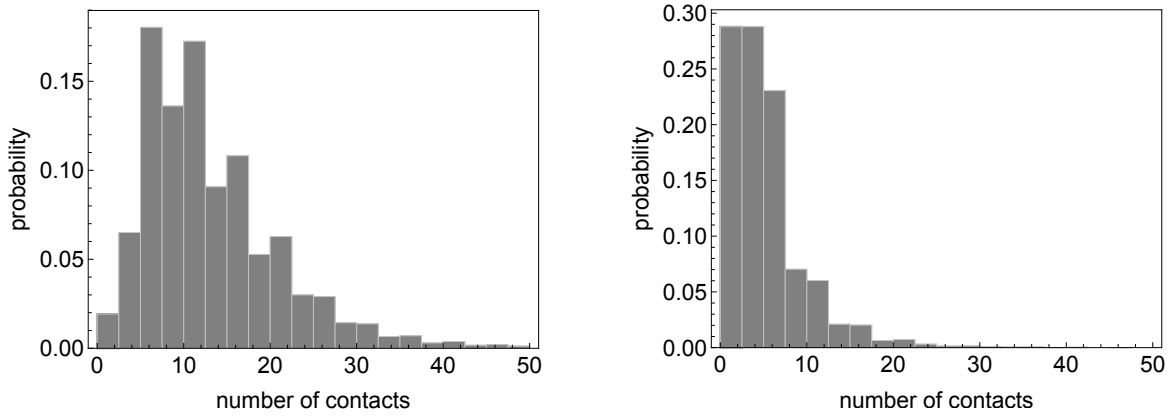


Figure S2. (A) Distribution of overall number of contacts per day in the model based on data from the Netherlands [5]. (B) Distribution of overall number of contacts per day in the scenario with contact reduction.

For the process of transmission, it is possible that contact persons are already infected at some point during the infectious period of the index case. To account for the probability of a contact person still being susceptible at day τ of the infectious period of the index case, we defined the saturation functions S_h and S_c for close and casual contacts as follows:

$$S_h(\tau) = \prod_{i=1}^{\tau-1}(1 - P_T(i))$$

and

$$S_c(\tau) = \prod_{i=1}^{\tau-1}(1 - qP_T(i)) \ ,$$

where q denotes the reduction factor of transmission in casual contacts as compared to close contacts.

Furthermore, contact numbers can be reduced in a scenario with physical distancing. This is implemented in the model by applying a reduction factor to the means of the distributions, i.e. if these factors are denoted by r_h and r_c for close and casual contacts, the means of the contact number distributions for a physical distancing scenario will be $r_h\mu_1$ and $r_c\mu_2$. If for example $r_h = 0.2$, we say that the number of close contacts is reduced by 80%.

In summary, the number of contacts per day of the infectious period is described by a random variable $C(\tau) = C_1(\tau) + C_2(\tau)$ where

$$C(\tau) \sim Poisson(r_h\mu_1 S_h(\tau)) + NegBin(r_c n S_c(\tau), p) \ .$$

In the following, $\mu_1(\tau) = r_h\mu_1 S_h(\tau)$ and $\mu_2(\tau) = r_c(np/(1-p))S_c(\tau)$ denote the mean number of contacts per day τ of the infectious period.

2.3 Basic reproduction number

The basic reproduction number for this model can be calculated explicitly. It is given by

$$R_0 = \sum_{\tau=1}^{D_I}(\mu_1(\tau)P_T(\tau) + \mu_2(\tau)qP_T(\tau)) \ ,$$

where q is the factor by which casual contacts are less transmissible than close contacts. We denote by $R_0(\tau)$ the number of secondary cases produced on day τ of the infectious period, which is given by the summand in the above equation. Using $R_0(\tau)$, the proportion of onward transmission generated up to day τ of the infectious period as

$$\rho(\tau) = \frac{1}{R_0}\sum_{i=1}^{\tau} R_0(i) \ .$$

2.4 Diagnosis and tracing

The probability of being diagnosed in the model is determined by the probability of developing symptoms. However, there can be a delay D_1 between symptom onset and diagnosis. Therefore, the probability of being diagnosed per day of the infectious period is given by $P_D(\tau) = 0$ for $\tau < D_1$, and $P_D(\tau) = P_S(\tau - D_1 + 1)$ for $\tau \geq D_1$. If not everybody who develops symptoms

is tested, the probability of diagnosis is reduced by a factor f_t, which represents the fraction of symptomatic persons, who get tested. If, for example, only persons who are using a mobile tracing app get tested, the fraction f_t represents the proportion of the population using the app. In summary

$$P_D(\tau) = \begin{cases} 0, & \text{if } \tau < D_1 \\ f_t P_S(\tau - D_1 + 1) & \text{if } D_1 < \tau \leq D_I \end{cases} .$$

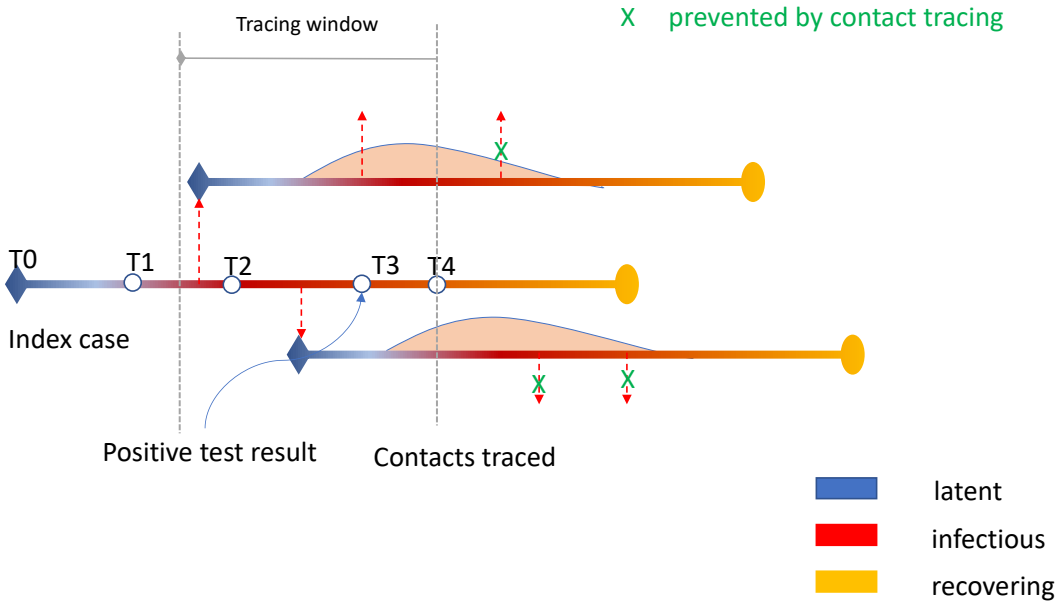


Figure S3. Schematic of the infection time line of an index case, and cases prevented by contact tracing. The red area under the curve represents the probability distribution of onward transmission of the infected contacts. The part of the distribution to the right of the dashed line marked "contacts traced" can be prevented by isolating these contacts. For explanations of the time points $T_0, ..., T_4$ see Table S1.

Table S1: Description of events during contact tracing.

Time	Event	Comments	Model implementation
$\mathbf{T_0}$	Time of infection of the index case.	Not observed	Start of the latent period, which lasts 1-3 days. Per day of the latent period, an infected person moves to the infectious period with a given probability.
$\mathbf{T_1}$	Time the index case becomes infectious.	Presymptomatic transmission may take place from time T_1 onwards.	After 1-3 days after infection, the infectious stage starts, which lasts 10 days with variable infectiousness. Between 33% and 50% of transmission takes place before symptom onset [7].
$\mathbf{T_2}$	Time that the index case becomes symptomatic and eligible for testing.	T_0 until T_2 reflects the time window, in which prevention is not possible with CTS.	The incubation period in the model is taken in agreement with published literature [4].
$\mathbf{T_3}$	Time that the index case is tested positive.	T_2 until T_3 is the testing delay, which may range from 0-7 days. The proportion being tested varies from 0%-100% in increments of 20%. During this period we expect subjects to self-quarantine, with effectiveness ranging from 0%-100% in increments of 20%.	After a testing delay D_1 after symptom onset, an individual receives a positive test result and gets isolated. If an individual self-isolates immediately, $D_1 = 0$. After isolation, no transmission takes place.
$\mathbf{T_4}$	Time that contacts of the index case are traced and quarantined.	T_3 until T_4 is the tracing delay, which may range from 0 (for instance with app technology) to 3 days (with current approach of health services). Here we can also vary the proportion with short post-test delay (those with apps).	After a tracing delay D_2, contacts of the index case are traced, and infected contacts are isolated. D_2 and the tracing coverage (proportion of contacts found and isolated) may differ between close and casual contacts. If household contacts self-isolate immediately with the index case, it means that $D_2 = 0$ and coverage is 100% for close contacts. Non-adherence reduces the tracing coverage, thus in the baseline scenario we assume 80% coverage.

The probability that an infected contact person gets traced and isolated, depends on his infector being diagnosed. For a contact person, who gets infected on day τ of his infector's infectious period, we can compute the probability that the infector gets diagnosed on day $\tau + i$ of the infectious period. Tracing then occurs on day $\tau + i + D_2$, where D_2 is the delay between isolation of the index case and successful tracing and isolation of the infected contact person. On day $\tau + i + D_2$, contacts in the time window $[\tau + i + D_2 - w, \tau + i + D_2]$ can be identified and tested, and if they are infected will be isolated. The proportion of these contacts that are successfully isolated is called tracing coverage and is denoted by C. This means that the probability to be traced and isolated for a contact infected on day τ of the index case's infectious period is given by

$$P_{ct}(\tau) = \sum_{i=\tau}^{Min(D_I, \tau+w)} C\phi(i)P_D(i) \ .$$

where

$$\phi(\tau) = \prod_{i=1}^{\tau-1}(1 - P_D(i))$$

is the probability that an infected index case is not yet diagnosed on day τ of its infectious period.

An infected contact person may already have infected others at the moment they are traced and isolated. This means that we may only prevent a fraction of the potential onward transmissions of that contact person. To account for that, we introduced a weighting function $\lambda(\sigma)$, that describes the fraction of onward transmission that has occurred on day σ after infection of the contact person. Here σ can run from 1 to $D_I + w$, because a contact person at the moment tracing takes place can be from 1 day after infection up to $D_I + w$ days after infection. The latter occurs when the contact person was infected on the first day of the index case's infectious period, the index case was diagnosed on the last day of his infectious period, and the tracing delay equals the window period. If the tracing delay is longer than the window period, no contacts will be traced.

For an infected contact person, who is on day σ since acquiring infection, the proportion of onward transmissions (s)he has already generated, can be computed as

$$\lambda(\sigma) = \sum_{i=1}^{D_E} \prod_{j=1}^{i-1}(1 - P_I(j))P_I(i)\rho(\sigma - i) \ ,$$

which implies that the proportion that can be prevented is $1 - \lambda(\sigma)$. A contact person, who is infected on day τ of the index case's infectious period, may be traced on a day between $\tau + 1$ and $D_I + D_2$ after that. If $D_I + D_2 - w < \tau$ the contact will be isolated. A fraction $1 - \lambda(\sigma)$ of his onward transmissions can be prevented.

Combining λ with the probability of diagnosis of the index case, leads to the tracing probability

$$\psi(\tau) = \sum_{i=\tau}^{D_I} \phi(i)P_D(i)C(1 - \lambda(\tau + i + D_2)) \ .$$

Therefore, tracing the contact will decrease the effective reproduction number by a factor $1 - \psi(\tau)$. As delay and coverage may differ between close and casual contacts, we distinguish between $\psi_h(\tau)$ and $\psi_c(\tau)$.

Table S2: Description of variables and parameters.

Notation	Description	Note
P_I	Probability of becoming infectious per day of latent period	vector of length D_E
P_T	Probability of transmission upon contact per day of infectious period	vector of length D_I
P_S	Probability of symptom onset per day of infectious period	vector of length D_I
P_D	Probability of being diagnosed per day of infectious period	vector of length D_I
P_{ct}	Probability of contact being traced per day of infectious period of infector	vector of length D_I
$\mu_1(\tau), \mu_2(\tau)$	Mean daily number of contacts for close and casual contacts	vector of length D_I
S_h, S_c	Saturation factors describing reduction of susceptible contacts due to repeated contact	vector of length D_I
r_h, r_c	Reduction factors for physical distancing	fractions
q	Ratio of transmissibility between casual to close contacts	fraction
f_t	Fraction of population who gets tested	fraction
w	Tracing window period	integer (days)
C	Tracing coverage	fraction
$\phi(\tau)$	Probability of not being diagnosed by day τ	vector of length D_I
$\rho(\tau)$	Proportion of onward transmission by day τ	vector of length D_I
$\lambda(\sigma)$	Proportion of onward transmissions by day σ since acquiring infection	vector of length $D_E + D_I$
$\psi(\tau)$	Probability of being traced by day τ of the infectors infectious period	vector of length D_I

3 Reproduction numbers

3.1 Effective reproduction numbers

In the case, where diagnosis and isolation can occur, the number of secondary cases is reduced. An infected person can only transmit to his contacts on day τ of the infectious period, if he has not been diagnosed and isolated on the previous days of the infectious period, which is given by

$\phi(\tau)$. We then define the effective reproduction number with testing and isolation as

$$R_{iso} = \sum_{\tau=1}^{D_I} (\mu_1(\tau) P_T(\tau) + \mu_2(\tau) q P_T(\tau)) \phi(\tau) \ .$$

Similarly, if contacts of an infected person, who is diagnosed at day τ of his infectious period are traced and isolated, the number of secondary infections are reduced. Contact persons, who were already infected in a time interval w before diagnosis of the index case will be found and isolated after a delay D_2. At the point of isolation, a fraction $\lambda(\tau)$ of their onward transmissions have already occurred, i.e. only the remaining fraction $1 - \lambda(\tau)$ can be prevented. As explained above, this reduces the effective reproduction number by factors $\psi_h(\tau)$ and $\psi_c(\tau)$. This leads to the definition of the effective reproduction number with tracing as

$$R_{cts} = \sum_{\tau=1}^{D_I} (\mu_1(\tau) P_T(\tau)(1 - \psi_1(\tau)) + \mu_2(\tau) q P_T(\tau)(1 - \psi_2(\tau))) \phi(\tau).$$

3.2 Individual reproduction numbers

Individual reproduction numbers can be generated by drawing from the distributions underlying the definitions of the reproduction numbers in section 3.1. For every day of the infectious period of an individual, numbers of close and casual contacts are drawn, say c_1 and c_2. The number of secondary infections is then generated by drawing from binomial distributions $Binom(c_1, P_T(\tau))$ and $Binom(c_2, qP_T(\tau))$. For determining whether the individual is diagnosed and isolated on day τ, a Bernoulli trial is performed with probability $P_D(\tau)$. Once an individual is diagnosed, the transmission probability is set to zero for the remaining infectious period.

For the tracing of contacts and isolation, the weighting function $\lambda(\tau)$ is used as a probability to determine whether a transmission is generated or not. An infected contact who has already passed a larger part of his infectious period has a higher probability of being generated as a secondary case, than a more recent contact. In other words, the expected number of secondary contacts of an index case is reduced by the proportion of their onward contacts that can be prevented by tracing.

Using the sampling process for generating individual reproduction numbers, we can assess the stochastic variability of the branching process and analyse the distribution of numbers of secondary cases per index case under various assumptions on diagnosis, isolation, and tracing of infected contacts. We can analyse how the delay between symptom onset and diagnosis D_1 and the delay between diagnosis and tracing and isolating infected contacts D_2 influence the distribution of individual reproduction numbers.

4 Sensitivity analyses

4.1 Sensitivity to generation time and incubation time

To account for the uncertainty in our choice of parameters which govern the distribution of the generation time and the distribution of the incubation time, we sampled parameters based on Nishiura et al. [3] and Backer et al. [4]. In [3] the mean serial interval was estimated to be 4.8 days with a 95% confidence interval of (3.8-6.1) and the standard deviation was estimated

to be 2.3 days with a 95% confidence interval of (1.6-3.5) days and a Weibull distribution gave the best fit to the data. In [4] the mean incubation was estimated to be 6.4 days with a 95% confidence interval of (5.6-7.7) and the standard deviation was estimated to be 2.3 days with a 95% confidence interval of (1.7-3.7) days and a Weibull distribution gave the best fit to the data.

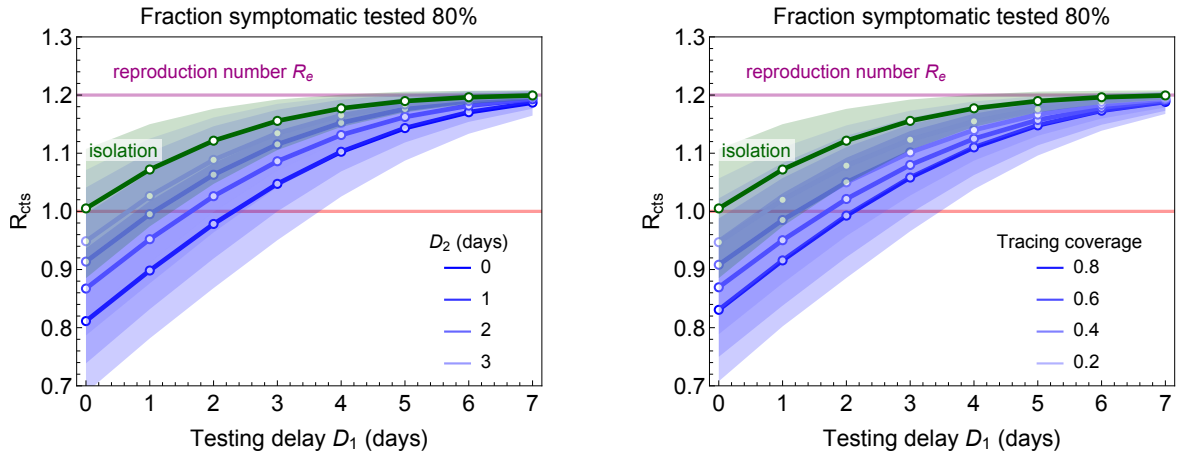


Figure S4. Impact of contact tracing on the effective reproduction number as a function of various delays and tracing coverages. In these analyses, 80% of those who develop symptoms get tested. For comparison, the reproduction number R_{iso} with only isolation of index cases without contact tracing is plotted (green) The shading shows 95% uncertainty intervals obtained by sampling parameters determining $P_T(\tau)$ and $P_S(\tau)$. (A) Influence of varying testing delay D_1 on the x-axis. The curves plotted in blue show varying tracing delays D_2, while tracing coverage is assumed to be 100%; (B) Here the tracing coverage is varied in the curves plotted in blue, while there is assumed to be no delay in tracing of contacts.

Independently for all 4 parameters (mean serial time, mean incubation time, standard deviation of the serial time and standard deviation of the incubation time) we have drawn 1000 values in the following way. Denote m as the mean of the parameter and l and u as the lower and upper bound of the 95% CI respectively. First we draw a random number r in the interval $(0, 1)$. If $r < 0.5$, we determined the value x of a normally distributed random variable with mean m and standard deviation $(m - l)/1.96$, such that the cumulative distribution function of the random variable equals r. If $r \geq 0.5$, we determined the value x of a normally distributed random variable with mean m and standard deviation $(u - m)/1.96$, such that the cumulative distribution function of the random variable equals r. In this way, we obtained 1000 sets of values for the 4 parameters. Next we determined for each set of the parameters the two Weibull distributions which have the mean and the standard deviation of that set. These Weibull distributions were discretized to probabilities per day since infection to develop symptoms and to an infectivity profile per day. We have calculated the reproduction numbers under different

conditions for each of the 1000 parameters and we have reported the mean and the 2.5% and the 97.5% percentiles.

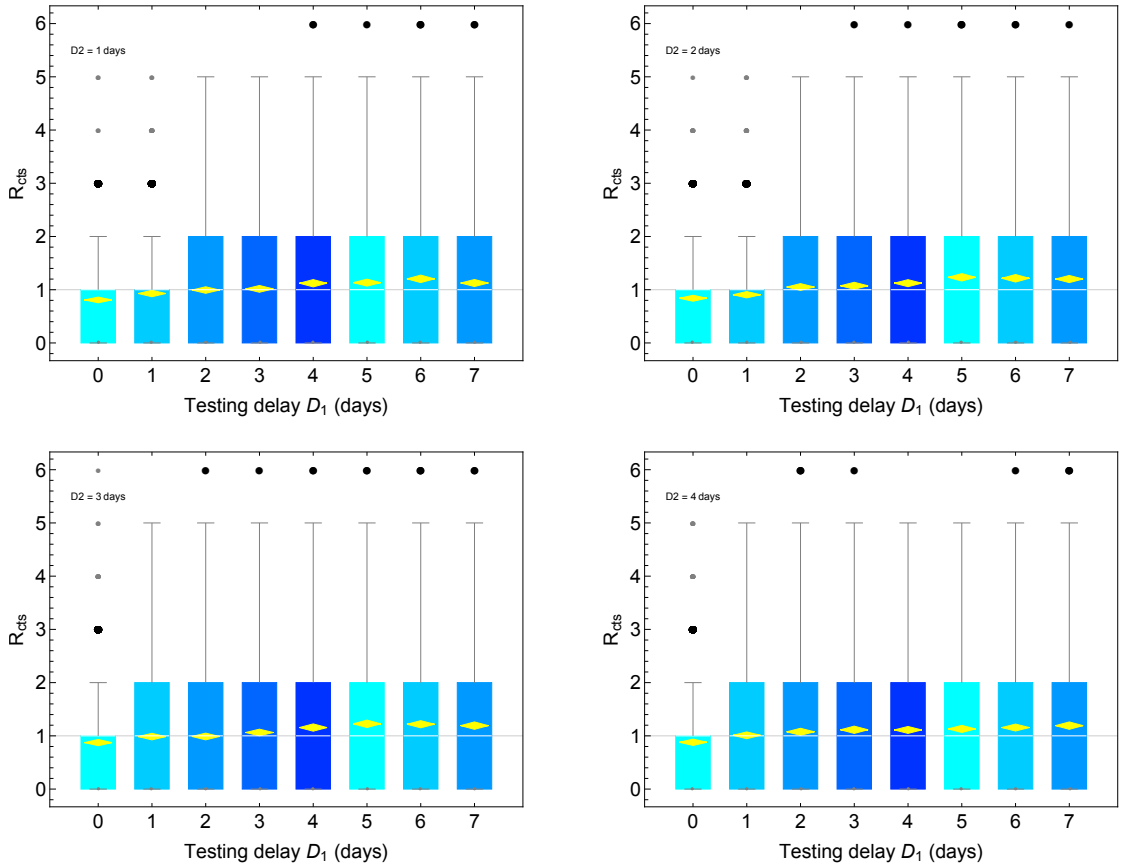


Figure S5. Impact of varying testing and tracing delays on individual reproduction numbers. Tracing coverage was assumed to be 80%.

4.2 Stochastic variability of individual reproduction numbers

We evaluated the distributions of individual reproduction number under contact tracing interventions with varying tracing delays D_2 (Figure S5) and tracing coverage (Figure S6). For both we varied also the testing delay between symptom onset and isolation D_1 on the x-axis. In all scenarios, the mean effective reproduction number was below 1 only if the testing delay was less than 2 days.

4.3 Varying testing coverage

To assess the impact of different levels of testing symptomatically infected individuals, we varied the testing fraction between 20% and 80%. It was assumed that the tracing delay is 0 days and tracing coverage is 80% (Figure S7).

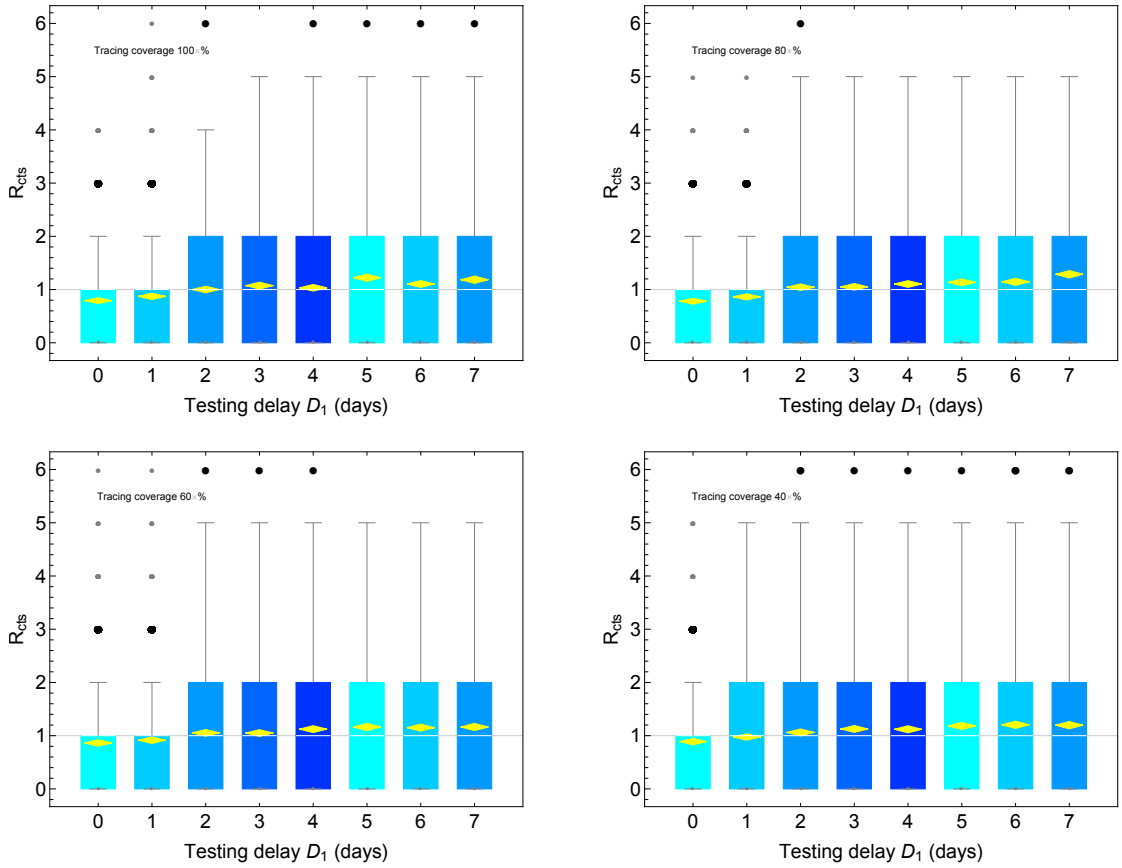


Figure S6. Impact of varying testing delay and tracing coverage on individual reproduction numbers. Tracing delay was assumed to be 0 days.

4.4 No physical distancing

While the results presented in the main text are formulated in the context of a situation with an effective reproduction number of around 1, they also apply to situations with higher values of the reproduction number. In that case, the CTS interventions cannot reduce R_{cts} to below 1, but the proportional changes in the reproduction number remain similar. To show the impact of CTS in a population without physical distancing, we ran the simulations with $r_h = r_c = 1$. The basic reproduction number R_0 is 2.5 in this case.

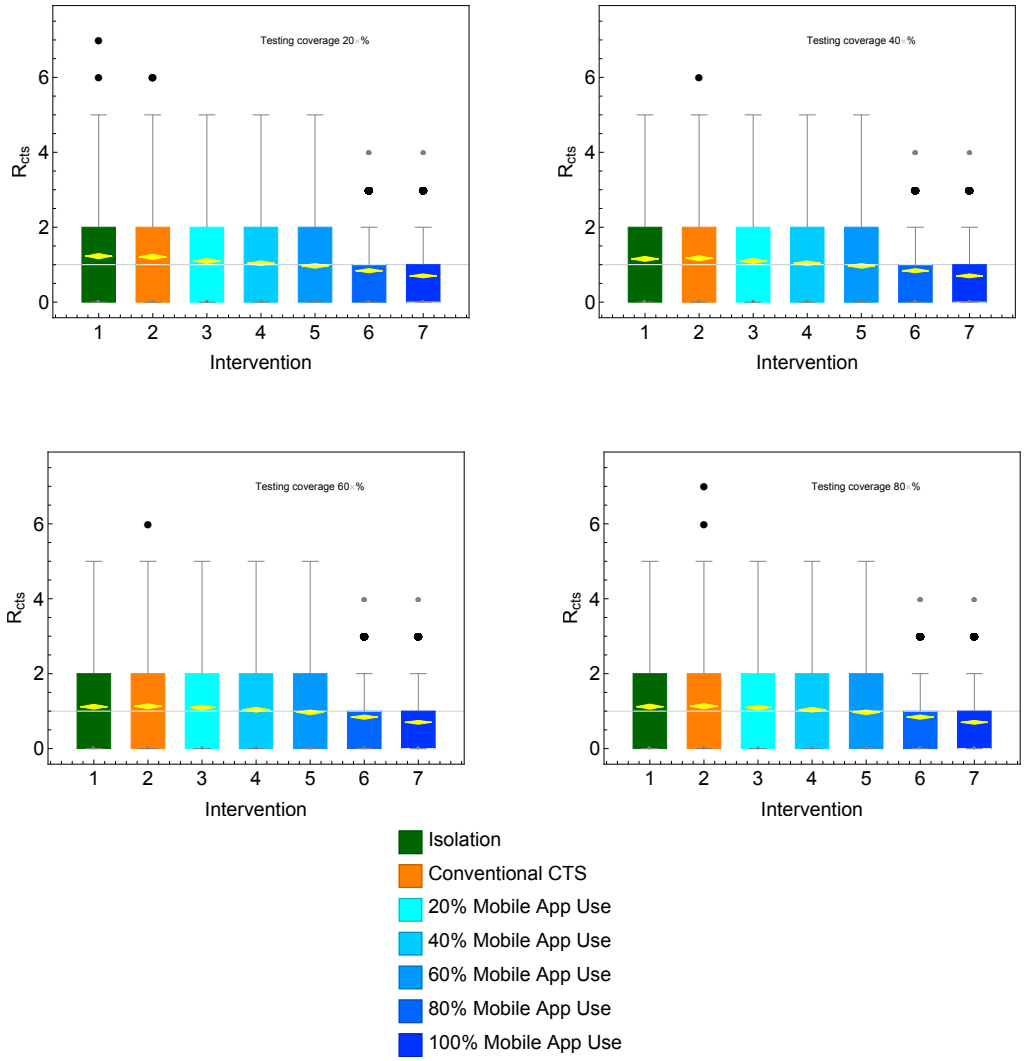
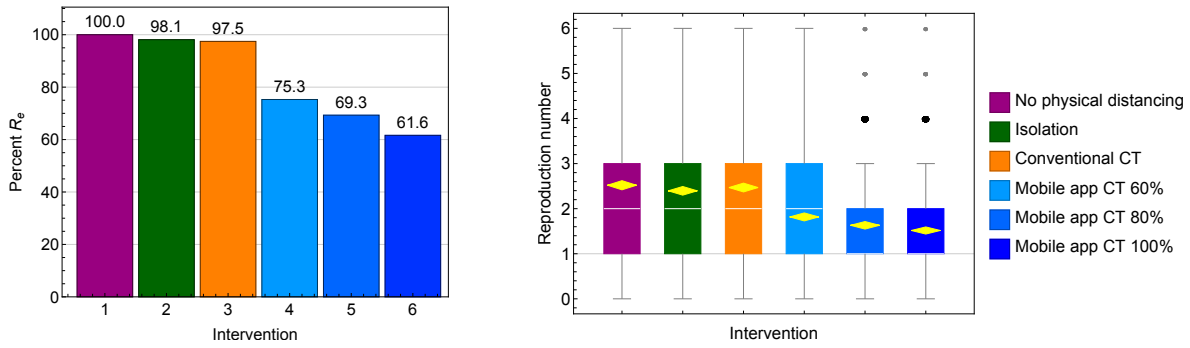


Figure S7. Impact of varying coverage of testing symptomatically infected individuals on individual reproduction numbers. Tracing delay was assumed to be 0 days, tracing coverage 80%.



(A) (B)

Figure S8. The reduction of the basic reproduction number for various CTS. (A) The reproduction number with CTS, R_{cts}, is shown as a percentage of the basic reproduction number R_0. (B) The distribution of individual reproduction numbers is shown for 1000 individuals. For the isolation scenario and conventional tracing scenario we assumed that there is a delay of 4 days between symptom onset and isolation of the index case. Testing coverage was assumed to be 80% in the isolation and conventional CT scenarios; app use prevalence was assumed to be 80% in the tracing app scenario.

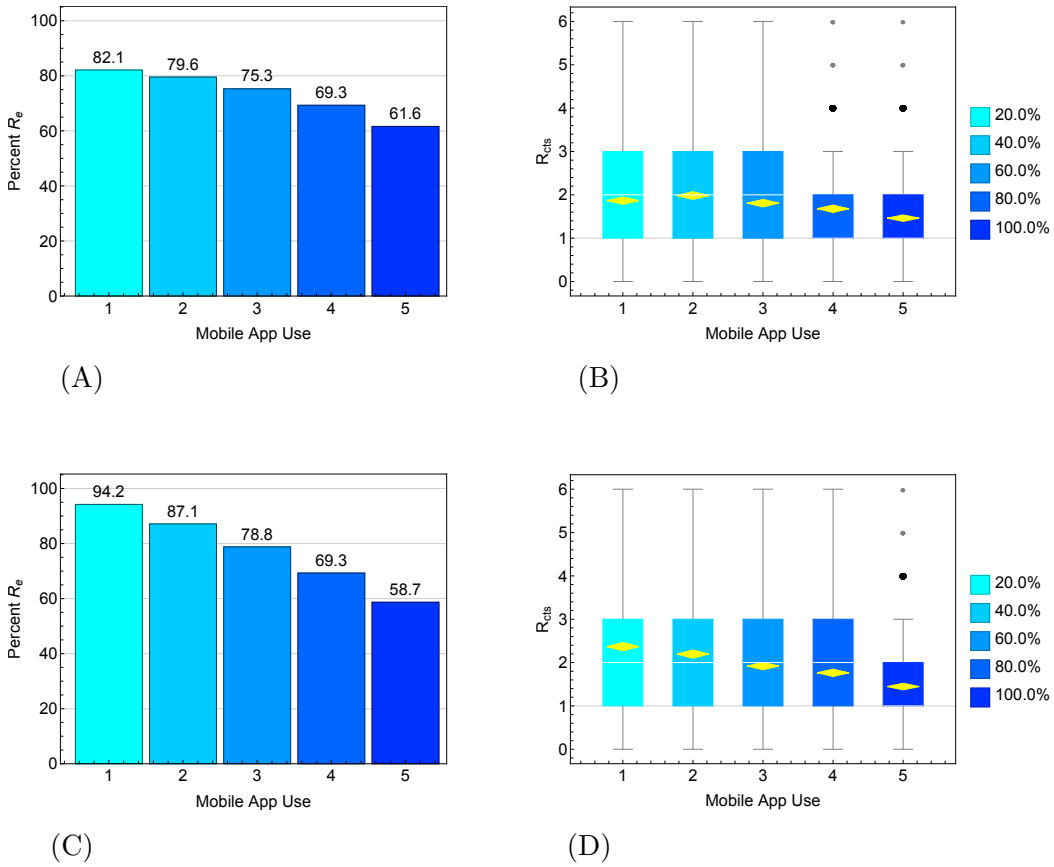


Figure S9. The impact of mobile app use on R_{cts} for varying levels of app use. In S9A and S9B, we assume that there is also testing of those who do not use the mobile app, so app use only is used for tracing contacts. In S9C and S9D, only app users, who develop symptoms, are tested. Panels A and C show percentage reductions of R_0 achieved by the CTS; panels B and D show the impact of various CTS on distributions of individual reproduction numbers.

References

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