
THE EFFECT OF SOCIAL DISTANCING, ISOLATION AND DIGITAL CONTACT TRACING ON COVID-19

A TECHNICAL REPORT

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ABSTRACT

A combination of Social distancing, isolation and digital contact tracing is modelled using an adapted deterministic SEIR model.

1 Introduction

New Zealand is developing a business case [3] for deploying new technology that enables digital contact tracing in order to reduce R_{eff} — the effective reproduction number — to less than 1. The new technologies are based on research by Ferritti et al. [1], who have shown that manual contact tracing alone cannot reduce $R_{\text{eff}} < 1$. They conclude that digital contact tracing and isolation can reduce $R_{\text{eff}} < 1$ if it works rapidly, and they define the requirements of a mobile app to achieve this.

This paper adapts the SEIR model equations [4] to analyse social distancing, isolation and digital contact tracing for New Zealand conditions. The adapted model is then used to define policy settings required to stop the transmission of the SARS-CoV-2 virus in New Zealand.

2 Adapted model equations, assumptions and parameter values

The SEIR model is adapted to account for the effect of aggressive testing, contact tracing and isolation. The compartment model for this system is displayed in Figure 2.

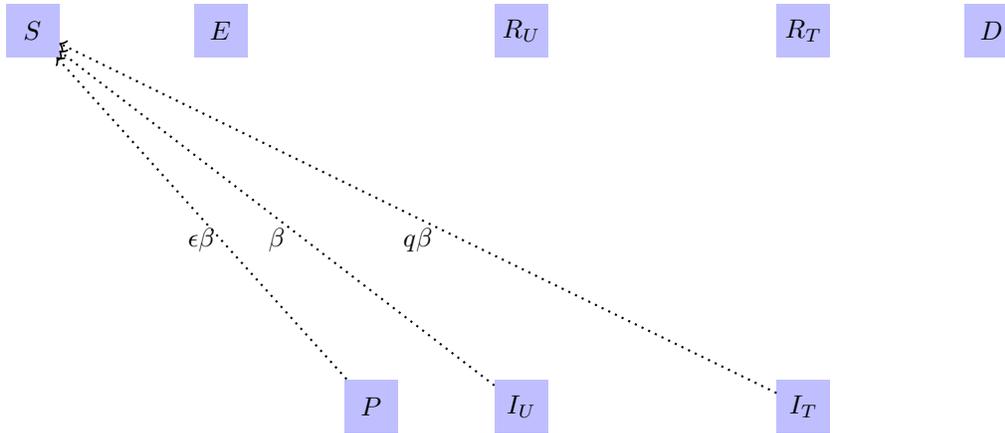


Figure 1: Sources of infection: the Pre-symptomatic and Infectious individuals infect the Susceptibles, who then become Exposed (see next figure).

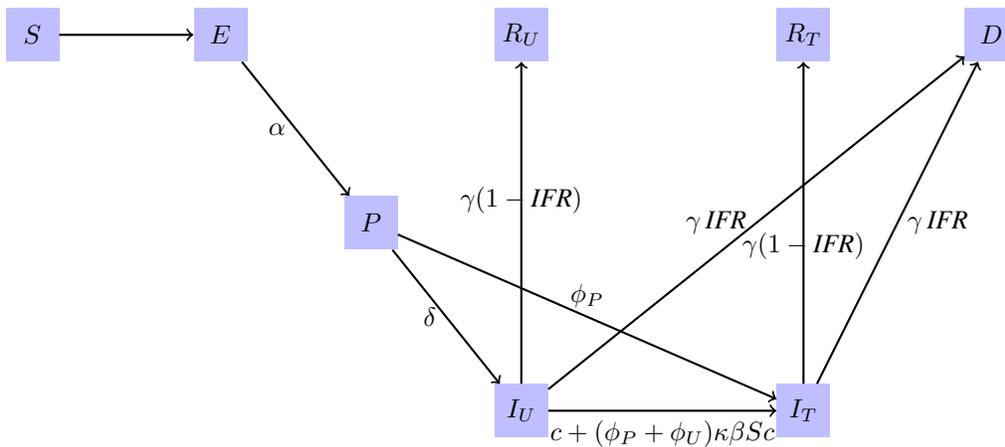


Figure 2: Sinks of infection: Susceptible individuals progress through the stages to either Recover or Die.

Continuous model equation

The equations for this model are as follows:

$$\begin{aligned} \frac{dS}{dt} &= -\beta S(\epsilon P + I_U + qI_T) & (1) \\ \frac{dE}{dt} &= \beta S(\epsilon P + I_U + qI_T) - \alpha E & (2) \\ \frac{dP}{dt} &= \alpha E - \phi_P \kappa \beta S c I_U - \delta P & (3) \\ \frac{dI_U}{dt} &= \delta P - \phi_U \kappa \beta S c I_U - (c + \gamma) I_U & (4) \\ \frac{dI_T}{dt} &= c I_U + (\phi_P + \phi_U) \kappa \beta S c I_U - \gamma I_T & (5) \\ \frac{dR_U}{dt} &= \gamma(1 - IFR) I_U & (6) \\ \frac{dR_T}{dt} &= \gamma(1 - IFR) I_T & (7) \\ \frac{dD}{dt} &= \gamma IFR (I_U + I_T) & (8) \end{aligned}$$

As a consistency check on any simulation, one should be able to compute that

$$S + E + P + I_U + I_T + R_U + R_T + D = 1 \quad (9)$$

for all t , since the expression on the left has derivative zero.

The first and most significant adaptation in the system is the introduction of a **quarantine parameter** q , which represents the extent to which individuals that have positive tests are prevented from infecting other individuals. In nations with advanced public health systems, it is reasonable to expect that this factor q is close to 0.

The effect of quarantining has been absent in deterministic models used to date. For example, James et al. [4] use a value of $q = 1$, implying that tested infected individuals I_T continue to infect susceptible individuals S at the same rate as before — which seems unlikely in the New Zealand situation. If highly effective quarantining ($q \approx 0$) of infected tested individuals is the norm, which is an obvious and sensible public health policy, then R_{eff} is significantly reduced. Ferritti et al. estimate that this measure alone would reduce R_{eff} by 40%.

Digital contact tracing, testing and isolation introduces new pathways into the model equations. Specifically, individuals can move from the Presymptomatic compartment P to the Infectious Tested compartment I_T directly. This new pathway introduces a new sinks from compartments P and I_U , and new sources to compartment I_T , as displayed in Figures 1 and 2. In the new model we assume that compartments P , I_U and possibly I_T are sources of infections to compartment S , but that compartment E is not a source of new infection. We also assume that individuals in compartment E will not test positive for the SARS-CoV-2 virus but that individuals in compartments P and I_U will.

In addition we assume that individuals who test positive, i.e. who enter I_T at time t , have until that point already infected $\kappa\beta S$ individuals, and that these individuals are contained in compartments E , P and I_U at time t . The new parameter κ is the **tracing period constant**, and it represents the average number of prior days over which the contacts of a newly infected-tested individual will be traced.

It remains to allocate proportions of these individuals into the various compartments E , P and I_U . We have used two methods for this proportioning of infections among compartments, as displayed in the table below.

Proportion	Value	Description
Method 1		
ϕ_E	$\frac{\alpha^{-1}}{\alpha^{-1} + \delta^{-1} + c^{-1}}$	Time-based proportioning of infected individuals into compartment E
ϕ_P	$\frac{\delta^{-1}}{\alpha^{-1} + \delta^{-1} + c^{-1}}$	Time-based proportioning of infected individuals into compartment P
ϕ_U	$\frac{c^{-1}}{\alpha^{-1} + \delta^{-1} + c^{-1}}$	Time-based proportioning of infected individuals into compartment I_U
Method 2		
ϕ_E	$\frac{E}{E + P + I_U}$	Population-based proportioning of infected individuals into compartment E
ϕ_P	$\frac{P}{E + P + I_U}$	Population-based proportioning of infected individuals into compartment P
ϕ_U	$\frac{I_U}{E + P + I_U}$	Population-based proportioning of infected individuals into compartment I_U

The model has all the same assumptions as the Hendy et al [4] model with the addition of the following:

- The quarantine constant q is introduced to model the isolation of individuals in compartment I_T .
- The tracing period κ is introduced to quantify the average number of prior days over which the contacts of a new Infected-tested person will be contact-traced.

- The assumption is that contact tracing, testing and isolation is instantaneous. In reality this process may take a day or so. The important feature is isolation, which is a matter of public health policy: contacts of an infectious person could be quarantined **before** testing, and then released if they test negative.
- The model assumes that exposed individuals E test negative.
- The model assumes that presymptomatic individuals P test positive.
- The model does not include social distancing measures related to the COVID-19 Alert Level mitigations implemented in New Zealand. These measures alone (e.g. [5]) have been shown to considerably reduce R_{eff} .

The adapted equations introduce two new parameters:

Parameter	Symbol (units)	Value
Quarantine constant	q	A measure of the effectiveness of quarantining individuals who have tested positive. Perfect quarantine means $q = 0$. No quarantine means $q = 1$.
Tracing period	κ (days)	Average number of prior days over which the contacts of a new Infected-tested person will be traced and tested.

The other parameter values used when simulating the SEIR model are:

$$\beta = \gamma R_0, \quad \epsilon = 0.15, \quad \alpha = 0.25, \quad \delta = 1.0, \quad c = 0.1, \quad \gamma = 0.1.$$

Here R_0 is the basic reproduction number. Its value will be chosen in simulations to reflect different social distancing settings.

Discrete model equation

The discrete equations for the same model are as follows:

$$S(n+1) = S(n) - \beta S(n)(\epsilon P(n) + I_U(n) + qI_T(n)) \quad (10)$$

$$E(n+1) = E(n) + \beta S(n)(\epsilon P(n) + I_U(n) + qI_T(n)) - \alpha E(n) \quad (11)$$

$$P(n+1) = P(n) + \alpha E(n) - \phi_P(n)\kappa\beta cI_U(n-2)S(n-2) - \delta P(n) \quad (12)$$

$$I_U(n+1) = I_U(n) + \delta P(n) - \phi_U(n)\kappa\beta cI_U(n-2)S(n-2) - (c + \gamma)I_U(n) \quad (13)$$

$$I_T(n+1) = I_T(n) + cI_U(n) + (\phi_P(n) + \phi_U(n))\kappa\beta cI_U(n)S(n-2) - \gamma I_T(n) \quad (14)$$

$$R_U(n+1) = R_U(n) + \gamma(1 - IFR)I_U(n) \quad (15)$$

$$R_T(n+1) = R_T(n) + \gamma(1 - IFR)I_T(n) \quad (16)$$

$$D(n+1) = D(n) + \gamma IFR(I_U(n) + I_T(n)) \quad (17)$$

The discrete model allows a delay to be directly incorporated between testing of the infectious person and testing of their contacts. See equations (12)–(14), where a 2-day delay is hard coded. This delay could easily be added as an additional parameter in the discrete system. We have not yet run simulations with the discrete model.

The remainder of this technical report uses the continuous version of these equations, where contact tracing and isolation are assumed to be instantaneous.

3 Results

The modified model is used to simulate the epidemic progression when varying values of R_0 , κ and q through the following ranges:

- $R_0 = \{0, 0.5, 1.0, 1.5, 2.0, 2.5, 3.0\}$
- $\kappa = \{0, 2, 4, 6, 8, 10, 12, 14, 16\}$
- $q = \{0.0, 0.2, 0.4, 0.6, 0.8, 1.0\}$.

The simulations were run over 24 months, with each variable being changed to investigate its impact on R_{eff} as a function of time.

Each of these variables represents some tangible policy setting. The basic reproduction number R_0 is a proxy for social distancing measures, which in New Zealand are defined in policy by the COVID19 Alert Levels [8]. The quarantine

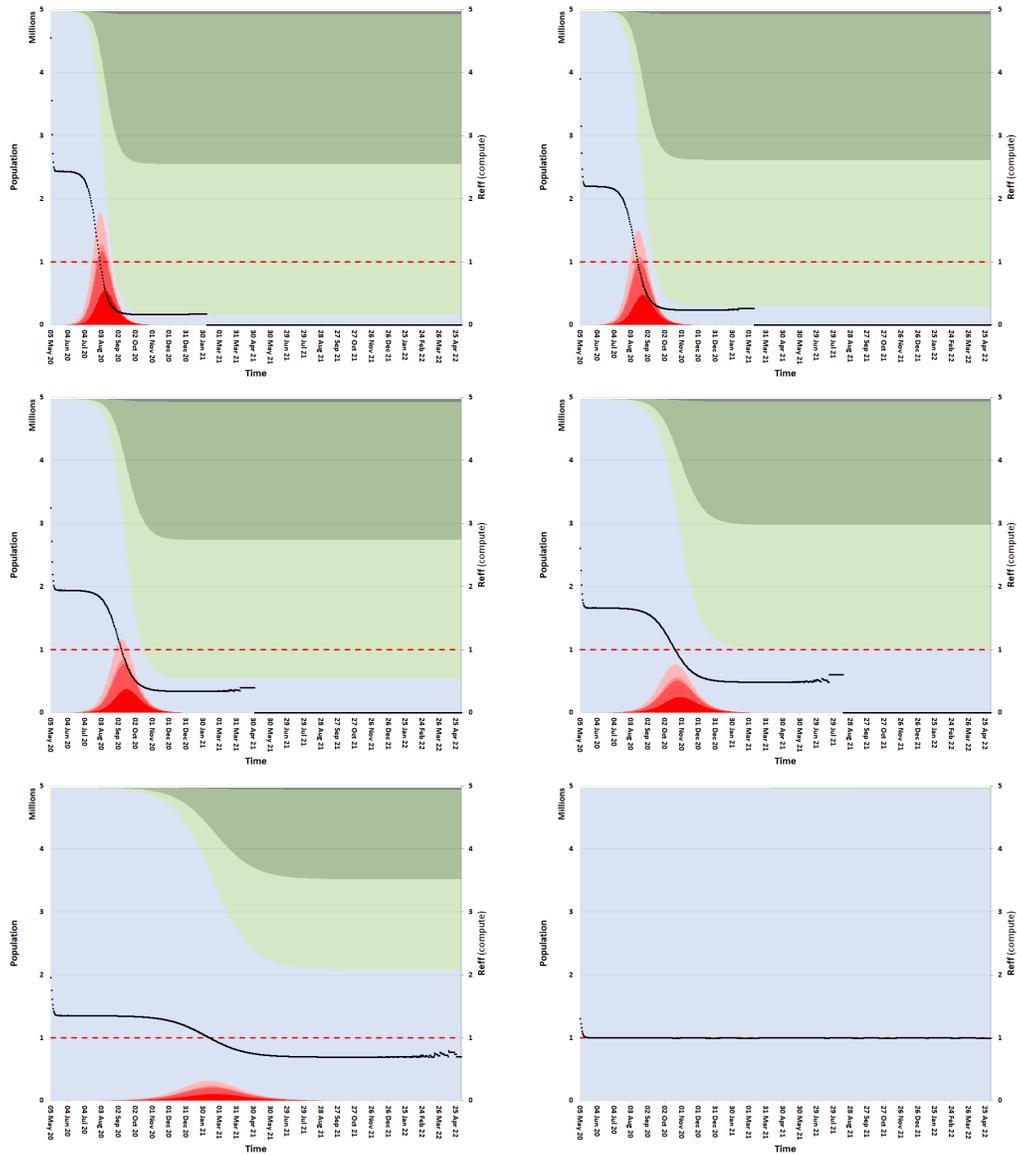


Figure 3: This series of graphs varies the social distancing setting R_0 , with no quarantining ($q = 0$) and no digital contact tracing ($\kappa = 0$). R_0 varies from 3.5 down to 1.0 in steps of 0.5. The susceptible population S is displayed in light blue; the infected tested I_T , infected untested I_U , pre-symptomatic P and Exposed E populations in lightening shades of red; the recovered untested R_U and recovered tested R_T populations in lightening shades of green; and the population of fatalities D in black. The R_{eff} (computed) values displayed as black squares are the effective reproduction number as a function of time, calculated using equation (18). Finally, the critical line of $R_0 = 1$ is shown as a red dash. Top Left: $R_0 = 3.5$, Top Right: $R_0 = 3.0$, Middle Left: $R_0 = 2.5$, Middle Right: $R_0 = 2.0$, Bottom Left: $R_0 = 1.5$, Bottom Right: $R_0 = 1.0$. The start time of the simulation was 5 May 2020, with total population $N = 4,975,871$ and initial compartment values $NS = 4963686$, $NE = 25$, $NP = 6$, $NI_U = 62$, $NI_T = 164$, $NR_U = 10593$, $NR_T = 1302$, $ND = 20$.

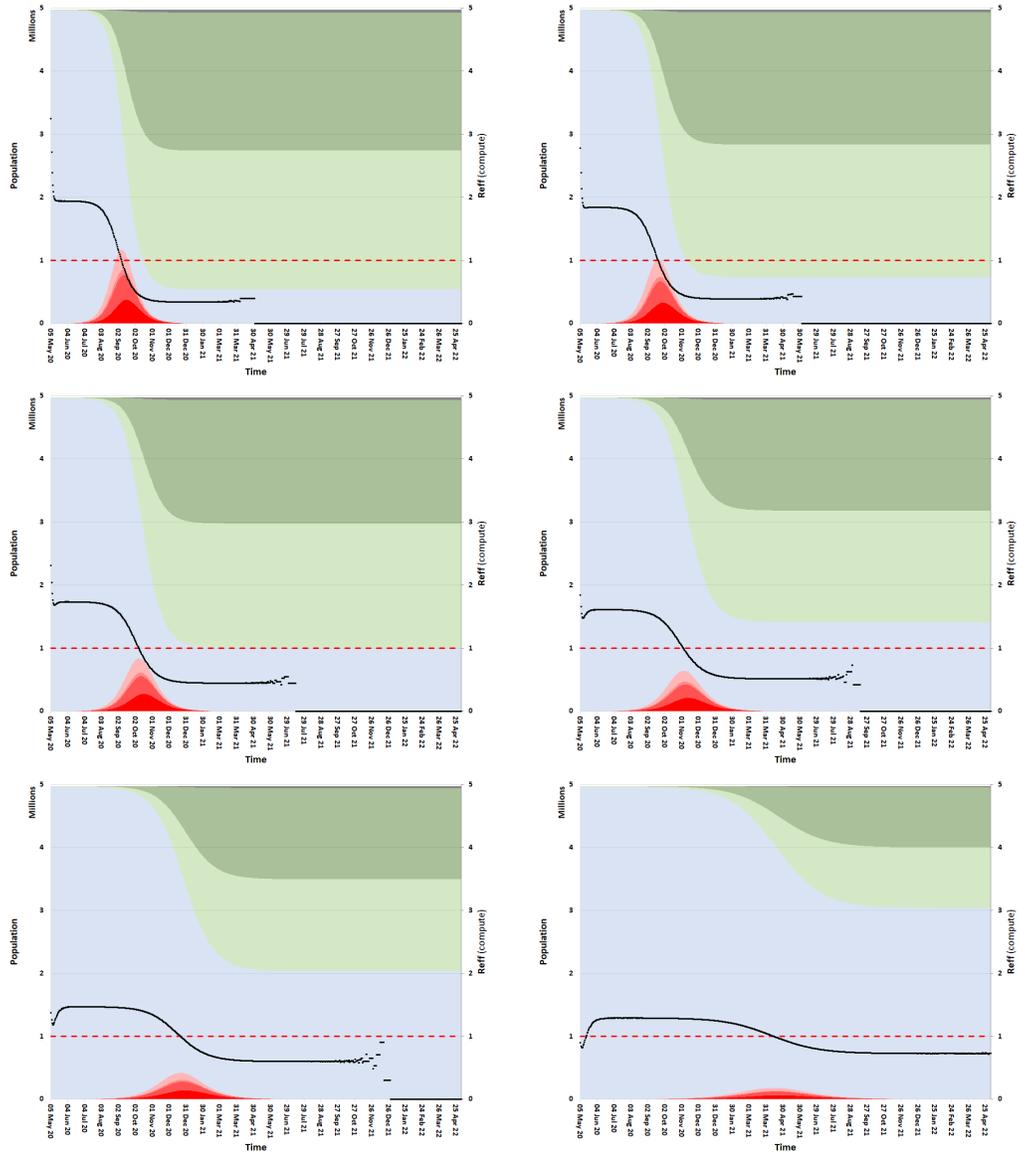


Figure 4: This series varies the quarantine setting q from 1.0 down to 0.0 in steps of 0.2, while holding social distancing fixed ($R_0 = 2.5$), with no digital contact tracing ($\kappa = 0$). Top Left: $q = 1.0$, Top Right: $q = 0.8$, Middle Left: $q = 0.6$, Middle Right: $q = 0.4$, Bottom Left: $q = 0.2$, Bottom Right: $q = 0.0$. The initial conditions are the same as for Figure 3.

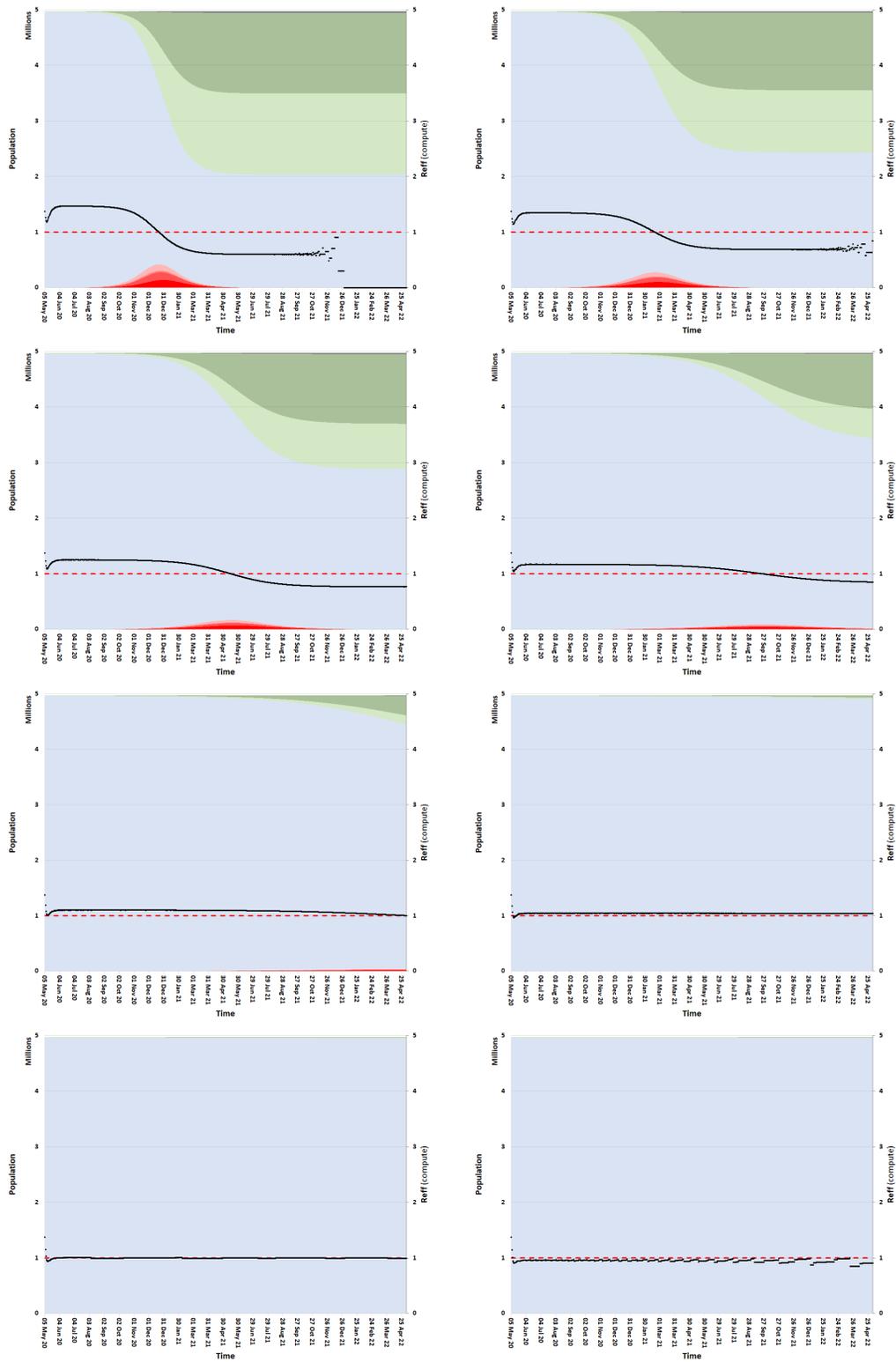


Figure 5: This series varies the digital contact tracing settings κ from 0 up to 14 in steps of 2 days, and fixes the social distancing constant ($R_0 = 2.5$) and quarantining constant ($q = 0.2$). Top Left: $\kappa = 0$, Top Right: $\kappa = 2$, Upper Middle Left: $\kappa = 4$, Upper Middle Right: $\kappa = 6$, Lower Middle Left: $\kappa = 8$, Lower Middle Right: $\kappa = 10$, Bottom Left: $\kappa = 12$, Bottom Right: $\kappa = 14$. The initial conditions are the same as for Figure 3.

constant q reflects sensible medical policy, and is a measure of how well the infected tested population I_T is isolated from the susceptible S population. Finally, the tracing constant κ is a new measure of the ability of digital contact tracing to identify potentially infected individuals from the contact list of a person that has just tested positive.

R_{eff} has been calculated and plotted for each of the simulations using the following equation:

$$R_{\text{eff}} = (\alpha^{-1} + \delta^{-1} + \gamma^{-1}) \frac{\beta S(\epsilon P + I_U + q I_T)}{E + P + I_U + I_T} \quad (18)$$

The first factor in this equation represents the average number of days a person takes from initial infection to recovery, while the second factor gives the number of new infections generated per day per infected person (counting here as infected everyone in compartments E, P, I_U, I_T).

The goal of these combined policies is to lower $R_{\text{eff}} < 1$, and hence to "eliminate" [9] the transmission of COVID19 in New Zealand.

3.1 Observations

Each graph exhibits the following general features. There is a plateau with $R_{\text{eff}} > 1$, then R_{eff} decreases as the Susceptible population becomes infected, and plateaus again but this time with $R_{\text{eff}} < 1$, until the disease fades out due to lack of Susceptible individuals to sustain transmission. The goal is to reduce $R_{\text{eff}} < 1$ earlier in the epidemic, before the Susceptible population becomes heavily infected. This goal can be achieved by changing the public health policy settings, as shown below.

First, consider the effect of varying R_0 using just social distance measures, which can be seen in Figure 3. The figures show the impact on changing R_0 from 3.5 to 1.0 on the disease transmission. Here we assume no digital contact tracing ($\kappa = 0$) and no isolation of infected tested individuals ($q = 1$). The figures show that the infection peak is lowered and delayed in time by lowering R_0 . This is an expected feature.

Second, consider the effect of varying the quarantine constant q using conventional medical policy. In Figure 4 we hold $R_0 = 2.5$ constant — reflecting a mild social distance constraint — and vary the value of q . Here we assume no digital contact tracing ($\kappa = 0$). The figures show the impact of changing q from 1.0 (no isolation) to 0.0 (complete isolation) of infected tested individuals I_T . Quarantining also dramatically lowers and delays the infection peak.

Lastly, consider the effect of varying the tracing constant κ using new digital contact tracing technology. In Figure 5 we hold $R_0 = 2.5$ and $q = 0.2$ — reflecting a reasonable isolation choice — and vary the value of κ . The figure show the impact of changing κ from 0 to 14 days in steps of 2 days. Digital contact tracing is seen, like quarantining, to be effective at reducing and delaying the infection peak.

3.2 Summary

Various lock down policies have been implemented by governments around the world, and almost all of them have been shown to be effective in lowering $R_{\text{eff}}(t)$ (e.g. see [5]). The aggressive, quick, and decisive action taken by the New Zealand government has been shown to lower $R_{\text{eff}}(t)$ immediately after COVID19 Alert Level 4 was implemented on 26 March 2020. Laugesen et al. [5] estimate that $R_{\text{eff}} \geq 3$ before 24 March 2020. This value is internationally high but probably reflects that the dominant pathway of disease transmission was international air flight arrivals and not community transmission at this time. Those authors estimate that after the lock down was implemented, $R_{\text{eff}} \approx 0$ from the second week of April 2020 onward.

Quarantining has long been a highly effective public health policy, dating back at least to the bubonic plague of 1665 [12] and more recently with SARS and MARS epidemics in 2002 and 2013, respectively. COVID-19 epidemiology is more difficult, because a number of infectious individuals will remain asymptomatic. These individuals will continue to transmit the disease, if only those people who display symptoms are isolated and their contacts are not traced and tested. This phenomenon can be seen in the Marist College cluster in New Zealand, where initially only symptomatic individuals were tested. Transmission continued via asymptomatic individuals until relatively recently [10, 11], despite the country being in COVID19 Alert Level 4 lock down. These asymptomatic individuals would likely have been young school students who continued to spread the SARS-CoV-2 virus throughout the school community before the lock down took place.

If $R_0 \geq 2.5$ then even perfect quarantining ($q = 0$) is not enough to reduce $R_{\text{eff}} < 1$ and stop the spread of the disease. This can be seen in Figure 4, where there is no contact tracing. The figure shows that all values of q result in $R_{\text{eff}} > 1$.

Digital contact tracing is a new technology in epidemiology. Therefore, relatively little is known about applying it to new COVID-19 disease transmission. However, our calculations have shown that it is an effective third public policy

tool. Immediate isolation of individuals who came into contact with an individual that has just tested positive is highly effective at lowering R_{eff} . The implementation details of the policy settings can vary, but the important point is that all contacts be isolated as soon as possible. Any delay in isolation of the contacts will increase R_{eff} .

All three policies (social distancing, quarantining, and contact tracing) are required to get $R_{\text{eff}} < 1$, according to our calculations, and the policies work together to suppress the disease.

Trade-offs can be made. Cost is an important factor, and of the three policies, social distancing carries substantially the greatest costs.

Which raises the question: what is the optimal combination of these policy settings?

When analysing this mix of policies (and hence variables), we would opt for the most liberal social distance measures, reflected in a choice of $R_0 = 2.5$. Strict but reasonable quarantining measures are defined by $q = 0.2$. This combined with digital contact tracing of $\kappa > 6$ days has been shown to reduce to $R_{\text{eff}} < 1$.

Various refinements of the models could be considered. For example, the delay in testing and isolation could readily be modelled using the discrete equations. This would allow a comparison between the effectiveness of digital contact tracing verses the current manual contract tracing processes.

4 Conclusion

Social distancing, quarantining, and new digital contact tracing technology can combine to reduce $R_{\text{eff}} < 1$. This is shown to occur when:

- $R_0 = 2.5$, representing liberal social distancing policies,
- an 80% reduction in ongoing infectiousness of tested individuals is achieved by quarantining them,
- new digital contract tracing technology is used to enable rapid isolation and testing of people who came in contact during the past 12 days with individuals who have newly tested positive.

A Heuristic relation between quarantining, contact tracing and R_{eff}

To check the qualitative consistency of our results, this appendix develops formulas relating contact tracing and quarantining to the effective reproduction number, R_{eff} . The methods are completely different from the rest of the paper, but the conclusions are remarkably consistent.

Write d for the number of days between a contact being infected and them testing positive as a result of the contact tracing. We assume each contact has the same d -value. Consider the fractions f and i defined by:

$$\begin{aligned} f &= \text{fraction of contacts who are traced,} \\ i &= \text{fraction of each contact's infectious period that they will spend in quarantine,} \\ &\quad \text{if the contact tests positive } d \text{ days after infection.} \end{aligned}$$

For COVID-19, a reasonable formula for i in terms of d is:

$$i = \begin{cases} 1 & \text{if } d \leq 5, \\ \frac{15-d}{10} & \text{if } 5 < d \leq 15, \\ 0 & \text{if } d > 15. \end{cases} \quad (19)$$

This formula assumes that infected individuals become infectious on day 6 of their infection, and are removed after day 15, on average. The formula could be modified with additional terms, to follow the progression of the disease more realistically.

The first infectious person in the population can be expected to infect R_0 individuals in the first generation, by definition. These individuals can either be contact-traced or not. The first generation individuals who are not contact traced will then each infect an average of R_{eff} individuals in the second generation, leading to an N_{nc} infections on average:

$$N_{nc} = (1 - f)R_0R_{\text{eff}}.$$

The first generation individuals who are contact-traced will be quarantined for fraction i of their infectious period, which means they can each infect people only during the fraction $1 - i$ of that period, leading on average to $(1 - i)R_{\text{eff}}$ new

infections in the second generation. Thus the first generation individuals who are contact-traced lead to N_c infections in the second generation:

$$N_c = fR_0(1 - i)R_{\text{eff}}$$

The combined number of new infections in the second generation is then

$$\begin{aligned} (R_{\text{eff}})^2 &= N_{nc} + N_c \\ &= (1 - f)R_0R_{\text{eff}} + fR_0(1 - i)R_{\text{eff}}, \end{aligned}$$

which simplifies to

$$\boxed{R_{\text{eff}} = (1 - fi)R_0}. \quad (20)$$

(An alternate derivation of this formula is given below, in terms of conditional expectations.) We conclude that $R_{\text{eff}} < 1$ if and only if the following condition is true:

$$\boxed{fi > 1 - 1/R_0}. \quad (21)$$

The R_0 value for COVID-19 is 2.5, therefore one needs $fi > 0.6$ in order to get $R_{\text{eff}} < 1$.

Formula (21) illuminates the quantitative trade off between the fraction of contacts traced and the speed with which tracing occurs. Using equation (19), we see the requirement (21) for getting $R_{\text{eff}} < 1$ is equivalent to

$$f > \begin{cases} 6/(15 - d) & \text{if } d \geq 5 \\ 0.6 & \text{if } d < 5 \end{cases} \quad (22)$$

where d is the number of days to trace the infection. Since $f \leq 1$, we conclude that the requirement for getting $R_{\text{eff}} < 1$ cannot hold if $d \geq 9$.

The practical conclusion is that for contact tracing and quarantining alone to reduce the effective reproduction number of COVID-19 to less than 1, the tracing must be completed within 9 days from the date of infection, and preferably sooner, so that only a smaller fraction of contacts need be successfully traced.

Perfect quarantining ($q = 0$) is assumed in the discussion above. If quarantining only partially effective ($0 < q < 1$) then i should be multiplied by $1 - q$, so that the condition (21) for getting $R_{\text{eff}} < 1$ becomes $(1 - q)fi > 1 - 1/R_0$.

The results are in good agreement with the simulations in Figures 5 earlier in the paper. The sixth graph in that figure shows the epidemic is completely suppressed when $R_0 = 2.5$, $q = 0.2$ and $\kappa = 10$ days.

Derivation of equation (20) in terms of conditional expectation.

In probabilistic language, f is the probability of an infected person being identified by contact tracing, which we write $P[\text{traced}]$. The effective reproduction number is the expected number of “descendant” infections that each infected person generates, and so

$$\begin{aligned} R_{\text{eff}} &= E[\text{descendants}] \\ &= E[\text{descendants}|\text{traced}] P[\text{traced}] + E[\text{descendants}|\text{not traced}] P[\text{not traced}] \\ &= (1 - i)R_0f + R_0(1 - f) \\ &= (1 - fi)R_0, \end{aligned}$$

which gives equation (20). This derivation assumes that an infected person who is not identified by contact tracing will go on to infect R_0 people, on average, while if the person is traced then they will be quarantined for fraction i of their infectious period and so will infect only $(1 - i)R_0$ people.

Literature related to inequality (21).

Müller et al. [6] take $i = 1$, meaning that tracing and quarantining occur before the contacts become infectious. They arrive at $f > 1 - 1/R_0$. Fraser et al. [2] take $f = 1$, meaning all contacts are successfully traced, and arrive at $i > 1 - 1/R_0$ (which is expressed in their notation as $\theta < 1/R_0$). Thus both these formulas are special cases of (21).

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