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# Addendum - Effect of COVID-19 variants with increased transmission rates on the effectiveness of Alert Level 4 for eliminating a community outbreak

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## EXECUTIVE SUMMARY

New variants of COVID-19 have emerged with mutations that increase their transmissibility by 30-70%<sup>1</sup>. We use an Aotearoa-specific, individual-based network contagion model to quantify the likely implications of a community outbreak involving one of these more transmissible variants. We do this by simulating the spread of a variant of COVID-19 with 50% higher transmissibility. We have previously reported metrics relating to spread of these new variants and the effectiveness of non-pharmaceutical interventions comparable to Alert Level 3 (AL3)<sup>2</sup>.

**This addendum report provides a summary of the impact of Alert Level 4 (AL4) on the transmission of the new variant, and compares it to the impact of AL4 on an outbreak of the old variant. Our simulations again represent the situation of community outbreak, with no clear epidemiological link to the border. **Our results show that AL4 results in elimination of 100% of model simulations for both the old and new more transmissible variant.** Furthermore, in contrast to the long periods of heavy contact tracing load at AL3, AL4 results in ‘complete isolation’ of most simulated outbreaks (78%) within 60 days post detection for the new variant.**

### Key points:

- All (100%) simulations of both the old and new variants under AL4 led to elimination within 200 days, with the median time to elimination (all cases recovered) being 68 [53, 83] days for the new variant and 54 [40,69] days for the old variant.
- AL4 is sufficient for achieving complete isolation of a community outbreak within 60 days in a high proportion (78%) of simulations for the new variant, with many of our simulations (38%) reaching elimination of an outbreak within this time.
- The time to ‘complete isolation’ of cases\* is 40 [26, 58] days (*median [LQ, UQ]*) for the new variant and 27 [17, 41] days for the old variant.

\*Complete Isolation is defined as all active cases being confirmed or in isolation as close contacts.

- From our simulations we calculate the median  $R_{\text{eff}}$  of the new variant under AL4 as 0.72 [0.68, 0.77]. This compares to a median  $R_{\text{eff}}$  of 0.65 [0.58, 0.71] for the old variant under AL4. Note, this is a 13% increase in  $R_{\text{eff}}$ , despite a 50% increase in infectivity, due to non-linear interactions with alert level and contact tracing interventions.
- For the new variant, AL4 is sufficient to keep new daily confirmed cases below the capacity limits of both the National Contact Tracing Solution (NCTS) and the Managed Isolation and Quarantine (MIQ) system. However, our results show that the number of isolations resulting from contact tracing is dependent on the size of outbreak upon detection. Outbreaks of larger size (e.g. over 100 cases) place substantially more demand on contact tracing resources than smaller outbreaks.
- These results suggest that AL4 is an effective strategy for elimination of outbreaks of both old and new variants of COVID-19, but early detection of outbreaks is still extremely important for reducing the duration the Alert Level intervention would need to be applied for.

## Characterisation and parameterisation of model simulations

We have developed a set of interaction, testing, and tracing parameters that are intended to reproduce as accurately as possible the transmission situation in the weeks prior to 14 February 2021, and the subsequent change to Alert Level 3 on February 15th.

In this addendum, we extend the scenarios to a stronger control, which we term Alert Level 4 (AL4). This involves the closure of more contexts of transmission, increased measures to reduce transmission, and increased propensities for symptomatic individuals to test. We also explore the effect of a more transmissible variant under this set of control measures.

We ran 500 simulations for the old variant and 500 simulations for the more transmissible variant, with AL4 applied post-detection. 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 Alert Level 1 (AL1), and were the same for both old and new variants. Once the first case is detected we turn on the AL4 simulation parameters. 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. However, this also 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.

### Increased transmission variants (‘New Variant’)

Based on technical reports<sup>3,4</sup> from the UK’s New and Emerging Respiratory Virus Threats Advisory Group, we investigate the impact of a variant of COVID-19 with a 50% increase in transmissibility, relative to older variants. We simulate this by increasing the  $\beta$  parameter, which characterises the infectivity of COVID-19 in the network contagion model, by 50%. For the ‘Old Variant’ simulations, we use a  $\beta$  parameter that corresponds to the infectivity of older variants of COVID-19 used in previous reports<sup>2,5-7</sup>. Other aspects of disease progression for the ‘New Variant’ are unchanged. There is some evidence for increased duration of infection in B.1.1.7<sup>8</sup>, but we do not include this here.

### Alert Level 1

For AL1 (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<sup>†</sup>, based on levels of testing in Auckland estimated from FluTracking data<sup>9</sup>. We assume a test positivity rate of 80%<sup>10</sup>, 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 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  $\approx 7\%$  whereas over 60s will have a case detection of  $\approx 16\%$ . We know from FluTracking data<sup>9</sup> 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.

These parameters for AL1 are consistent with earlier reports<sup>2,6,7</sup>.

### Alert Level 4

In AL4, we assume that there is widespread reduction in transmission through various control policies. We assume that all schools are closed, with no capacity for any students. Workplaces will be closed, with exceptions for essential work only (estimated to be 30% of workers still working on site<sup>11</sup>). For essential workplaces, strict measures are taken to ensure worker safety, such as the use of physical distancing, increased hygiene measures, contactless interaction, and the use of

<sup>†</sup>severe cases are those that would be expected to seek medical attention for breathing difficulties, pneumonia, etc.

personal protective equipment (PPE) to further reduce transmission. In large dwellings, such as university accommodation, we assume that measures will be taken to reduce mixing between groups of individuals, and increased hygiene measures be implemented. We also assume a widespread adoption of mask-wearing and distancing, as well as strong travel restrictions and reduction in interactions. Overall, we expect these measures to completely eliminate the transmission in schools, reduce close contact transmission in workplaces by around 80%, and reduce close contact in community settings by 91%. Casual contact transmission risk in large dwellings is decreased by 36%, and in all other contexts (workplace and community) by around 95%.

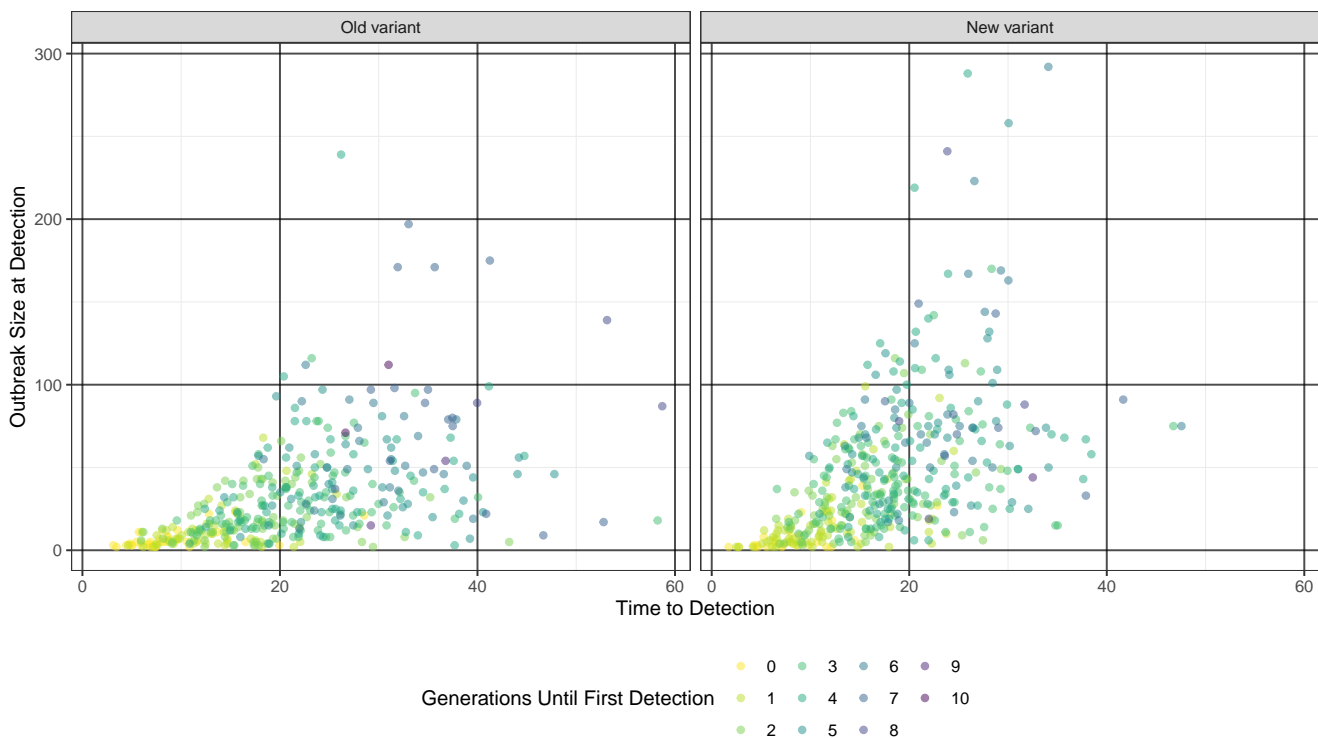
Once the first case has been detected, we assume there is a testing surge and 80% of mild symptomatic community cases get tested (the 80% test positivity rate means 64% of cases test positive) and 100% of serious symptomatic community cases get tested (80% of cases test positive). Tested individuals are notified of their test results in a mean of **4 days post symptom onset**, matching rates seen in the Auckland August outbreak.

All other parameters related to testing and trace-and-isolate remain the same as the Baseline scenarios in the earlier Alert Level 2.5 and 3 reports<sup>2,7</sup>.

## Simulation results

### Pre-detection phase

Even though the transmission settings in the simulation are identical for the two variants during the pre-detection phase, the distribution of the outbreak sizes at detection differs between the two sets of simulations, due to the increased transmissibility.



**Figure 1. Outbreak size at detection vs Time to detection (days) for the the old and new variants.** This plot shows the distribution of initial outbreak sizes and time to detection for the old and new variant — these use identical simulation conditions for the pre-detection phase. The colour of the dots indicates which generation the first detected case is. Those which are yellow (generation 0 or 1) are those where the detected case would have a direct connection to the border.

In Figure 1 we look at a scatter plot of Outbreak Size at Detection against Time to Detection for identical simulation conditions for the pre-detection phase. From this we can see that the general pattern is that the longer it takes to detect the outbreak, the larger it will be, but that there is a large amount of run to run variability. The simulations which are coloured yellow (generation 0 or 1) are those where the detected case would have a direct connection to the border. These are typically smaller, but there is a large amount of variation. It is important to note here that we do not consider an elevated rate of testing, or any regular testing to the 'seed' cases who would have a connection to the border.

Time to Detection looks to be shifted to earlier for the New Variant, and the Outbreak Size at Detection is higher. Since the

outbreak size at detection is an important factor in the progression of an outbreak, post-detection, we compare the distribution of outbreak sizes at detection for the simulation runs that are used for the AL4 scenarios. The distribution of the size of outbreak at detection for the 1000 simulations we ran for the AL4 interventions is given in Table 1. Overall, there is a statistically significant difference in outbreak sizes between the model simulations for the old variant and the new variant, with outbreaks of the new variant being larger at detection than for the old variant. Outbreaks of the new variant are also detected sooner, as found in the earlier ‘Alert Level 3’ report<sup>2</sup>.

Scenario	Simulation runs	Cases at Detection	Time to Detection (days)
Old Variant	386	22 [10, 44]	20 [14, 27]
New Variant	429	34 [14, 65]	17 [12, 22]

**Table 1.** Outbreak size at detection and Time to Detection from the pre-detection phase of the simulations with a new higher transmissibility variant and with the old variant. Results shown are *median [lower quartile, upper quartile]* unless otherwise stated.

In the following sections, as well as looking at all simulation runs together, we will break the simulation results into bins based on outbreak size at detection to allow for comparison between the variants with the same conditions at detection. When we look more specifically within different outbreak size bins (Table 2), we can see that outbreak sizes for the old and new variants are similar.

Scenario	Distribution within bins of different initial outbreak sizes				
	2–10 (n)	11–20 (n)	21–50 (n)	51–100 (n)	101+ (n)
Old Variant	5 [3, 7] (99)	15 [12, 17] (84)	33 [26, 41] (130)	68 [57, 81] (63)	155 [113, 174] (10)
New Variant	5 [3, 8] (78)	15 [13, 17] (64)	33 [27, 43] (139)	70 [61, 78] (111)	128 [110, 167] (37)

**Table 2.** Distribution of initial outbreak sizes at the point of applying the AL4 interventions within each size band from the pre-detection phase of the simulations with a new higher transmissibility variant and with the old variant. 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.

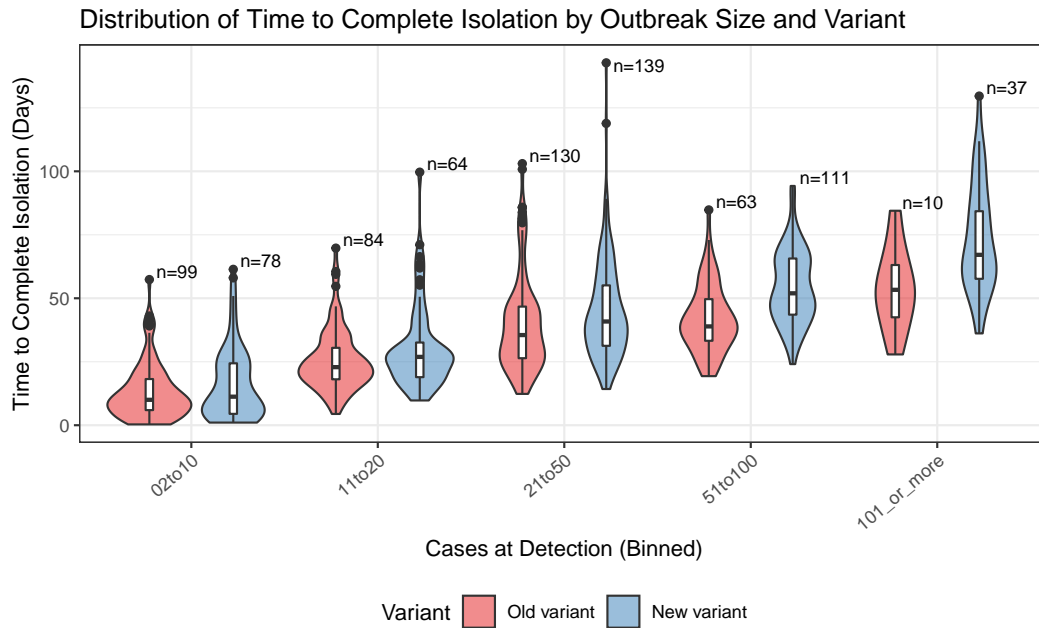
### Post-detection phase

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 200 days from detection, that is after a period of over half a year at Alert Level 3. Additionally, we report the estimated value of  $R_{\text{eff}}$  during the period of the simulation when the intervention (AL3 or AL3+) was active for both old and new variants, 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’.

In our simulations we do not implement any capacity constraints in terms of the maximum number of people who can be in quarantine at any one time or the maximum number of people who can be contact traced in a day. We therefore report medians and interquartile ranges for the peak number of cases in isolation and the peak number of successful contact tracing attempts per day.

### Probability of elimination and time taken

We find that for both the old and the new variant, 100% of the runs with Alert Level 4 (AL4) applied post-detection resulted in the elimination of cases detected within 200 days of the first infection. For the old variant both AL3 and AL4 lead to elimination (95% for AL3, 100% for AL4), but for the new variant we find that AL4 is much more effective as an intervention for eliminating an outbreak compared to AL3 (40% for AL3, 100% for AL4). In addition to having improved chances of elimination, AL4 tended to take less time to reach elimination of cases detected (see Figure 2). The median time taken to eliminate the old variant for AL4 was 54 [40, 70] days, compared to 70 [48, 100] for AL3. For the new variant, AL4 tended to take 68 [53, 83] days to reach elimination. We cannot compare this to AL3 because AL3 did not tend to result in elimination within 200 days for most runs with a new variant. Overall, 38% of simulations for the new variant reached elimination under AL4 within 60 days, compared to 62% for the old variant, with the percentage that reach elimination within 60 days decreasing as the size of outbreak at detection increases (Table 3).



**Figure 2. Time to complete isolation (days) by scenario and outbreak size.** In general, the time to complete

Scenario	All runs	By size of outbreak at detection				
		2-10	11-20	21-50	51-100	101+
Old Variant	62%	98%	79%	48%	22%	0%
New Variant	38%	85%	69%	28%	10%	0%

**Table 3. Percentage of all outbreaks that reach elimination within 60 days** for different initial outbreak sizes at detection and variants. The number of runs in each bin of outbreak sizes is noted in Table 1.

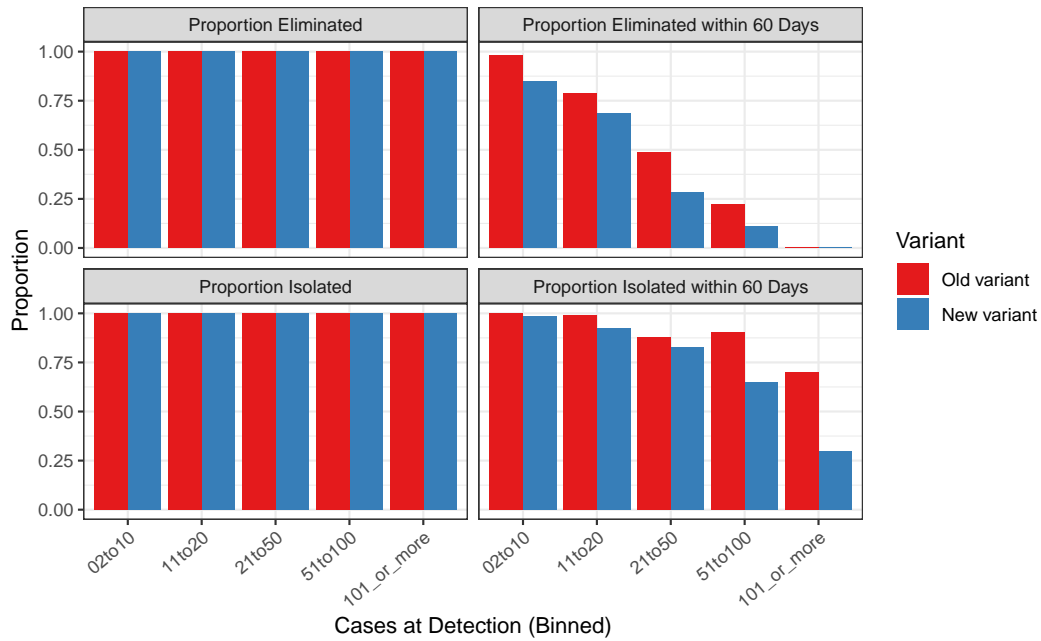
The time to ‘complete isolation’, is shorter than the time to elimination and is a more relevant measure of the duration of time needed for community wide Alert Level changes. The average time taken to reach ‘complete isolation’ under AL4 was 27 [17, 41] days for the old variant, and 40 [26, 58] days for the new variant. These times are given in Table 5. Overall, 78% of simulations for the new variant had ‘complete isolation’ under AL4 within 60 days, compared to 93% for the old variant. We report the proportion of simulations that reached ‘complete isolation’ within 60 days in Table 4 and in Figure 3. Splitting simulations into groups depending on the outbreak size at detection, we see that larger outbreaks (detected later) take longer to completely isolate.

Scenario	All runs	By size of outbreak at detection				
		2-10	11-20	21-50	51-100	101+
Old Variant	93%	100%	99%	88%	90%	70%
New Variant	78%	98%	92%	83%	65%	30%

**Table 4. Percentage of all outbreaks that reach ‘complete isolation’ within 60 days** for different initial outbreak sizes at detection and variants. The number of runs in each bin of outbreak sizes is noted in Table 1.

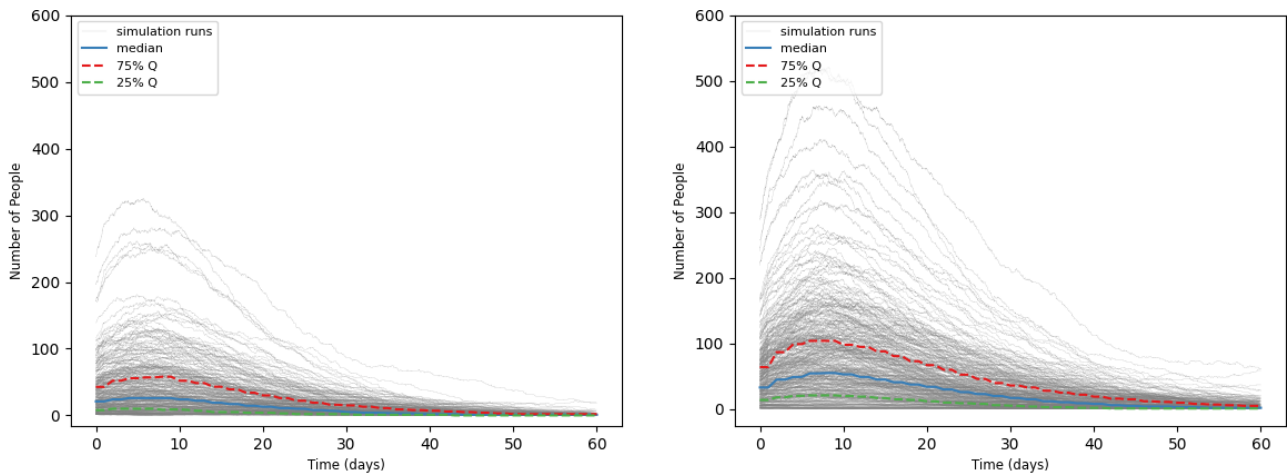
Scenario	All runs	By size of outbreak at detection				
		2-10	11-20	21-50	51-100	101+
Old Variant	27 [17, 41]	10 [6, 18]	23 [18, 30]	36 [26, 47]	39 [33, 50]	53 [43, 63]
New Variant	40 [26, 58]	11 [4, 24]	27 [19, 33]	41 [31, 55]	52 [44, 66]	67 [58, 84]

**Table 5. Time to ‘Complete Isolation’** for different initial outbreak sizes at detection and variants. The number of runs in each bin of outbreak sizes is noted in Table 1.



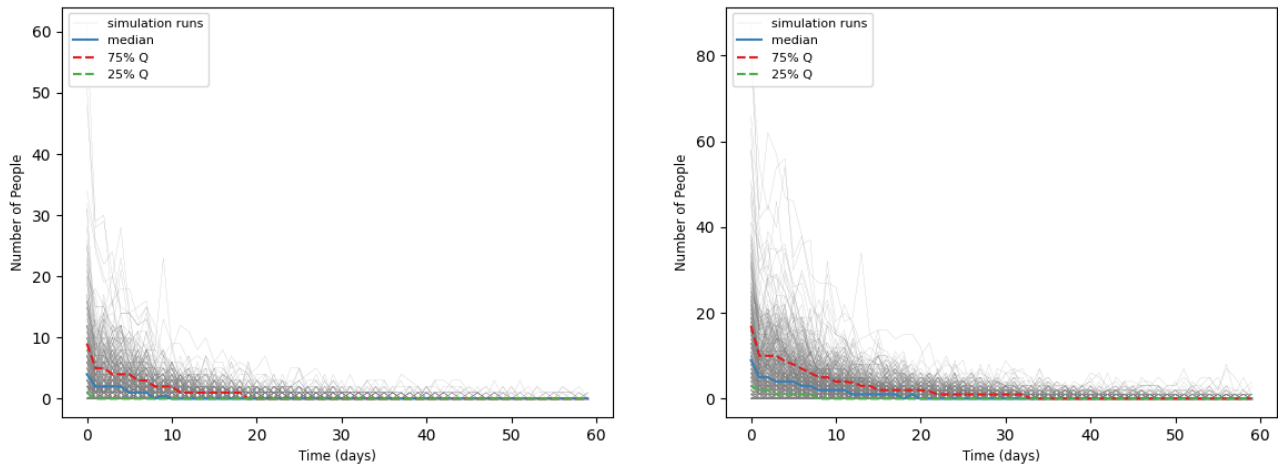
**Figure 3.** Proportions of simulations that reach elimination or isolation by scenario and outbreak size.

Figure 4 show trajectories, under AL4, for the total ‘active cases’ (known and unknown) along with the corresponding median and upper and lower quartiles for the old and new variants. These figures show that the number of active cases tends to stop growing within 10 days, but at a higher peak for the new variant, with the majority of active cases reducing to 0 within 60 days.



**Figure 4.** Total active cases through time (after detection) during an outbreak with AL4 applied for the old variant (left) and the new variant (right), for 60 days post-detection. Note this includes confirmed (known) and unknown cases.

We can get a better idea of how much AL4 is reducing spread, by looking at the number of new infections (on their day of exposure/infection) through time (Figure 5). Here we see that the number of new infections drops sharply as soon as the first case is detected and AL4 is applied. We see that for the old variant, in over 75% of simulations, there are no new cases after 19 days. For the new variant, it takes longer to get containment, and in over 75% of simulations, there are no new cases after 32 days.



**Figure 5.** Daily new infections through time (after detection) during an outbreak with AL4 applied for the old variant (left) and a new variant (right), for 60 days post-detection under AL4. *Note that these plots are on different y-axis scales.*

### Estimate of $R_{\text{eff}}$

An important feature of this modelling is that  $R_{\text{eff}}$  is not an input of our model, hence the case numbers can be used to independently calculate an effective reproduction number for a given combination of interventions<sup>12</sup>. In the present work we post-process our results using the simple approximation<sup>13,14</sup>  $R_{\text{eff}} \approx r \times \text{generation time} + 1$  to provide an indication of this, where  $r$  is the observed exponential epidemic growth rate and is calculated using a linear approximation on the log-scale:  $\log(\text{Active Cases}) \approx r \times t$ .

For the old variant, during the simulation period when AL4 is in effect, we calculate a median  $R_{\text{eff}}$  of 0.65 [0.58, 0.71]. This rises for the new variant, to a median  $R_{\text{eff}}$  of 0.73 [0.68, 0.77] during AL4.

### Size of outbreak at 15, 30, 60, and 150 days post-detection

To better quantify the nature of the outbreaks seen under AL4 for the different variants we report the outbreak sizes at 15, 30, 60 and 150 days post-detection, with these highlighted in Table 6.

For the old variant under AL4, there are a median of 49 [21, 101] cumulative cases from the first seed case until 15 days post-detection. If we consider only ‘known’ (confirmed through testing) cases, the cumulative case counts are a median of 23 [10, 49] after 15 days post-detection.

For the new variant under AL4, there are a median of 93 [38, 178] cumulative cases from the first seed case until 15 days post-detection. If we consider only ‘known’ (confirmed through testing) cases, there are a median of 46 [20, 86] after 15 days post-detection.

Days Post-Detection	Cases	Old Variant	New Variant
0 Days	Confirmed	1	1
	Total	22 [10, 44]	34 [14, 65]
15 Days	<b>Confirmed</b>	<b>23 [10, 49]</b>	<b>46 [20, 86]</b>
	<b>Total</b>	<b>49 [21, 101]</b>	<b>93 [38, 178]</b>
30 Days	Confirmed	28 [12, 58]	62 [26, 116]
	Total	52 [21, 109]	105 [42, 199]
60 Days	Confirmed	29 [13, 62]	68 [27, 127]
	Total	52 [21, 111]	109 [44, 207]
150 Days	Confirmed	29 [13, 62]	69 [27, 133]
	Total	52 [21, 111]	109 [44, 210]

**Table 6.** Cumulative Cases (confirmed cases and total cases) at days 0, 15, 30, 60, and 150 post-detection under AL4. We highlight 15 days post-detection, and break this up by size of outbreak at detection in Table 7. Results shown are *median [lower quartile, upper quartile]*.

As can be seen in Table 6, *confirmed* and *total* cases do not increase much after 15 days post-detection. For the old variant, total cases increase to 49 [21, 101]. For the older variant, we can also see that by 60 and 150 total cases remain relatively unchanged from day 15.

For the new variant, total cases increase to 93 [38, 178] by day 15. Due to the AL4 intervention, there is not much change after day 15, with the number of total cases increasing slightly to 105 [42, 199] by day 30, and 109 [44, 207] by day 60.

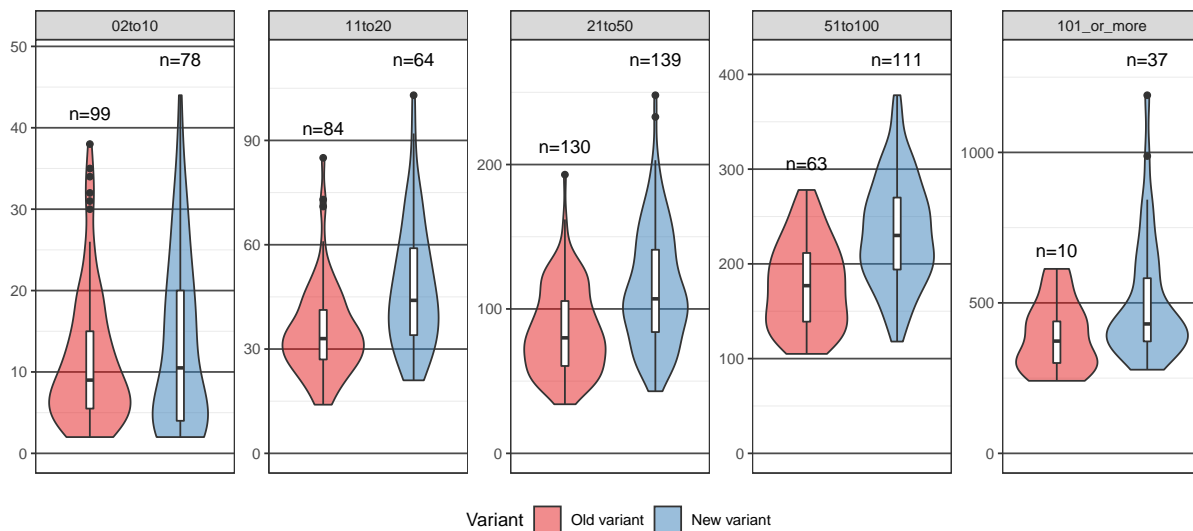
At 15 days post-detection with AL4, outbreaks of the new variant with a size at detection in the range 2–10 had a median of 9 [4, 17] total cases compared with a median of 41 [31, 50] for outbreaks with a size at detection in the range of 11–20. Table 7 reports cumulative number of total and ‘known’ cases at 15 days post-detection.

Scenario	Cases at 15 Days	Size of outbreak at detection				
		2-10	11-20	21-50	51-100	101+
Old Variant	Confirmed	5 [3, 8]	15 [12, 19]	35 [26, 44]	74 [62, 89]	180 [126, 212]
	Total	9 [6, 14]	32 [25, 38]	73 [56, 96]	154 [128, 197]	347 [273, 414]
New Variant	Confirmed	5 [2, 9]	20 [18, 25]	44 [36, 57]	93 [81, 108]	180 [144, 233]
	Total	9 [4, 17]	41 [31, 50]	92 [73, 113]	193 [166, 230]	363 [301, 461]

**Table 7. Cumulative Cases (confirmed cases and total cases) at day 15 post-detection** for different initial outbreak sizes at detection under AL4. Results shown are *median [lower quartile, upper quartile]*.

Comparing *confirmed* and *total* cases at 150 days (end of the outbreak) in Table 6 and the break down by outbreak size at detection for cases at day 15 (Table 7), we can see that our simulations are predicting that around 40% of cases never get identified (confirmed). This

Figure 6 shows the distribution of the total cumulative outbreak sizes at elimination for a range of different initial outbreak sizes for the old and new variant. Overall, outbreaks of a new variant tend to have a greater number of cumulative cases compared to the old variant, with this especially evident for outbreaks of larger sizes.



**Figure 6. Distribution of Total Cumulative Cases at Elimination for AL4** by variant and controlling for different outbreak sizes at initial detection. This plot shows the distribution of the total cumulative number of cases (i.e. both confirmed cases and unknown cases). Results are split by outbreak size at initial detection (five sub-figures). Density plots indicate the lower quartile, median, upper quartile, and distribution of initial outbreak sizes across the set of simulations for each outbreak size and intervention scenario. *NB. Scales are different for each sub-plot. This is to zoom in on the differences between the two variants, but care needs to be taken if comparing the number of cases between different sub-plots (size of outbreak at detection).*



## Capacity constraints

We do not impose any capacity constraints in our model. Specifically, we assume that:

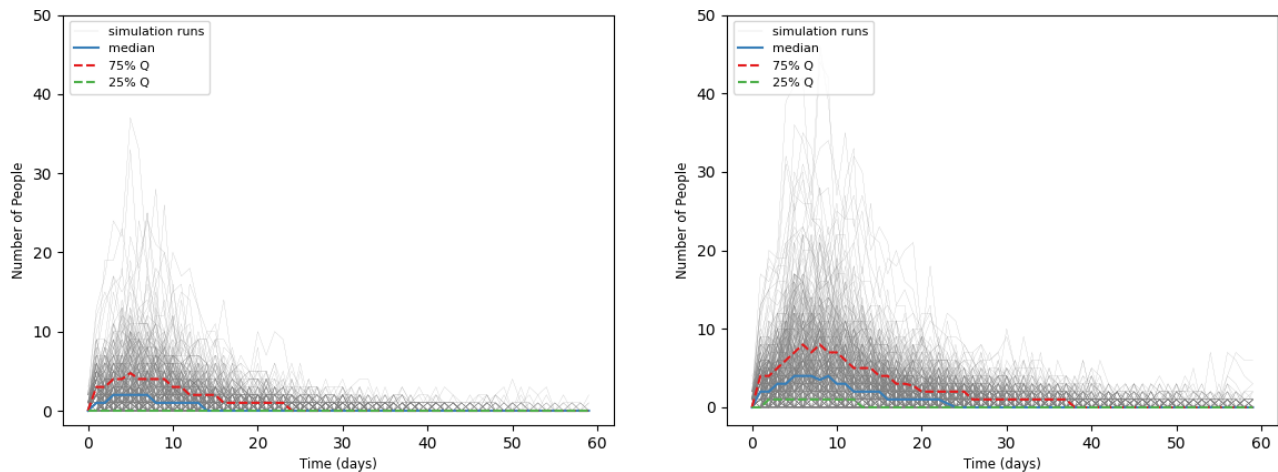
- contact tracing effectiveness (proportion of contacts identified and speed of contacting them) will be the same even as the number of cases rises
- there is testing capacity for the very high testing levels of the symptomatic population
- the time to get a test result is not affected by the large number of people who would need to be tested
- there is space in the MIQ facilities for all confirmed cases

We can use our simulation results to investigate whether any of these capacity constraints might be met.

### *New confirmed cases*

Figure 7 shows that under AL4 the peak of new confirmed cases occurs around 5-10 days post-detection (with a slightly later peak for the new variant). In some runs that are up to 50 new confirmed cases per day, but in most simulations there are fewer than five new confirmed cases per day on most days. We note that the number of new confirmed cases is different to the total number of new cases as it does not include infections that are undetected, and only includes them on the day of positive test result, not at the day of infection (c.f. Figure 5).

The number of daily new confirmed cases gives an indication of the level of resourcing that might be required for contact tracing and managed isolation services. Our estimates of daily cases under AL4 are firmly within the official limits of the NCTS which can handle a surge capacity of up to 1000 new cases per day managed centrally by the National Investigation and Tracing Centre (NITC) and up to 350 new cases per day managed by Public Health Units (PHUs)<sup>15</sup>.

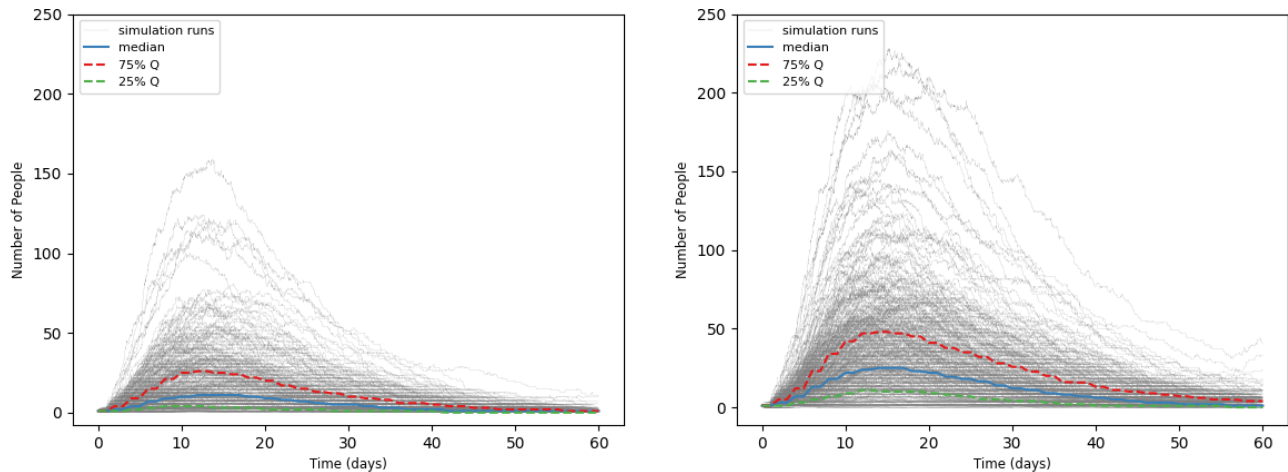


**Figure 7.** Daily new confirmed cases through time (days since first case detected) for an outbreak of a old variant (left) and new variant (right), for 60 days post-detection, under AL4.

### Confirmed cases to move to MIQ

In the current model, we implement a policy where confirmed cases get transferred to an MIQ facility and are then unable to infect household members (unlike close contacts in self-isolation, who can still infect close contacts in their dwelling). The majority of confirmed cases are moved to the Jet Park facility in Tāmaki Makaurau where the capacity for COVID-positive cases is 222 beds<sup>16</sup>. We note that this assumes that there are no other confirmed cases from MIQ facilities needing beds at the Jet Park facility.

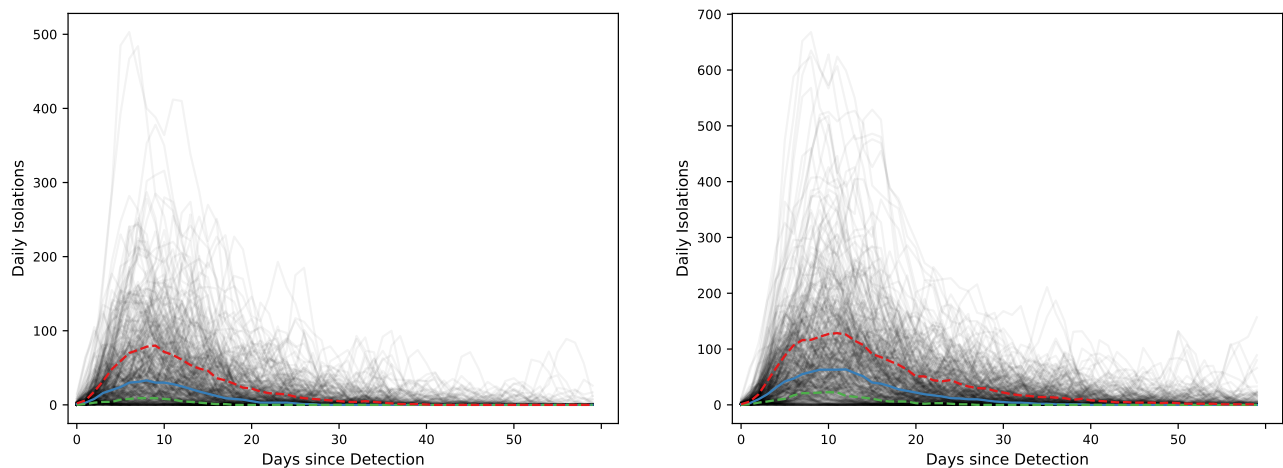
Looking at the number of active confirmed cases (Figure 8) it can be seen that most outbreaks require fewer than 50 beds at a time (upper quartile peaks at below 50), with the majority of outbreaks remaining within the capacity of the Jet Park facility.



**Figure 8.** Number of active confirmed community cases in managed isolation (MIQ) through time (since detection) for an outbreak of an old variant (left) and a new variant (right), for 60 days post-detection, under AL4.

### Close contacts to identify and contact

We plot the number of close contacts identified and successfully contacted each day in Figure 9. Results of model simulations show that for outbreaks of sizes 2-10 at detection, the peak number of people isolated from contact tracing is around 20 [6, 38] for the new variant under AL4 (see Table 8). With greater outbreak sizes at detection, the peak number of people being contacted to isolate increases. Outbreaks of size 11-20 had a peak number of 55 [39, 80] isolations per day, while outbreaks sizes of 100 or more had a peak number of 376 [285, 460] isolations per day. This contrasts with the old variant under AL4, which had slightly fewer isolations overall, due to the lower case numbers (see Table 8).



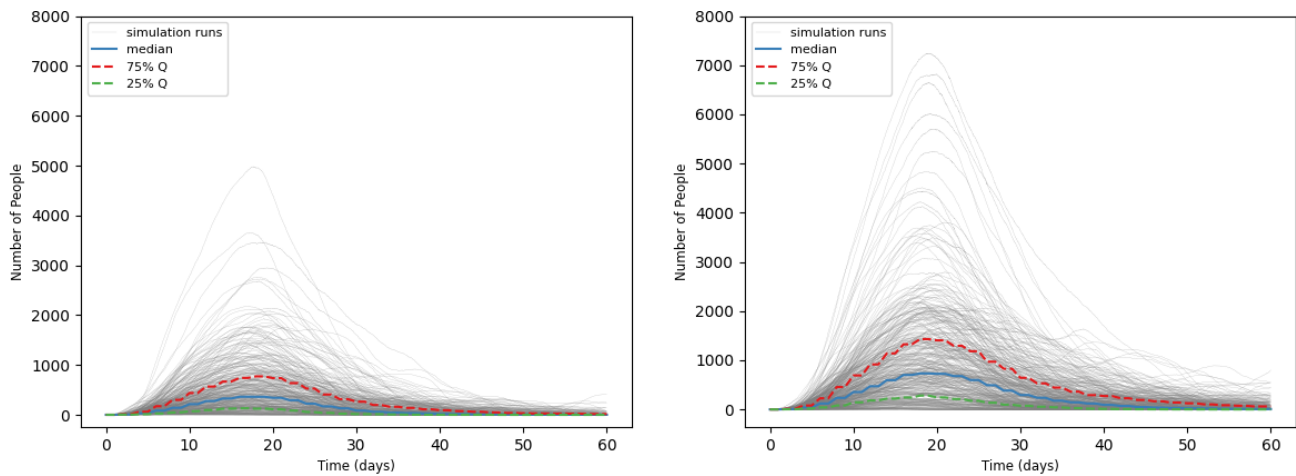
**Figure 9.** Number of close contacts successfully identified and contacted each day for an outbreak of old variant (left) and new variant (right), for 60 days post-detection under AL4. The y axis scales are not the same for the two plots. The peak for the new variant (right) is much higher than for the old variant (left).

Scenario	Size of outbreak at detection				
	2-10	11-20	21-50	51-100	101+
Old Variant	18 [8, 36]	47 [35, 68]	85 [67, 111]	162 [129, 221]	280 [222, 355]
New Variant	20 [6, 38]	55 [39, 80]	109 [80, 138]	187 [153, 237]	376 [285, 460]

**Table 8. Peak number of people isolated in a single day from contact tracing** for different initial outbreak sizes at detection and interventions. Results shown are *median [lower quartile, upper quartile]* unless otherwise stated.

Unlike AL3, which produces suppression behaviour, AL4 is more likely to reach elimination, and reach it faster, for both the old and new variant. This means that we would not need to maintain a high capacity of contact tracing over a number of months.

Despite the lower number of close contacts to isolate each day, these close contacts must stay in isolation, with repeat testing, for 14 days. This means that AL4 can still lead to a large number of people in self-isolation who need to be supported and monitored. Figure 10 shows the sum of active cases and people currently in self-isolation at any given time. By subtracting from this the number of active cases (Figure 8) we can get an idea of the level of resourcing required.



**Figure 10. Number of people currently in isolation (both confirmed cases in MIQ and close contacts in self isolation)** through time (since detection) for an outbreak of the old variant (left) and a new variant (right), for 60 days post-detection, under AL4.

The number of people in self-isolation is especially high if an outbreak is large upon detection, as shown in Table 9. For example, only around 103 [21, 190] total close contact isolations would be required for outbreaks of a new variant of size 2-10 under AL4, but outbreaks of size 21-50 would require around 1133 [905, 1576] isolations, and outbreaks of size 101+ would require 4850 [4360, 6463] isolations.

Scenario	Size of outbreak at detection				
	2-10	11-20	21-50	51-100	101+
Old Variant	78 [31, 171]	330 [207, 509]	772 [622, 1086]	1833 [1469, 2210]	3624 [2743, 4740]
New Variant	103 [21, 190]	448 [304, 612]	1133 [905, 1576]	2560 [2034, 3049]	4850 [4360, 6463]

**Table 9. Total cumulative number of isolations from contact tracing** in the outbreak for different initial outbreak sizes at detection. Results shown are *median [lower quartile, upper quartile]* unless otherwise stated.

## Discussion

The results presented here show that **Alert Level 4 is still enough to lead to elimination for COVID-19 variants with increased transmission rates**. Our estimates for  $R_{\text{eff}}$  at AL4 (based on post-processing our simulations) for the Old Variant are 0.65 [0.58,0.71] and increase to 0.72 [0.68, 0.77] for the New Variant. For both the Old and New Variant, an AL4 intervention results in elimination within 200 days in 100% of model simulations. Furthermore, ‘complete isolation’ of active cases is achieved within 60 days for the majority of model simulations for the Old Variant (93%) and New Variant (78%).

However, as is the case in our previous report on the effectiveness of an AL3 intervention<sup>2</sup>, **early detection of outbreaks remains extremely important for reducing the duration required for an alert level intervention to achieve elimination or containment**. Outbreaks of larger size at detection require more time before ‘complete isolation’ of active cases is accomplished, and the probability of elimination within a shorter time-frame (e.g., 60 days) is reduced (Tables 3-5).

Comparing our results to the  $R_{\text{eff}}$  estimates from Aotearoa New Zealand during March and April 2020<sup>17</sup>, we find that our model produces higher estimates for  $R_{\text{eff}}$ . This can in part be attributed to the fact that the introductions in March 2020 were from returning travellers who were of a reasonably homogeneous demographic, most of whom were not essential workers who would be working under AL4. This brings up an aspect of our current implementation of Alert Level 4 restrictions that it is worth commenting on further. In implementing the lockdown restrictions at AL4 we reduce the *rate* at which all people contact each other through each specific context (work, school, etc.), rather than reducing the *number* of contact links between people depending on the type of contact (e.g. supermarket workers vs IT professionals). For example, we do not shut down the 70% of workplaces (or 70% of workers) who are assumed to be not working on site during AL4. Instead, we reduce the *interaction (transmission) rate* for all workers by 70%. This has the potential limitation of underestimating the amount of *variance* in the simulations, though the predicted *average* amount of transmission is expected to be comparable.

Comparing *confirmed* and *total* at 15 days (Table 6), we can see that our simulations are predicting that around 50% of all cases are not identified (confirmed) at this point. This is conserved across different sizes of outbreaks (Table 7). Some of this could be because some cases, which will be identified in future, either haven’t developed symptoms and been tested or haven’t been contact traced yet. However, looking at the proportion of cases that were identified (confirmed) even at the end of the outbreak (150 days in Table 6), we see that there remain around 40% of cases that never get identified during the outbreak.

We suspect that the actual proportion of never detected cases in the recent outbreaks (including August Auckland and Valentine’s Day outbreaks) is much lower. If this is the case, there are a number of factors that might explain the difference. The key parameters that might be affecting this are:

- contact tracing ‘known’ proportions (for close contacts);
- speed of contact tracing;
- proportions of casual contacts who would know they were casual contacts and would seek testing;
- proportions of infections that are asymptomatic;
- testing rates for the symptomatic general population (although we assume almost 100% in AL4);
- PCR testing sensitivity (we assume 80%); and
- testing policies for close contacts.

These factors will be important to investigate to improve the accuracy of the model simulations, especially as they are crucially linked to how much control the Test/Trace/Isolate process is providing, and what extra widespread control measures (Alert Levels) are needed.

Our simulations are also relatively pessimistic about various behavioural aspects, including: infected individuals not isolating until they have received a positive test, even if they are presenting with symptoms; assumptions that possibly underestimate the number of contacts (close and casual) that can be contacted, and the speed at which tracing occurs; and assumptions about the propensity for individuals to seek tests. If we are being too pessimistic in these assumptions, then a realistic outbreak would be more likely to be controlled with similar restrictions than our model shows. In particular, these factors could influence the exact thresholds that suppression or elimination could occur at. We are awaiting feedback from contacts within the Ministry of Health, and contact tracing teams, around whether to revise these assumptions and estimates.

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## References

1. Volz, E. *et al.* Transmission of SARS-CoV-2 Lineage B. 1.1. 7 in England: Insights from linking epidemiological and genetic data. *medRxiv* (2021).
2. Harvey, E. *et al.* Effect of COVID-19 variants with increased transmission rates on the effectiveness of Alert Level 3 for eliminating a community outbreak. Tech. Rep., Te Pūnaha Matatini (2021).
3. Public Health England. Investigation of novel SARS-CoV-2 variant: Variant of Concern 202012/01 — Technical briefing 3. Retrieved from: [https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment\\_data/file/950823/Variant\\_of\\_Concern\\_VOC\\_202012\\_01\\_Technical\\_Briefing\\_3\\_-\\_England.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/950823/Variant_of_Concern_VOC_202012_01_Technical_Briefing_3_-_England.pdf) (2021). Accessed: 2 Feb 2021.
4. Public Health England. Investigation of novel SARS-CoV-2 variant: Variant of Concern 202012/01 — Technical briefing 5. Retrieved from: [https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment\\_data/file/959426/Variant\\_of\\_Concern\\_VOC\\_202012\\_01\\_Technical\\_Briefing\\_5.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959426/Variant_of_Concern_VOC_202012_01_Technical_Briefing_5.pdf) (2021). Accessed: 2 Feb 2021.
5. 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).
6. Harvey, E. *et al.* Network Modelling of Elimination Strategy Pillars: Prepare for it; Stamp it out. Tech. Rep., Te Pūnaha Matatini (2020).
7. Harvey, E. *et al.* Alert Level 2.5 is insufficient for suppression or elimination of COVID-19 community outbreak. Tech. Rep., Te Pūnaha Matatini (2021).
8. Kissler, S. M. *et al.* Densely sampled viral trajectories suggest longer duration of acute infection with b. 1.1. 7 variant relative to non-b. 1.1. 7 sars-cov-2. *medRxiv* (2021).
9. Harvey, E. & Turnbull, S. 2020-12-18 fluTracking Testing Calculations. Tech. Rep., Te Pūnaha Matatini (2020).
10. 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).
11. Statistics NZ. Household labour force survey: June 2020 quarter. Retrieved from: <https://www.stats.govt.nz/assets/Uploads/Labour-market-statistics/Labour-market-statistics-June-2020-quarter/Download-data/household-labour-force-survey-june-2020-quarter-supplementary-tables.xlsx> (2020). Accessed: 9 Dec 2020.
12. Breban, R., Vardavas, R. & Blower, S. Theory versus data: how to calculate R0? *PLoS One* **2**, e282 (2007).
13. Ma, J. Estimating epidemic exponential growth rate and basic reproduction number. *Infect Dis Model.* **5**, 129–141 (2020).
14. Wallinga, J. & Lipsitch, M. How generation intervals shape the relationship between growth rates and reproductive numbers. *Proc. Biol. Sci.* **274**, 599–604 (2007).
15. Smith, R. NCTS – Metrics for Modelling. Tech. Rep., National Contact Tracing Solution (NCTS) (2020).
16. Jet Park Hotel Auckland Airport. Rooms & Suites Jet Park Hotel Auckland Airport. Retrieved from: [view-source:https://www.jetparkauckland.co.nz/rooms/](https://www.jetparkauckland.co.nz/rooms/) (2021). Accessed: 15 Feb 2021.
17. James, A. *et al.* Modelling support for the continued elimination strategy. Tech. Rep., Te Pūnaha Matatini (2020).