Alert Level 2.5 is insufficient for suppression or elimination of COVID-19 community outbreak

Report provided to officials February 15th, 2021;
this version published after internal peer review July 22nd, 2021

Author list alphabetical

Emily Harvey[1,2,*]**, Oliver Maclaren**[3]**, Dion O'Neale**[1,4,*]**, Frankie Patten-Elliott**[3]**, Steven Turnbull**[1,4,5]**, and David Wu**[3]

[1]Te Pūnaha Matatini, University of Auckland, NZ
[2]M.E. Research, Takapuna, Auckland, NZ
[3]Engineering Science, University of Auckland, NZ
[4]Physics Department, University of Auckland, NZ
[5]Faculty of Education and Social Work, University of Auckland, NZ
[*]Corresponding author e-mail addresses: emily@me.co.nz; d.oneale@auckland.ac.nz

EXECUTIVE SUMMARY

We use an Aotearoa-specific, individual-based network contagion model to simulate the spread of COVID-19 in the community with control measures representing Alert Level 2.5 turned on when the first case is detected.

Our simulations for a community outbreak with no direct link to the border – similar to the 2020 Auckland August outbreak situation – find that Alert Level 2.5 would be unlikely to suppress or eliminate the outbreak.

Only $\sim 19\%$ of simulations with a case detected eliminated the outbreak within 150 days of detection. All others had uncontrolled growth with $R_{\text{eff}} > 1$. Furthermore, we find that Alert Level 2.5 would still be insufficient, even if augmented by improved contact tracing through widespread use of QR code scanning, Bluetooth tracking of close contacts and faster manual contact tracing. These contact tracing improvements slightly decreased R_{eff} and the total number of cases at 150 days but had no statistically significant increase in the fraction of simulations with elimination in 150 days of detection or less.

The probability of elimination in our simulations is strongly linked to the outbreak size at initial detection when the Alert Level 2.5 intervention is applied. Outbreaks with 10 or fewer total cases (including unknown cases) at the time of alert level elevation have an approximately 60% chance of being eliminated within 150 days of detection, while if the outbreak size is 11 or more at the point when alert levels are elevated, the probability of elimination falls to under 12%. This threshold behaviour underlines the importance of the second component of the *Go Hard, Go Early* strategy of the pandemic response pursued in Aotearoa.

We note that the magnitude of the impact of improved contact tracing on contagion control observed at Alert Level 2.5 would be different at other alert levels: the effects of various interventions combine non-linearly in our model. Furthermore, we note that we are assuming a reasonably high level of contact tracing in the 'baseline', both in terms of the fraction of contact that are knowable by the National Contact Tracing Service (NCTS) and the rate of successfully contacting them, with no capacity constraints in the system.

Introduction

We use a detailed individual-based network contagion model that explicitly represents ~ 5 million individuals along with the the contexts in which they interact. This network model includes stochasticity, spatial information, and individual demographic information, along with multiple distinct 'transmission contexts' including dwellings, workplaces, schools, and more generally in the community. It also includes an explicit representation of the contact tracing process.

We use this network-based contagion model to address the question of whether Alert Level 2.5 (AL2.5) is enough to eliminate a community outbreak with no clear epidemiological link to the border —similar to that seen in the 2020 Auckland August outbreak. This situation is distinct from (and more concerning than) the case of a positive test in a known MIQ worker or person with an epidemiological link to a MIQ worker. We simulate the outbreak under two scenarios: firstly AL2.5 as it was implemented in Auckland at the tail-end of the Auckland August outbreak (i.e. with the contact tracing processes and NZ COVID Tracer app usage as observed) and secondly with AL2.5 augmented by improvements in contact tracing technology and processes (i.e. higher rates of NZ COVID Tracer app usage, Bluetooth contact tracing, and improved speed of manual contact tracing).

Characterisation and parameterisation of Alert Level 2.5

Motivated by the question of "Could Auckland have eliminated the August outbreak using AL2.5?" we have developed a set of interaction, testing, and tracing parameters that is intended to reproduce as accurately as possible AL2.5 as it was implemented at the end of the 2020 Auckland August outbreak. It is also possible to implement a combination of technological, behavioural and procedural changes that could increase the effectiveness of contact tracing at AL2.5, without altering the restrictions or gathering size limits that applied. The parameterisation and characterisation of both of these scenarios is given below. Further details of the network-based model and the implementation of the test/trace/isolate (contact tracing and testing) programme is given in the Method section.

Alert Level 2.5 (AL2.5)

For AL2.5 only, we assume a reduction in transmission occurs via various control policies. These reductions are relative to the model's calibrated default values, not relative to other scenarios.

We assume that schools are still open with attendance at 94% of usual, but there are some transmission reduction measures in place such as reduced activities (like assemblies). These changes translate into our model as a close contact transmission risk 94% of default (no interventions) and a causal contact risk of about 80% of default. These measures roughly translate to an overall reduction in the likelihood of transmission in schools by around 6%, as the transmission risk for close contacts is much larger.

Workplaces can remain open under AL2.5, but working from home is encouraged where possible. Furthermore, additional measures to keep workers safe are typically used, such as physical distancing, mask-wearing, and increased hygiene measures. We model this using transmission rates in workplaces of around 70% of default for close contacts and around 60% of default for casual contacts.

In the community under AL2.5, 'close' gatherings of over 10 people are not allowed, with appropriate considerations for weddings, funerals, and tangihanga. We also expect a decrease in the number of events attended. We assume widespread adoption of mask-wearing and distancing, which reduces casual contact transmission rates. These interventions translate into our model as a reduction in all (non-dwelling) community interactions by around 50%. We do not strictly enforce the rule of no groups over 10 but enforce no groups over 100 people. We note that these community gatherings are modelled as either 'close' or 'casual', with no specification on their type (e.g. public transport, weddings, religious gatherings). That is, all interaction contexts, or group nodes, represented by the community layer are drawn from the same group size distribution and all follow the same interaction mechanism, parameterised as either 'close' or 'casual' contact.

We include contact notification and tracing processes in our model. In reality, casual contacts are notified through media announcements, NZ COVID Tracer app 'exposure notifications', and some manual contact tracing. Casual contacts are advised to get a test regardless of symptoms. These translate to the following model parameter changes: Once the first case has been detected, we assume there is a testing surge and 50% of mild symptomatic community cases get tested (the 80% test positivity rate means 40% of cases test positive) and 80% of serious symptomatic community cases get tested (64% of cases test positive). Tested individuals are notified of their test results in a mean of **4 days post symptom onset**, matching rates seen in the Auckland August 2020 outbreak.

Close contacts are traced at a rate fitted to fit to metric S0003 in the National Contact Tracing Performance reports. Specifically, we use a Weibull distribution with parameters: scale = 3.04, shape = 2.66, which gives a median time (since confirmed test) to notify a close contact of 2.65 days. There is a prioritisation in contact order such that household (dwelling) contacts are contacted sooner than other contacts.

It is assumed that all members of a confirmed case's dwelling, 95% of close workplace or school contacts, and 80% of community close contacts are known and reachable by contact tracers. Contact tracing attempts are then made with a 10% chance of failure per attempt for contacts that do not share a dwelling with the confirmed case. If an attempt fails, up to 5 more attempts are made at making contact, with an inter-attempt time modelled by an exponential distribution with rate = 4.

In the baseline AL2.5 scenario, we model the casual-plus category by assuming that 50% of casual contacts in dwellings*, 50% of casual contacts in schools and workplaces, and 10% of casual contacts in the community would know they were a casual contact and seek a test. For this percentage, the delay between the confirmed case notification and the casual contact seeking a test is between 2.5 and 7 days, with the times modelled as a scaled Beta distribution with parameters $a = 3, b = 5$.

Alert Level 2.5 with improved contact tracing (AL2.5+)

We address the impact of QR codes, Bluetooth tracing, and manual improvements all together. In terms of parameter changes in our model, we: **increase the likelihood of casual contacts in the community getting tested to 25%** (from 10%); **increase the proportion of community close contacts known to 95%** (from 80%); and **increase the speed of close contact tracing** by adjusting the parameters of the Weibull Distribution to: scale = 2.6, shape = 1.7. This is a reduction of the median time (since confirmed test) to notify a close contact from 2.65 days in the baseline case to 2.10 days in this scenario.

Simulation results

We ran 500 simulations for each of the Alert Level 2.5 (AL2.5) and Alert Level 2.5 plus improved contact tracing (AL2.5+) scenarios. Each simulation was seeded by setting the state to infected (specifically to 'Exposed') for a single, randomly selected, individual in Auckland. Pre-detection testing rates and behaviour were the best estimate of AL1. Further details of the initial conditions and set-up are given in the Initial Conditions section.

Pre-detection phase

Since the simulation conditions **before detection of the first case** are identical for the AL2.5 and AL2.5+ scenarios, we can combine the simulation results for any analysis of this phase of the outbreak. We exclude from analysis any simulations where the infection died out without being detected (i.e. infections that do not spread and which remain unknown) or where there is no further transmission from the first detected case (i.e. the infected case is isolated at detection and no outbreak occurs). This leaves a remaining 766 (372 for AL2.5; 394 for AL2.5+) of the 1000 total simulations with an outbreak of total size of two or more cases.

The median time from the initial seed case to detection of the first case in a community outbreak ranges from two to just under four weeks (median = 20 days; [LQ = 14, UQ = 26]). The most common outbreak size at the time of detection is in the range of 10–40 total cases.

Post-detection phase

One of the best measures of whether a specific intervention, or combination of interventions, would be sufficient to control an outbreak is to count the fraction of outbreaks that are brought under control (either zero active cases, or zero non-isolated active cases) in a specified time period. Here we report the fraction of outbreaks with zero active cases 150 days from detection. Additionally, we report the estimated value of R_{eff} during the period of the simulation when the intervention (AL2.5 or AL2.5+) was active, along with the distribution of outbreak sizes at 60 and 150 days post-detection for both 'total cases' and the smaller subset of 'known (confirmed) cases'. Though R_{eff} is not a basic input of our model, we can post-process our overall results to provide estimates of it[1]. In the present work we post-process our results using the simple approximation[2,3] $R_{\text{eff}} \approx r \times$ generation time + 1 to provide an indication of this, where r is the observed exponential epidemic growth rate.

Probability of elimination

We find that in simulations with AL2.5 applied post-detection, only 72 (19.4%) of the 372 simulations with a case detected completely eliminated the outbreak within 150 days of detection. All others had uncontrolled growth with $R_{\text{eff}} > 1$. Similarly, we find that for Alert Level 2.5 with improved contact tracing (AL2.5+) applied post-detection, only 84 (21.3%) of the 394 simulations with a case detected completely eliminated the outbreak within 150 days of detection . All others had uncontrolled growth with $R_{\text{eff}} > 1$. A two-sample test for equality of proportions indicates no statistically significant difference between the proportion of simulations that eliminate completely within 150 days of detection. That is, both **AL2.5 and AL2.5+ are insufficient to eliminate an outbreak** and AL2.5+ gives no appreciable improvement of the likelihood of elimination. (The evidence is that there is either no effect, or that the effect is too small to see in 500 simulation runs.)

It is worth noting that this does not imply that improved contact tracing measures have no effect on the probability of elimination in other contexts. It is expected that the impact of such measures is non-linear and may for example, show an

---

*all dwelling contacts will be close contacts except in large shared dwellings (occupancy over 12). NB: apartment complexes are not large dwellings, as these are considered separate, and unlinked, dwellings in Census records.

improvement in disease elimination at other Alert Levels where there are different transmission dynamics on account of different interaction patterns between individuals.

The probability of elimination is strongly dependent on the size of the outbreak at first detection; when outbreaks are detected sooner and are smaller, the likelihood of elimination within 150 days of detection is greatly increased. In Table 1 we group the outbreaks by their size (cumulative cases) at detection in size bins defined by the Ministry of Health in the earlier Elimination Strategy report[4]. We find that the probability of elimination for outbreaks of size 2–10 at detection is around ~60% while for outbreaks detected at size 11–20 the probability of elimination falls dramatically to around ~12%. Note: a two-sample test for equality of proportions showed no evidence of a statistically significant difference between the AL2.5 and AL2.5+ within any of the outbreak size bins.

Scenario	% of **all outbreaks** that reach elimination	By size of outbreak at detection			
		2-10	11-20	21-50	51-100
AL2.5	19%	58%	11%	2%	0%
AL2.5+	22%	65%	14%	0%	0%

Table 1. Percentage of simulations that reach elimination by day 150 for different initial outbreak sizes at detection and interventions. The number of runs in each bin of outbreak sizes is noted in table 4. Note: a two-sample test for equality of proportions showed no evidence of a statistically significant difference between the two scenarios for any of the outbreak sizes.

Figures 1 and 2 show trajectories, under AL2.5 for the cumulative cases and new daily cases, respectively, along with the corresponding median and upper and lower quartiles.
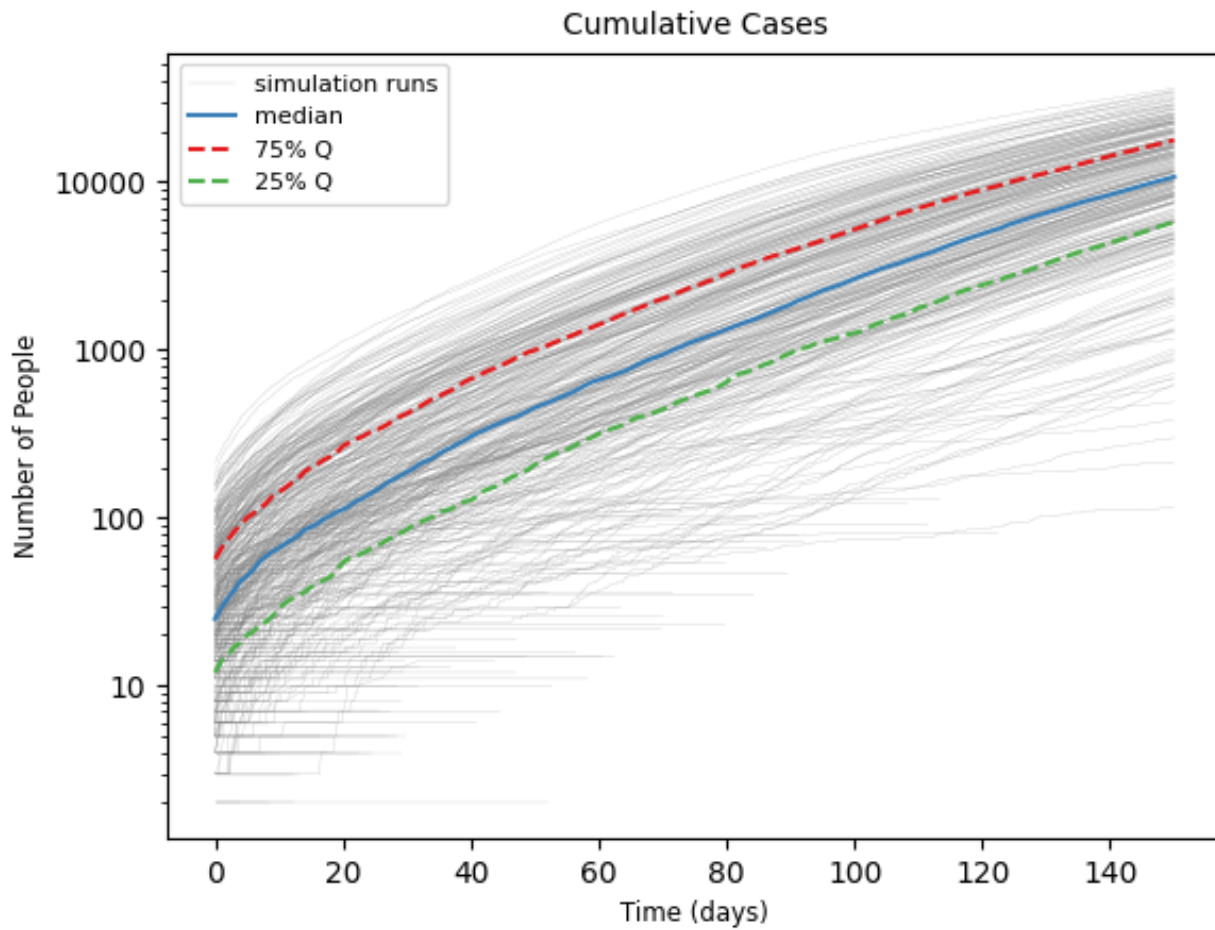
Cumulative Cases

Figure 1. Cumulative cases on a log scale, for 150 days post-detection under Alert Level 2.5. Although some simulations eliminate (as indicated by trajectories that flatten out and end before 150 days), the number of infected cases continues to grow exponentially for 80% of simulations.
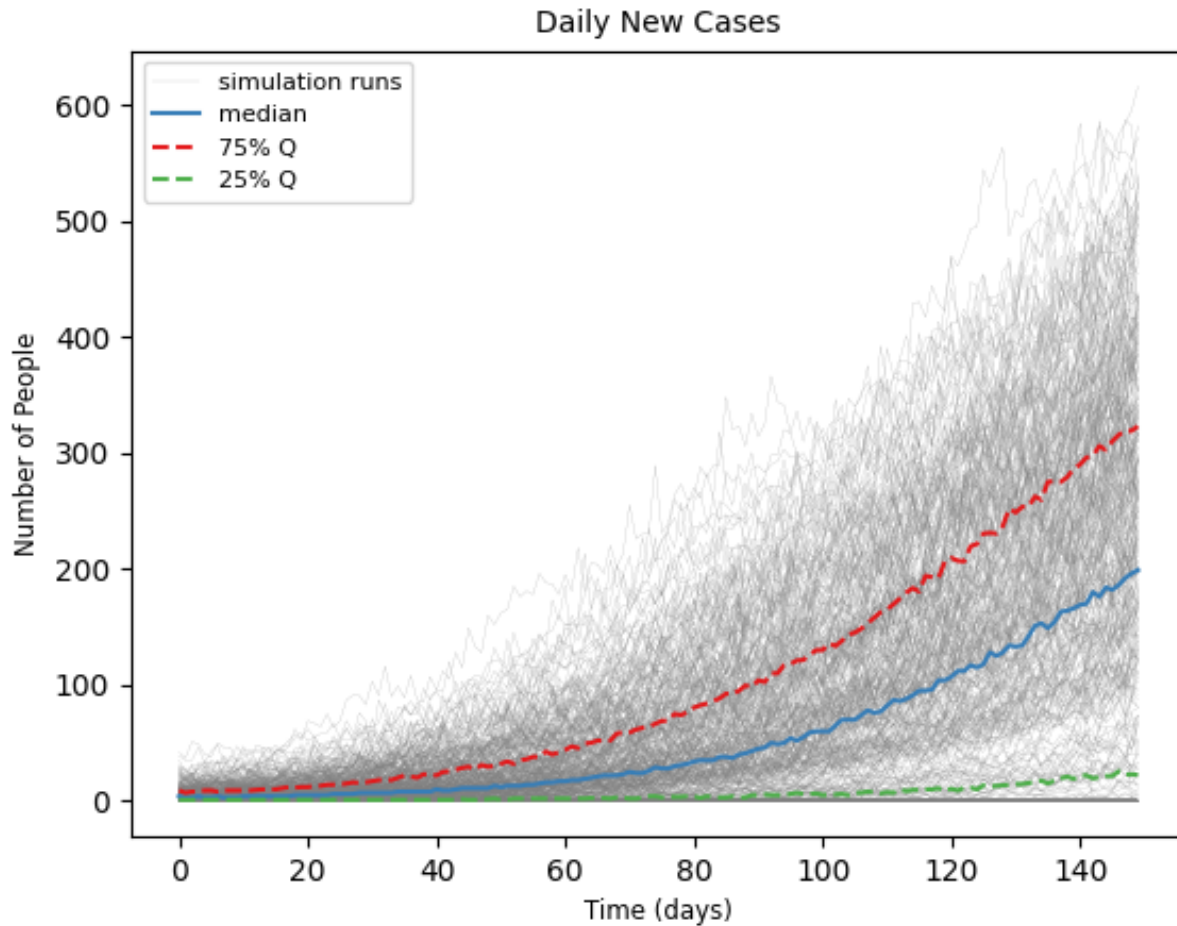
Figure 2. Daily new cases, for 150 days post-detection under Alert Level 2.5. Around 20% of trajectories die out, reaching zero daily new cases within 150 days of initial detection. However, the majority of simulations show an increasing number of new cases per day.

Estimate of R_{eff} during intervention period

During the simulation period when AL2.5 is in effect, we calculate a median R_{eff} of 1.12 [1.1,1.14] from the active number of cases. If AL2.5 intervention is replaced by AL2.5+ then the median R_{eff} is 1.11 [1.08,1.12]. The very slightly lower value of R_{eff} for AL2.5+ is statistically significant, however the difference is very small (95% confidence interval of 0.013-0.022) and since both values of R_{eff} are greater than 1, this difference is inconsequential in the context of an Elimination Strategy.

Size of outbreak at 60 and 150 days post-detection

To better quantify the nature of the outbreaks seen under AL2.5 and AL2.5+ we report the outbreak sizes at 60 and 150 days post-detection. The results for 60 days post-detection are reported in Table 2 and distributions of the cumulative outbreak sizes at 60 and 150 days post-detection are shown in Figure 3.

For AL2.5, there are a median of 493.5 [128, 1161] cumulative cases from the first seed case until 60 days post-detection, and a median of 8259 [1327, 15246] cumulative cases after 150 days post-detection. If we consider only 'known' (confirmed through testing) cases, the cumulative case counts are a median of 213 [67, 486] after 60 days post-detection, and a median of 3899 [621, 7516] after 150 days post-detection.

With the improved contact tracing under AL2.5+, there are a median of 453.5 [108, 973] cumulative cases from the first seed case until 60 days post-detection, and a median of 5054 [678, 9634] cumulative cases after 150 days post-detection. If we consider only 'known' (confirmed through testing) cases, the cumulative case counts are a median of 200 [48, 432] after 60 days post-detection, and a median of 2430 [365, 4861] after 150 days post-detection.

This suggests that even when it is insufficient to control an outbreak, improved contact tracing is likely to still play a role in reducing the *size* of an outbreak.

Scenario	Case type	Cumulative number of cases at 60 days	Cumulative number of cases at 150 days
AL2.5	Confirmed	213 [67, 486]*	3899 [621, 7516]*
	Total	493.5 [128, 1161]	8259 [1327, 15246]*
AL2.5+	Confirmed	200 [48, 432]*	2430 [365, 4861]*
	Total	453.5 [108, 973]	5054 [678, 9634]*

Table 2. Cumulative Cases (confirmed cases and total cases) at day 60 and 150 post-detection for all outbreaks. Results shown are reported as *median [lower quartile, upper quartile]*. Note: a Mann-Whitney-Wilcoxon test was performed and showed evidence (at the 0.05 level) of difference between the two Scenarios for the results indicated with an asterix *.
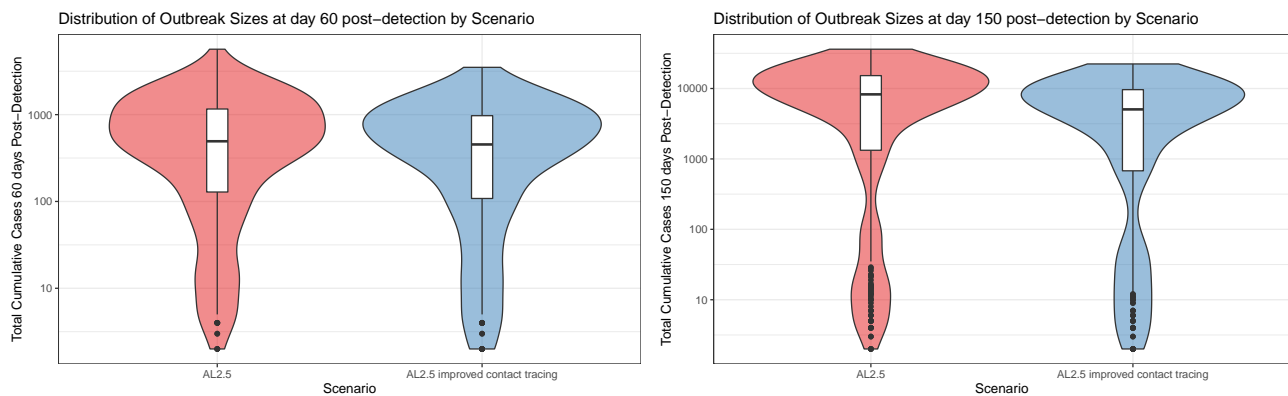

Figure 3. Distribution of Total Cumulative Cases at day 60 and day 150 by Scenario and Outbreak Size at Initial Detection. This plot shows the distribution of the total cumulative number of cases (i.e. both confirmed cases and unknown cases) at day 60 and day 150 after detection **on a log scale**. Note: the scale of the y-axis differs between the two times. Results are split across the scenarios of AL2.5, and AL2.5+. Density plots indicate the lower quartile, median, upper quartile, and distribution of outbreak sizes across the set of simulations for each intervention scenario.

As expected, the outbreak dynamics are influenced by the initial size of the outbreak. At 60 days post-detection, outbreaks with a size at detection in the range 2–10 and AL2.5 (respectively AL2.5+) had a median of 36.5 (resp. 25) total cases compared with a median of 374 (resp. 302.5) for outbreaks with a size at detection in the range of 11-20. Table 3 reports cumulative number of total and 'known' cases at 60 days post-detection, while Figure 4 shows the distribution of the total cumulative outbreak sizes at 60 and 150 days post-detection for a range of different initial outbreak sizes.

Scenario	Case type	Size of outbreak at detection			
		2-10	11-20	21-50	51-100
AL2.5	Confirmed	19 [5,67]	167 [95,237]*	351 [233, 538]*	802 [667, 972]*
	Total	36.5 [9, 144]	374 [212, 586]	823 [570, 1271]*	1891 [1498, 2418]*
AL2.5+	Confirmed	15 [4, 52]	137.5 [58, 239]*	321.5 [218, 468]*	691 [563, 887]*
	Total	25 [6,121]	302.5 [123.5, 589]	747 [483, 1100]*	1596 [1288, 2059]*

Table 3. Cumulative Cases (confirmed cases and total cases) at day 60 post-detection binned by different initial outbreak sizes at detection. Results shown are *median [lower quartile, upper quartile]* unless otherwise stated. Note: a Mann-Whitney test was performed and showed evidence of difference between the two Scenarios for the results with an asterix *.

Figure 4. Distribution of Total Cumulative Cases at day 60 and 150 post-detection by Scenario and Outbreak Size at Initial Detection. This plot shows the distribution of the total cumulative number of cases (i.e. both confirmed cases and unknown cases) at day 60 and 150 post-detection **on a log scale, with the scale of the y-axis differing for 60 and 150 days**. Results are split by outbreak size at initial detection (four sub-figures) and across the scenarios of AL2.5, and AL2.5+. Density plots indicate the lower quartile, median, upper quartile, and distribution of cumulative outbreak sizes across the set of simulations for each initial outbreak size and intervention scenario. Note that outbreaks that eliminated stay under around 100 cases in total, so the split that is evident especially in the 11to20 outbreak size bins is the split between simulations that eliminate and those that don't.

Method

Description of model and key assumptions

We implement a stochastic model of infection dynamics on a detailed interaction network of all ~ 5 million individuals in Aotearoa NZ. Each **individual** is represented by a node in this network; additional **group** nodes are used to represent the different **infection contexts** through which individuals can interact and transmit infection. Each individual has the demographic characteristics of age, sex, ethnicity, and geographic location (Statistical Area 2 (SA2)) of usual residence. These are sourced from Census 2018 figures. Individuals are placed in **dwellings**, with other individuals, in the same geographic location (SA2) based on Census 2018 dwelling size and age structure within that SA2. Besides dwellings, many individuals have places of **work** (tax data from the Statistics NZ Integrated Data Infrastructure (IDI)) and/or **education** (Ministry of Education roll data), and all individuals participate in so-called **community** events which capture all interactions which are not with other people in their dwelling, or work/school (i.e socialising, shopping, using public transport, and attending church or sporting events). The community interactions also include long-range travel within Aotearoa New Zealand, based on cellphone movement data[5]. As was noted earlier, we do not currently distinguish between different types of community interactions: the community interaction event groups sizes are drawn from a single distribution.

Group nodes are further classified as involving **close** or **casual** (background) contact behaviour. In small dwelling, school, and workplace groups, we assume that all contacts are both close and casual contacts. But if groups are larger (e.g. a whole school or a large workplace), we create smaller groups within the large group which represent the smaller number of close contacts such as a class within a school or a team within a workplace. Within the large school and workplace groups, we assume only a casual contact level of interaction. For community events, however, we categorise these as either close or casual contact type interactions in advance.

Close contacts are assumed to be contact traceable, if 'known' (by the National Contact Tracing Solution team), and the proportion of close contacts who would be 'known' varies by context (e.g. all dwelling close contacts are known, but only a lower proportion of social/community close contacts are known) and is influenced by contact tracing effectiveness and technology assumptions. In our model, casual contacts are not directly traced, but if they know that their casual contact(s) have been confirmed as COVID-19 positive (through e.g. media reports, NZ COVID Tracer app alerts), then they increase their likelihood of seeking a COVID test. The proportion of casual contacts who would know that they may have been exposed, and who subsequently, would seek a test varies by interaction context. This number is also influenced by the methods used by public health officials for notifying people and what the advice to casual contacts is. Our model also includes policy effects, representing non-pharmaceutical interventions such as Alert Levels, which reduce the chance of transmission in various interaction contexts, and increase community (general public) test-seeking behaviour.

We use the Gillespie algorithm[6] to simulate our contagion dynamics. This algorithm is a so-called exact algorithm for simulating realisations from a collection of independent *transition* processes with rates (or *hazards*) of the form:

$$\text{Probability of transition } i \text{ per unit time} = h_i(\text{system state}) \tag{1}$$

for $i = 1, ..., n$. In this context, a transition consists of one or more individuals changing their state; for example, a susceptible individual becoming exposed due to an encounter with an infected individual. This simulation approach was popularised in the stochastic chemical kinetics literature, but also has a long history of applications to population dynamics[7] and is now standard in the network contagion literature[8].

Key assumptions

Full model details are described elsewhere[9], but key assumptions and parameters include:

- Disease progression for infected individuals proceeds through a sequence of states. Initially, exposed individuals are infected but not yet infectious, they transition to either pre-symptomatic or asymptomatic states (both infectious). Cases that will go on to develop symptoms (pre-symptomatic) are further split into being 'mild' or 'severe' cases, with this varying by age. Note that this case severity is based on eventual outcome, and is not specifically the symptom severity at onset. Severe cases can become hospitalised and can die while the remainder of the infected cases recover. The parameters controlling transitions between these states are based on international literature — primarily from Fraser et al.[10].

- There is negligible difference in the rate of recovery from exposure between different symptom presentations.

- The proportion of infections that are asymptomatic varies with age, and equates to about 16% over the whole population, in line with findings from PCR based studies with inclusive symptom case definitions[11, 12]. Asymptomatic cases are assuming to have zero chance of being tested for COVID-19 unless they have been identified as a casual or close contact of a confirmed case.

- The split of (pre-)symptomatic cases into being 'mild' or 'severe' cases, also varies by age. Case severity determines primarily the probability of hospitalisation (zero for mild cases)[9], but also affects the likelihood of infected individuals to seek testing (severe cases are more likely to seek medical attention and thus have a higher testing probability).

- Infectiousness of individuals at any infectious (asymptomatic, pre-symptomatic, or symptomatic) stage of their infection is identical to any other individual in the same infectious stage of infection.

- Infectiousness of asymptomatic and pre-symptomatic individuals is identical to symptomatic individuals.

- Individuals have a probability of getting a test depending on their infection state and scenario settings. Given that they do get tested, the time it takes from symptom onset to receiving a positive result is modelled as an exponential distribution, with the speed dependent on scenario settings.

- Individuals will not isolate or change their behaviour until they either receive a positive test, or are contacted by contact tracing.

- Individuals will stay in self-isolation for 14 days, starting from when they are first contacted by contact tracing.

- Individuals that receive positive tests will stay in an MIQ facility until they recover.

- Infected individuals in self-isolation can infect others in their dwelling and have a small (1%) chance to infect others outside of isolation.

- Infected individuals in MIQ (confirmed cases) have a small (1%) chance to infect others outside of isolation/quarantine.

- Contact tracing traces a proportion of close contacts of a confirmed case. The proportion depends on the interaction group type, as well as scenario settings.

- Close contact tracing is modelled by a finite number of attempts at contact, each with a small chance of failure, dependent on the type of group (e.g. work vs dwelling) that connects the close contact with the confirmed case.

- Casual contacts of a confirmed case have a certain probability that they would both i) know they were a close contact, and then ii) would go to get a test; with some delay between the confirmed case notifying and a test being returned to the casual contact. The probability that a casual contact would seek a test depends on the interaction group type or context, as well as scenario settings.

Initial conditions

In order to create initial conditions for each Alert Level 2.5 intervention, we set 500 simulations running using parameters for our best estimate of a 'Baseline Alert Level 1'[4] to simulate infection spread prior to detection of the first case. Once the first infected case is detected and confirmed we turn on the Alert Level 2.5 simulation parameters described above.

This approach ensures that we start with not just an initial number of infections but with an epidemiologically based contagion tree to allow for contact tracing. This provides more realistic infection histories for each simulation, but means that the number of simulations and the size of the outbreaks at detection are not identical for each simulation run. This increases the run-to-run variability within and between different interventions.

For Baseline Alert Level 1 (pre-detection) we assume that there is some mask wearing and social distancing which will reduce casual community transmission by 10% below the model's calibrated default values. We set the proportion of symptomatic cases who would seek a test to 10% for mild/moderate cases and 50% for severe cases[†], based on levels of testing in Auckland estimated from FluTracking data[13]. We assume a test positivity rate of 80%[14], which equates to a probability of detection of 8% for mild/moderate cases, and 40% for severe. Finally, we assume the time from symptom onset to test result is exponentially distributed with a mean time from symptom onset to test result of 5 days. It is worth noting that the proportion of cases detected will vary depending on age solely due to the the higher proportion of asymptomatic cases and lower proportion of severe cases for younger individuals. For example, in the baseline case 0–14 year olds will have a case detection of ≈7% whereas over 60s will have a case detection of ≈16%. We know from FluTracking data[13] that testing rates are *much* lower in younger age groups even after accounting for symptom presentation. Based on this, we suspect that the parameters in our scenarios correspond to a higher rate of testing in under 15s than is actually observed.

Even though the transmission settings in the simulation are identical for the AL2.5 and the AL2.5+ scenarios during the pre-detection phase, the distribution of the outbreak sizes at detection can differ between the two sets of simulations, due to stochastic effects. Since the outbreak size at detection is an important factor in the progression of an outbreak, post-detection,

---

[†]severe cases are those that would be expected to seek medical attention for breathing difficulties, pneumonia, etc.

we compare the distribution of outbreak sizes at detection for the simulation runs that are used for the AL2.5 and AL2.5+ scenarios. See Table 4 and Figure 5.

Scenario	All runs	Distribution of different initial outbreak sizes			
		2-10 (n)	11-20 (n)	21-50 (n)	51-100 (n)
AL2.5	19 [9,41] (372)	5.5 [4, 7] (104)	15 [13, 18] (91)	32 [26, 41] (115)	71 [56, 82] (62)
AL2.5+	20.5 [9,37] (394)	6 [4, 8] (111)	15 [12, 19] (86)	33 [26, 38] (140)	67 [61,81] (57)

Table 4. Distribution of initial outbreak sizes within each size band for the simulations from the pre-detction phase of the AL2.5 and AL2.5+ scenarios. The number of simulations (with at least one post-detection transmission event) in each size band is indicated in parentheses (n). Results shown are *median [lower quartile, upper quartile]* unless otherwise stated.
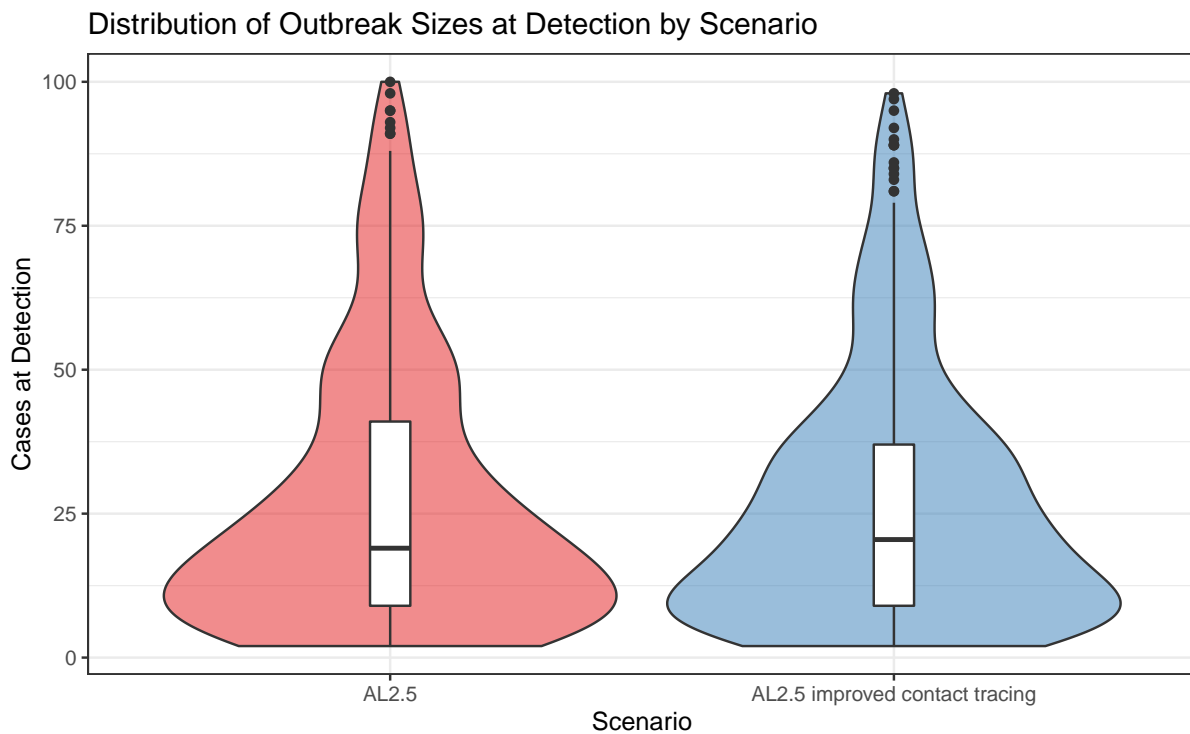

Figure 5. Distribution of Initial Outbreak Sizes by Scenario. This plot shows the distribution of initial outbreak sizes across the scenarios of AL2.5, and AL2.5+. The distributions of the initial outbreak sizes used for the simulations are comparable across intervention scenarios.
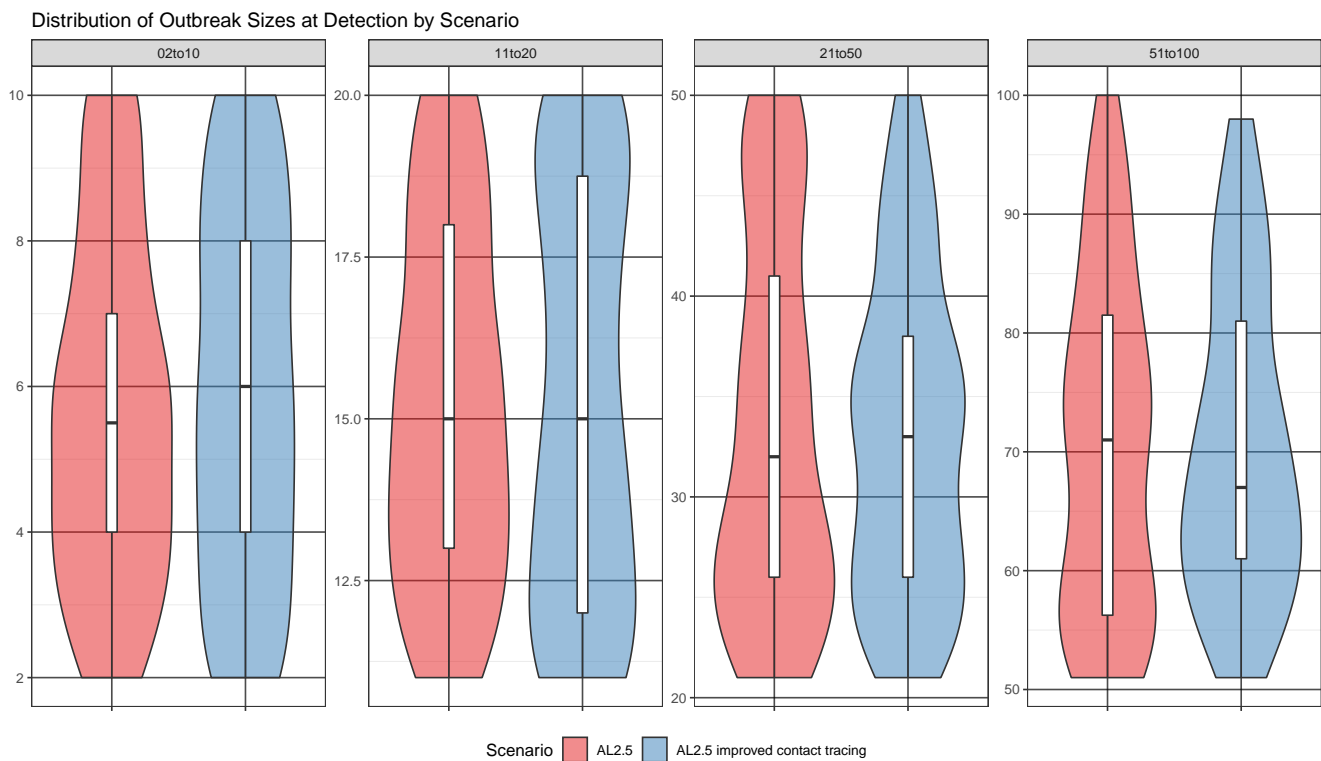
Figure 6. Distribution of Initial Outbreak Sizes within each size bin, by Scenario. This plot shows the distribution of initial outbreak sizes within each outbreak size bin, across the scenarios of AL2.5, and AL2.5+. The distributions of the initial outbreak sizes used for the simulations are comparable across intervention scenarios and within groups of initial outbreak size.

Discussion

The results presented here show that Alert Level 2.5 is unlikely to lead to elimination of a community outbreak of COVID-19, in a scenario similar to that observed in the 2020 Auckland August outbreak. Improving contact tracing through higher rates of QR code scanning, Bluetooth tracing and faster manual contact tracing has little to no effect on the probability of eliminating such an outbreak.

We find that both the probability of elimination and the total cumulative size of an outbreak are strongly linked to the size of the outbreak at initial detection. Outbreaks smaller than 10 cases at initial detection are around five times more likely to eliminate and around 10 times smaller in cumulative size than outbreaks with more than 10 cases at initial detection. It is important to note that the threshold for the initial outbreak size of greater or less than ten is not a 'magic number' of cases with different dynamics on either side of a sharply defined bound. The bin sizes used in this report (2–10, 11–20, 21–50, 51–100) are those used in a previous report prepared for the Ministry of Health[4]. **The key message from this finding is that the smaller an outbreak is when interventions, such as increasing Alert Levels, are first applied, the higher the probability of elimination and the smaller the total outbreak size.** A forthcoming report will specifically address the question of the effect of delays in elevating Alert Levels after initial detection of a case of community transmission.

Although the simulations here suggest that improved contact tracing at Alert Level 2.5 has little to no effect on increasing the chance of elimination, this will not necessarily be true at all Alert Levels. The effect of any interventions will typically be non-linear and context dependent and hence it is typically not possible to assume that the effect of applying an intervention in one scenario will lead to the same increase or decrease in R_{eff} in another scenario.

Furthermore, the parameters used here for the baseline level of contact tracing are relatively optimistic and assume no capacity constraints on the speed of identifying close contacts through case interviews or number of contact tracing attempts per day. Improvements in contact tracing technology may reduce outbreak size or duration, not because they improve the speed or effectiveness of contact tracing, but because they increase the number of contact tracing attempts that can be made before capacity constraints are reached. At lower Alert Levels, when few other contagion limiting interventions, such as restricting interactions, are in effect, contact tracing is likely to be a significant factor in controlling infection spread.

The parameters used in these simulations are the best that the authors were aware of at the time of running these simulations in late 2020 and the best available estimates for a mathematical parameterisation of interaction and COVID control measures under Alert Level 2.5. However, as with any model, they require making a number of assumptions and best guesses in order to incorporate limited empirical data into a mathematical model. Obviously, changes to these parameters will change the results of the simulations.

Uncertainty also arises from the stochastic nature of the simulations . Most of the results reported here are medians and in most cases we have also included interquartile (25th percential and 75th percential) ranges. Figures illustrating the run-to-run variability (Figures 1 and 2) show trajectories of all simulations. These give an indication of the degree of stochasticity in the simulations.

Finally, the simulations here do not consider the presence of newer and more highly transmissible variants of COVID. These will be addressed in a forthcoming report.

Acknowledgements

References

1. Breban, R., Vardavas, R. & Blower, S. Theory versus data: how to calculate R0? *PLoS One* **2**, e282 (2007).

2. Ma, J. Estimating epidemic exponential growth rate and basic reproduction number. *Infect Dis Model.* **5**, 129–141 (2020).

3. Wallinga, J. & Lipsitch, M. How generation intervals shape the relationship between growth rates and reproductive numbers. *Proc. Biol. Sci.* **274**, 599–604 (2007).

4. Harvey, E. *et al.* Network modelling of elimination strategy pillars: Prepare for it; stamp it out. Tech. Rep., Te Pūnaha Matatini (2020).

5. QriousNZ. Qrious inter-regional ground travel data. https://www.transport.govt.nz/mot-resources/research-papers/inter-regional-ground-travel-data-from-qrious/ (2019). Accessed: 2020-08-10.

6. Gillespie, D. T. A general method for numerically simulating the stochastic time evolution of coupled chemical reactions. *J. Comput. Phys.* **22**, 403–434 (1976).

7. Kendall, D. G. An artificial realization of a simple "Birth-and-Death" process. *J. R. Stat. Soc. Ser. B Stat. Methodol.* **12**, 116–119 (1950).

8. Kiss, I. Z., Miller, J. C. & Simon, P. L. *Mathematics of Epidemics on Networks: From Exact to Approximate Models* (Springer International Publishing, 2017).

9. Harvey, E. *et al.* Network-based simulations of re-emergence and spread of COVID-19 in Aotearoa New Zealand. Tech. Rep., Te Pūnaha Matatini (2020).

10. OpenABM-Covid19 model. https://github.com/BDI-pathogens/OpenABM-Covid19. Accessed: 2020-08-03.

11. Harvey, E., Maclaren, O. J., O'Neale, D. & Wu, D. Asymptomatic cases of COVID-19 in NZ: a study of data from the Auckland August re-emergence case data. Tech. Rep., Te Pūnaha Matatini (2020).

12. Byambasuren, O. *et al.* Estimating the extent of asymptomatic COVID-19 and its potential for community transmission: systematic review and meta-analysis. *medRxiv* DOI: 10.1101/2020.05.10.20097543 (2020). https://www.medrxiv.org/content/early/2020/09/13/2020.05.10.20097543.full.pdf.

13. Harvey, E. & Turnbull, S. 2020-12-18 fluTracking testing calculations. Tech. Rep., Te Pūnaha Matatini (2020).

14. Kucirka, L., Lauer, S., Laeyendecker, O., Boon, D. & Lessler, J. Variation in false-negative rate of reverse transcriptase polymerase chain reaction-based sars-cov-2 tests by time since exposure. *Annals Intern. Medicine* **173**, 262–267, DOI: https://doi.org/10.7326/M20-1495 (2020).