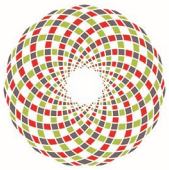

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Effect of COVID-19 variants with increased transmission rates on the effectiveness of Alert Level 3 for eliminating a community outbreak

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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

New variants of COVID-19 have emerged with mutations that increase their transmissibility by 30-70%[1]. 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. **Our simulations represent the situation of community outbreak, with no clear epidemiological link to the border — similar to the situation announced on 14 February 2021.**

Our results show that Alert Level 3 with a more transmissible variant would be unlikely to eliminate the outbreak within 200 days, except for very small outbreaks caught quickly. Alert Level 3 with improved contact tracing (AL3+) had a small effect on overall probability of elimination (4–14%), and no statistically discernible effect on elimination probability when controlling for outbreak size at detection. For reference, Alert Level 3 led to elimination within 200 days post-detection in nearly all cases for old variants.

While new variants have a much-reduced probability of elimination within 200 days under AL3/AL3+ interventions, **our estimates for R_{eff} are close to 1 under both AL3 and AL3+**. This R_{eff} indicates either suppression behaviour or that some simulations that do not eliminate within 200 days may be heading to elimination over a more extended period. However, **this requires sustaining AL3/AL3+ measures for long periods, which may place heavy burdens on the NZ population and contact tracing systems.**

The estimated generation number at detection was the same for both the new and old variants, with **a median estimate for the generation number at detection of 3 and interquartile range of 2–4 generations** in both cases. Despite this, the increased transmissibility of the new variants leads initial detection of **outbreaks from the new variants occurring slightly sooner (median of 17 days, compared with 20 days for the older variant) and outbreaks of the new variant are around 50% larger at detection (median of 34 compared with 21 for the older variants)**. The new variants also had more instances of large outbreaks (over 100 cases at detection).

Key points:

- Alert Level 3 is insufficient for achieving a high probability of elimination of a community outbreak within 200 days for new, higher transmissibility variants of COVID-19.
- Only around 40% of all simulations of the new variant under AL3 led to elimination within 200 days, and improved contract tracing (AL3+) had only a very small (but statistically detectable) effect on this. This compares to around 95% of all simulations of the old variant leading to elimination under AL3 interventions.
- Alert Level 3 can be sufficient for elimination of a small COVID-19 outbreak (fewer than 10 total cases at initial detection). For small outbreaks of the new variant (2-10 cases at detection), AL3/AL3+ led to elimination within 200 days in around 90% of the simulations.
- The probability of elimination dropped off significantly with outbreak size at detection: for intermediate size outbreaks (11-50 cases at detection) the probability of elimination under AL3/AL3+ was around 50%, while for outbreaks detected at size 51–100 the probability of elimination within 200 days falls to around 10%.
- Despite lack of elimination within 200 days for many simulations, our estimates for R_{eff} are close to 1 under both AL3 and AL3+. This R_{eff} indicates either suppression behaviour or that some simulations that do not eliminate within 200 days may be heading to elimination over a more extended period.
- This indicates that long periods under AL3/AL3+ interventions are required to suppress or eventually eliminate intermediate to large outbreaks, which may not be sustainable in practice. Even for those simulations that did eliminate the new variant within 200 days, this often took a long time: for example, only about 12% of new variant runs reached elimination within 60 days of detection under AL3 interventions.
- Under Alert Level 3, suppression of growth for a new, more transmissible variant of COVID-19 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, both systems would be required to operate at a significantly increased level for a sustained period of time and without failure — this may not be realistic.

Introduction

Novel variants of COVID-19, with increased transmissibility compared to the original variant[2,3] have recently appeared in various countries. On 14 February 2021, one of these novel variants, COVID-19 variant B1.1.7 (also known as VOC 202012/01 or Alpha), was identified in the community in Auckland, Aotearoa New Zealand[4]. Reports indicate that this novel variant, first identified in the UK, may have up to 30-70% higher transmissibility than the original COVID variant[1,5]. As of 15 February 2021, the Auckland case lacks a clear epidemiological link to the border. This missing or unconfirmed link prompted the New Zealand government to initiate a Level 3 COVID-19 Alert Level (AL3) for Auckland, and a Level 2 Alert Level (AL2) for the rest of New Zealand, starting at 11.59 pm Sunday 14 February 2021. The present report summarises the results of **network contagion model** simulations, detailing **whether Alert Level 3 is enough to eliminate a community outbreak of a COVID variant with increased transmissibility**.

We use a detailed individual-based network contagion model that explicitly represents ≈ 5 million individuals and 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, and schools. It also includes an explicit representation of the contact tracing process. This model has previously been used to simulate earlier community outbreaks and to quantify the expected performance of a range of non-pharmaceutical interventions (NPIs) as part of the New Zealand Government's 'Keep it Out, Stamp it Out, Eliminate it' strategy[6–8].

This report focuses on a scenario comparable to that on 14 February 2021, where a community outbreak was detected with no known epidemiological link to the border. (This is in contrast to the case of a positive test result being returned for a known high exposure risk individual — e.g. a MIQ worker or recent arrival in Aotearoa NZ, or someone with an epidemiological link to such a person.) While one of the individuals who tested positive for COVID-19 in the February 14th outbreak was deemed to be at a higher risk of exposure, due to working in an airline food and laundry servicing facility, their testing schedule was not reflective of this, being at most fortnightly[*], hence we do not treat them as having an increased frequency of testing in the weeks immediately prior to them developing symptoms.

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. We refer to this scenario as baseline Alert Level 3 (AL3).

Contact tracing plays an important role in reducing transmission of COVID-19 — it is also one of the NPIs where the effectiveness can be more directly influenced by choices from public health officials and government. Since contact tracing is an intervention that can be more or less effective, depending on a number of technological, procedural, and public uptake settings, we also consider a scenario where the Alert Level 3 parameters are augmented by a combination of technological, behavioural and procedural changes to contact tracing that could increase its effectiveness, without altering the restrictions or gathering size limits that applied. We refer to this scenario as 'Alert Level 3 with improved contact tracing' or AL3+. 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.

Increased transmission variants (new variant)

Based on technical reports[2,3] from the UK's New and Emerging Respiratory Virus Threats Advisory Group, we assume a variant of COVID-19 with a 50% increase in transmissibilty, relative to older variants. This corresponds to a 50% increase in the β parameter which characterises the infectivity of COVID-19 in the network contagion model. Other aspects of disease progression for the new variant are unchanged.

Baseline AL3 (AL3)

In the baseline for AL3 we assume that there is widespread reduction in transmission through various control policies. We assume that schools are closed, with limited capacity for the children of essential workers and some transmission reduction measures in place. Workplaces encourage working from home where possible, and measures are taken to keep workers safe, for example through physical distancing, increased hygiene measures, contactless interaction and use of PPE. We also assume that there is widespread adoption of mask-wearing and distancing, as well as travel restrictions and general reduction in interactions. Overall we expect these measures reduce the chances of transmission in schools by around 97%, workplaces by around 55% and in all other (non-dwelling) interactions by around 90%. These reductions are relative to the model's calibrated default values in the absence of interventions.

[*]The positive test results of the intial cases were returned after the infected individuals sought testing due to experiencing COVID-like symptoms. The most recent test from scheduled testing of the high exposure risk individual was reported as being on January 18th, almost a month prior[9].

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 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 knowable 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 $= 4$.

Casual contacts are notified through media announcements, NZ COVID Tracer app 'exposure notifications', and some manual contact tracing where capacity allows. Casual contacts are advised to get a test regardless of symptoms. In the baseline Alert Level 3 scenario we assume 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 $a = 3, b = 5$.

AL3 with improved contact tracing (AL3+)

Here we consider the impact of QR codes, bluetooth tracing, and manual improvements all together. In terms of parameter changes in our model, we estimate the impact of these would be to: **increase the chances 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 100 simulations for the old variant with Alert Level 3 (AL3) applied post-detection, and 500 simulations for the more transmissible variant for each of the Alert Level 3 (AL3) and Alert Level 3 plus improved contact tracing (AL3+) interventions (again 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 AL1, and the same for both old and new variants and for both AL3 and AL3+ settings. 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 new variant across the AL3 and AL3+ scenarios, we can combine the simulation results for our analysis of this phase of the outbreak. Combining these gives 1000 simulations total for the new variant pre-detection, though various metrics are subsequently reported conditional on detection. For these metrics, we then exclude any simulations where the infection died out without being detected, 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).

We also ran 1000 simulations of the pre-detection phase for the old variant with identical transmission settings to those used for the new variant. When calculating metrics conditional on detection, we again exclude any simulations where the infection died out without being detected, or where there is no further transmission from the first detected case.

For the 1000 simulations with the old variant, 79% of the simulations reached detection (and hence are retained in subsequent analysis), compared to 88% of the 1000 total simulations with the new more transmissible variant. Using a two-sample test for equality of proportions, we find that statistically significantly more re-incursions grow and reach detection for the new variant (95% confidence interval for difference in detection percentages of 6% – 12% for new variant minus old).

In Table 1 we compare the time to detection, the chances of a simulation reaching detection, the generation number at detection, and the outbreak size at detection, for the new and old variants.

We find that the time from the initial seed case to detection of the first case in a community outbreak of the original variant ranges from two to just under four weeks (median $= 20$ days; [LQ $= 14$, UQ $= 27$]). A new variant with increased

[†]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.

Scenario	Time to detection (days)	Number of simulations (/ 1000)	Generation number at detection	Outbreak size at detection
Old variant	20 [14, 27]	793	3 [2, 4]	21 [10, 42]
New variant	17 [12, 22]	883	3 [2, 4]	34 [15, 65]

Table 1. Time from re-incursion by an initial seed case to detection, generation number at detection, and size of outbreak at detection. Results are formatted as *median [lower quartile, upper quartile]*. Number of simulations vary, as not all incursions get detected before dying out.

transmissibility reduces this time to detection by around half a week (median = 17 days; [LQ = 12, UQ = 22]). This is expected to be due to the earlier presence of a greater number of cases and hence more symptomatic people who might seek a test. The generation number at detection is unchanged, however, with **a median estimate for the generation number at detection of 3 and interquartile range of 2–4 generations** in both cases.

Outbreak sizes are larger at detection for the new variant. For the original variant, we find that the outbreak size at the time of detection has an interquartile range of 10–42 total cases, whereas for a new, more transmissible, variant this increases to 15–65. Of particular note is that the number of outbreaks that are very large (>100) at detection increases markedly (orange dots in Figure 2).

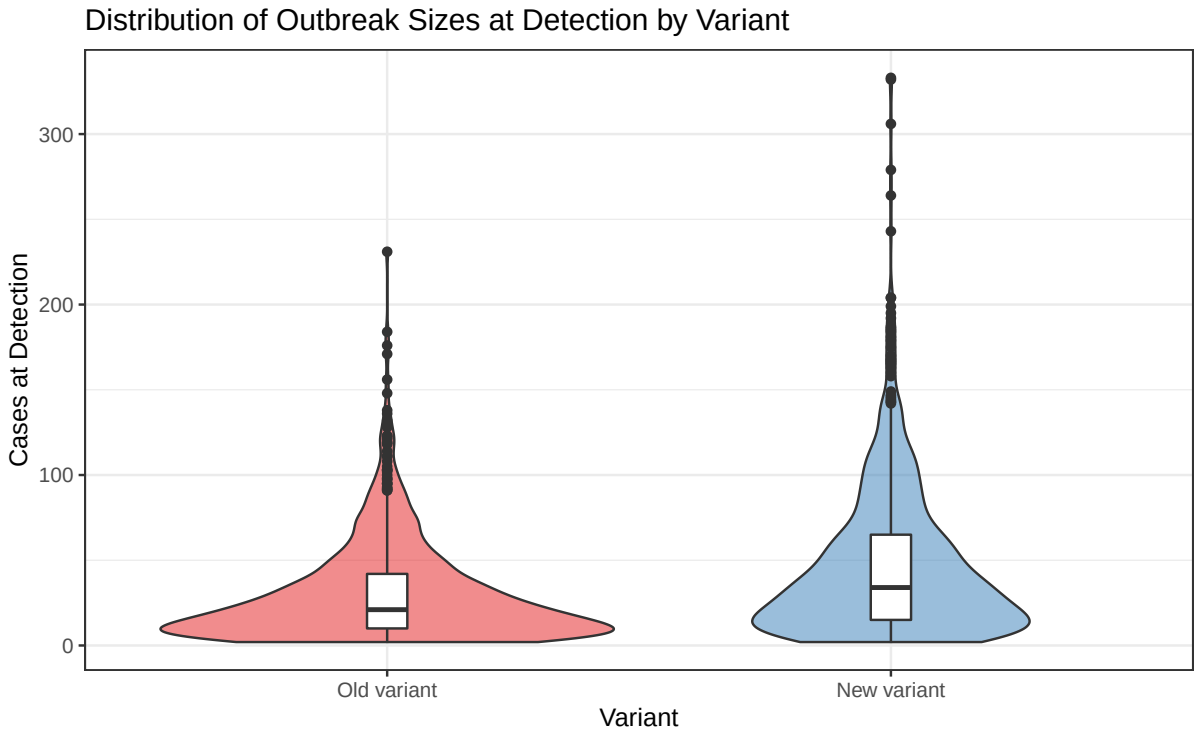

Figure 1. Distribution of Initial Outbreak Sizes by Variant. This plot shows the distribution of initial outbreak sizes for an old variant and a new variant with 50% increased transmission. Note: the pre-detection data for the 'Old variant' come from the pre-detection (i.e. AL1) phase of the 1000 simulations run for a previous report[7].

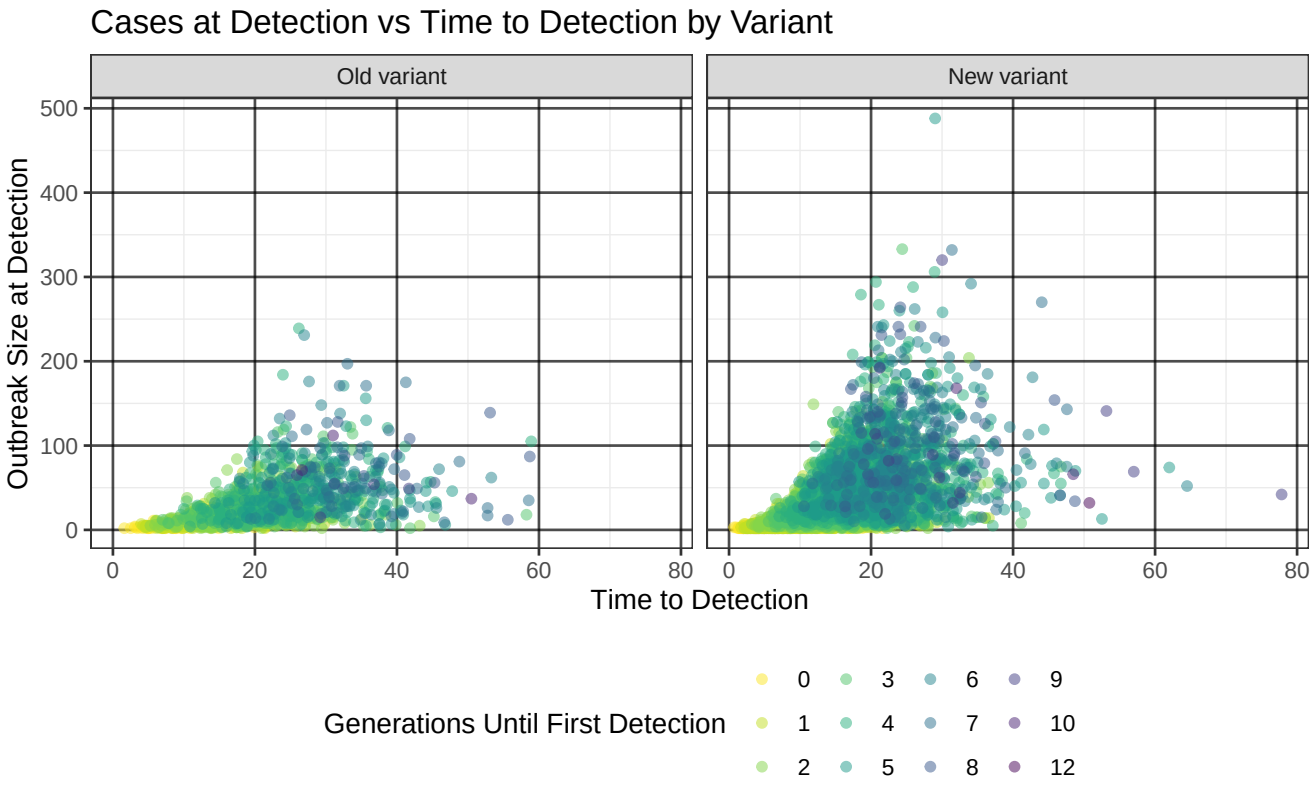

Figure 2. Cases at Detection against Time of Detection by Variant. This plot shows the relationship between initial outbreak sizes (cases at detection) and time to detection for an old variant (left) and a new variant with 50% increased transmission (right). The colour indicates the number of generation until the outbreak was detected. With the new variant, the first cases are detected slightly sooner and are typically significantly larger. For a given time of detection, the number of cases at detection is approximately 50% greater than for the same time of first detection with the old variant.

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_{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

We find that in simulations with the old variant with Alert Level 3 (AL3) applied post-detection, 77 (95%) of the 81 simulations with a case detected completely eliminated the outbreak within 200 days of the first infection. When we consider an outbreak of a new, more transmissible, variant, we find that with AL3 applied post-detection, only 175 (40%) of the 441 simulations with a case detected completely eliminated the outbreak within 200 days of the first infection. This is a substantial difference in the effectiveness of Alert Level 3 for eliminating a community outbreak (95% confidence interval for difference in elimination percentages of 48% – 63% for old variant minus new).

Scenario	% of **all outbreaks** that reach elimination	By size of outbreak at detection				
		2-10	11-20	21-50	51-100	101+
AL3 old variant	95%	100%	93%	93%	93%	100%
AL3 new variant	40%	86%	56%	39%	9%	5%
AL3+ new variant	47%	92%	74%	48%	15%	2%

Table 2. Percentage of simulations that reach elimination within 200 days of the first infection for different initial outbreak sizes at detection, variants and interventions. The number of runs in each bin of outbreak sizes is noted in Table 7.

For the new variant, the 175 runs that did eliminate within 200 days of the first seed case often took a long time to complete isolation of all active cases. For example, only 26 of the 175 runs that eliminated (or of the 441 runs with a case detected) reached complete isolation within 2 weeks of detection. Figure 3 shows the distribution of the times taken for outbreaks to reach complete isolation for each scenario and size of outbreak. This figure shows how the time to reach complete isolation are more varied for new variant compared to the old.

We also investigated the impact of improved contact tracing, and find that for the new variant Alert Level 3 with improved contact tracing (AL3+) led to elimination in only 207 (47%) of the 442 simulations with a case detected. A two-sample test for equality of proportions indicates a small but statistically significant difference (95% confidence interval of 4-14% more simulations would eliminate) between the proportion of simulations that eliminate completely within 200 days of the first infection. However, even with this slight improvement, both **AL3 and AL3+ are insufficient to reliably eliminate an outbreak, unless it is very small at detection (see Table 2) and Figure 4**.

For the old variant, Alert Level 3 led to elimination in close to 100% of outbreak[‡]. In contrast, for the new variant, 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 chances of elimination within 200 days of the first infection is greatly increased. In Table 2 and Figure 4 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[6]. We find that, for the new variant, the probability of elimination for outbreaks of size 2–10 at detection is around ∼90% while for outbreaks detected at size 51–100 the probability of elimination falls to around ∼10%.

Considering simulations with outbreak sizes at detection within the same 'bin' a two-sample test for equality of proportions did not show evidence of a difference in probability of elimination between AL3+ over AL3 for the new variant within any size bin, despite the raw numbers for the proportion that eliminated consistently being higher for AL3+. It is worth noting that the test does not prove that improved contact tracing measures have no effect on the probability of elimination at AL3, only that these results are compatible both with no effect and with non-zero effect sizes depending on sample size. It could thus be that the effect is too small to see in 500 simulation runs due to the run-to-run variability and the large variation in outbreak sizes at

[‡]We also note that while the proportion eliminated was 95%, the proportion completely contained was even higher at 99%, where completely contained means all cases are known and isolated.

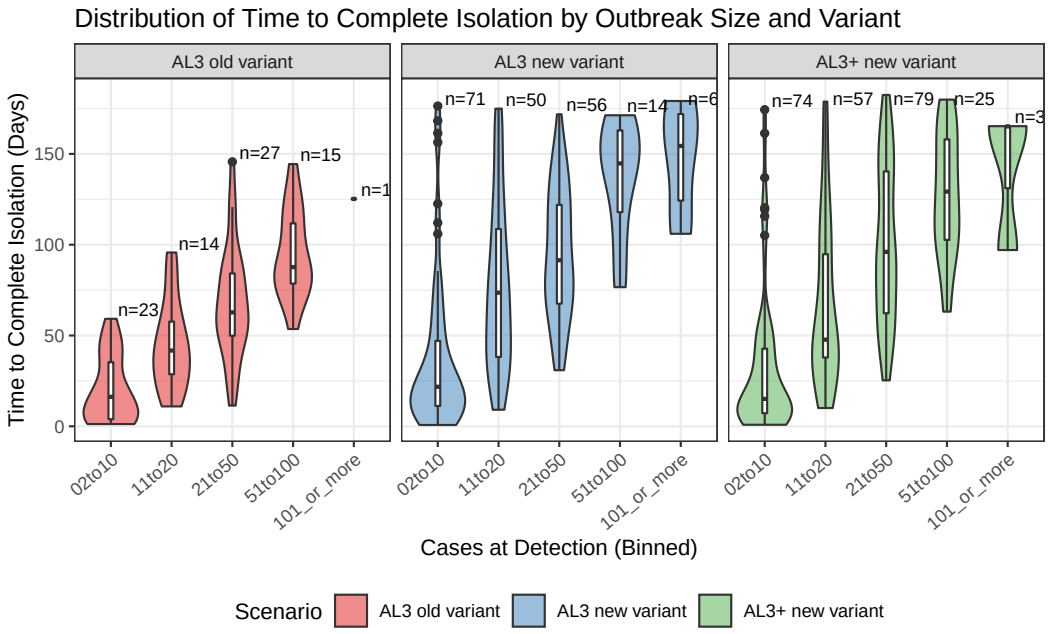

Figure 3. Time to complete isolation (days) by scenario and outbreak size. In general, the time to complete isolation of active cases was more varied as outbreak at time of detection increased.

detection between the two contact tracing levels (see Initial Conditions). However, we also note that the impact of improved contact tracing on contagion control depends on the alert level: the effects of various interventions combine non-linearly in our model. Thus the impact of improved contract tracing may be reduced in the presence of other measures.

Figures 5–7 show trajectories, under Alert Level 3, for the 'total cumulative cases', 'active cases' and 'daily new cases', respectively, along with the corresponding median and upper and lower quartiles.

Estimate of R_{eff}

An important feature of this modelling is that R_{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[10]. In the present work we post-process our results using the simple approximation[11,12] $R_{\text{eff}} \approx r \times \text{generation time} + 1$ 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 AL3 is in effect, we calculate a median R_{eff} of 0.75 [0.68,0.82]. This rises drastically for the new variant, to a median R_{eff} is 0.97 [0.88,1.00] during AL3. Although many of these R_{eff} values are below 1, they are close enough to 1 that many are simply 'suppressed', and for those that do eliminate, the time to elimination is very long (months), as discussed in the previous section.

When we consider AL3 with contact tracing improvements (AL3+), the median R_{eff} for the new variant is 0.94 [0.86,0.98]. This very slightly lower value of R_{eff} for AL3+ is statistically significant, however the difference is very small (95% confidence interval of 0.013-0.033), and similar behaviour, with suppression rather than elimination, is still observed.

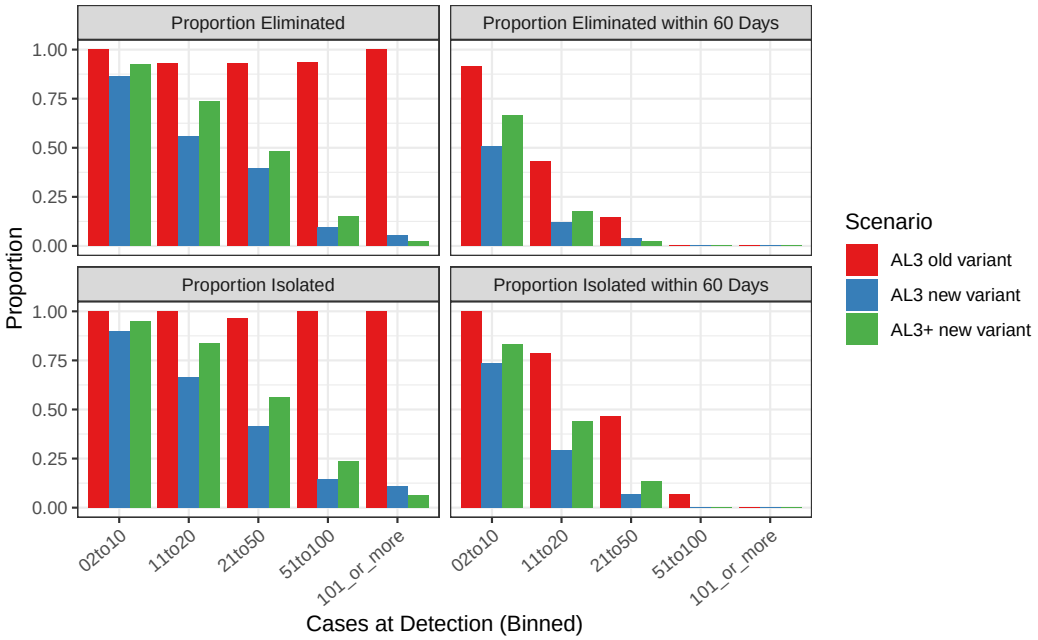

Figure 4. Proportions of simulations that reach elimination or isolation by scenario and outbreak size.

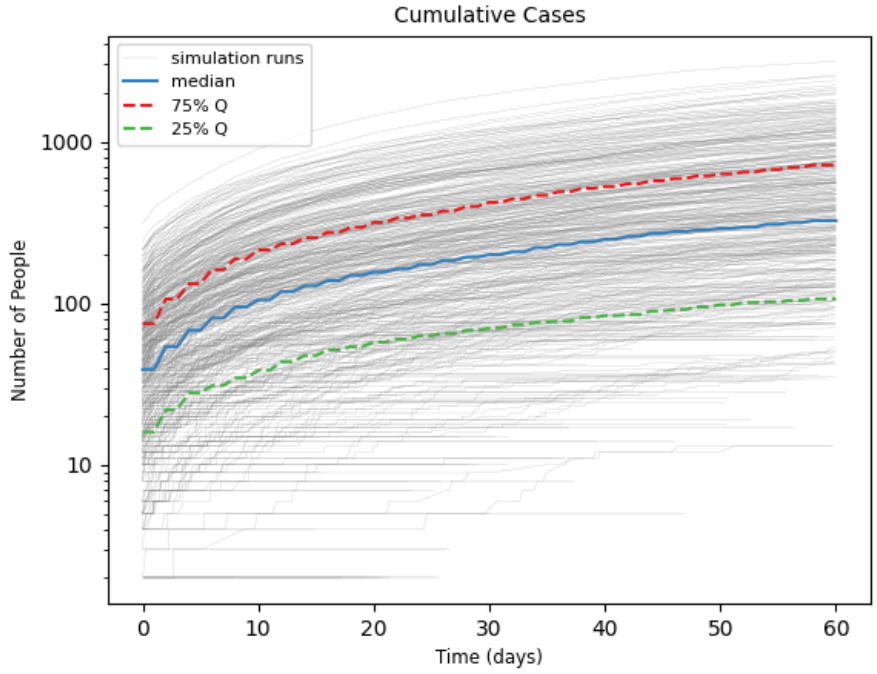

Figure 5. Cumulative cases on a log scale for an outbreak of a new variant, for 60 days post-detection under Alert Level 3. Although 40% of simulations eliminate within 200 days of the initial (seed) infection, only 12% eliminate within the first 60 days of Alert Level 3 (as indicated by trajectories that flatten out and end before 60 days), the remaining simulations are either suppressed with sub-exponential growth but continuing a steady level, or are heading towards elimination but very slowly.

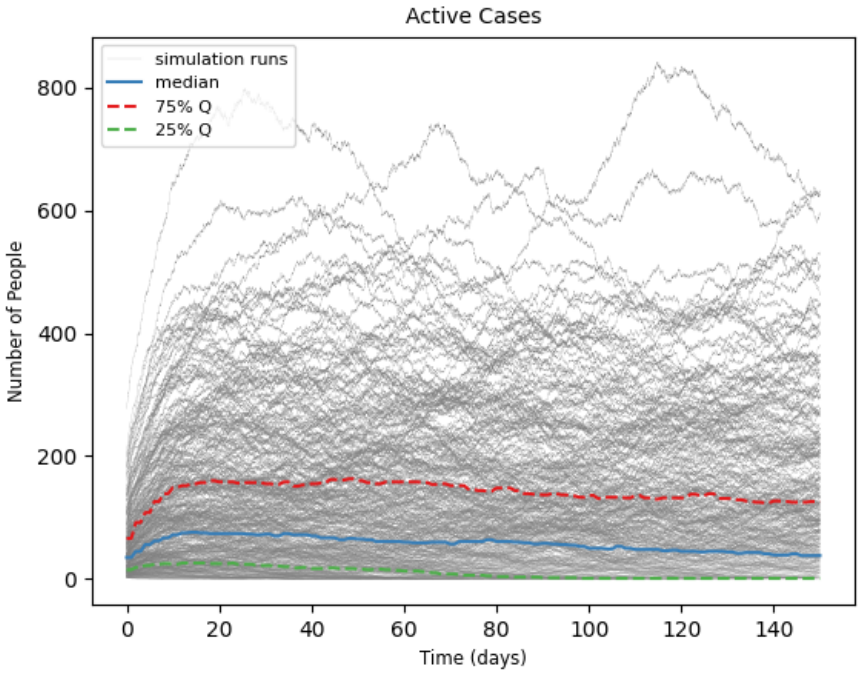

Figure 6. Active cases during an outbreak of a new variant, for 150 days post-detection under Alert Level 3. Around 40% of trajectories die out, reaching zero active cases within 150 days of initial detection. The remaining simulations show a very slowly decreasing number of active cases.

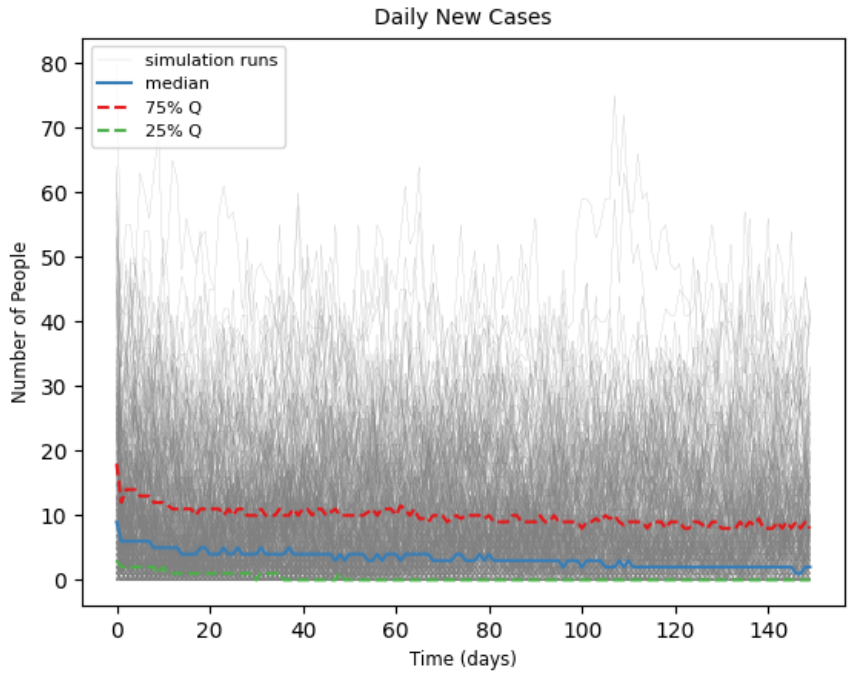

Figure 7. Daily new infections for an outbreak of a new variant, for 150 days post-detection under Alert Level 3. Around 40% of trajectories die out. However, the remaining simulations show a very slowly decreasing number of new cases per day, with Alert Level 3 being enough for suppression but not elimination.

Size of outbreak at 60 and 150 days post-detection

To better quantify the nature of the outbreaks seen under AL3 and AL3+ for the different variants we report the outbreak sizes at 60 and 150 days post-detection. The results for 60 days and 150 days post-detection are reported in Table 3 and distributions of the cumulative outbreak sizes at 60 and 150 days post-detection are shown in Figure 9.

For the old variant under AL3, there are a median of 74 [33, 189] cumulative cases from the first seed case until 60 days post-detection, and a median of 77 [33, 223] cumulative cases after 150 days post-detection. If we consider only 'known' (confirmed through testing) cases, the cumulative case counts are a median of 34 [17, 93] after 60 days post-detection, and a median of 35 [17, 118] after 150 days post-detection. These numbers are very similar at day 60 and day 150, as most simulations have no or low new cases after 60 days.

For the new variant under AL3, there are a median of 332 [111, 734] cumulative cases from the first seed case until 60 days post-detection, increasing to a median of 689 [151, 1518] cumulative cases after 150 days post-detection. If we consider only 'known' (confirmed through testing) cases, there are a median of 166 [54, 365] after 60 days post-detection, increasing to a median of 372 [86, 823] after 150 days post-detection.

With the improved contact tracing under AL3+, there are a median of 302.5 [90, 610] cumulative cases from the first seed case until 60 days post-detection, and a median of 478.5 [119, 1140] cumulative cases after 150 days post-detection. If we consider only 'known' (confirmed through testing) cases, the cumulative case counts are a median of 156 [51, 315] after 60 days post-detection, and a median of 259 [67, 624] after 150 days post-detection.

This suggests that the slight reduction in R_{eff} from the improved contact tracing is likely to still play a role in reducing the *size* of an outbreak.

Scenario	Cases	Size of outbreak at day 60	Size of outbreak at day 150
AL3 old variant	Confirmed	34 [17, 93]	35 [17, 118]
	Total	74 [33, 189]	77 [33, 223]
AL3 new variant	Confirmed	166 [54, 365]	372 [86, 823]
	Total	332 [111, 734]	689 [151, 1518]
AL3+ new variant	Confirmed	156 [51, 315]	259 [67, 624]
	Total	302.5 [90, 610]	478.5 [119, 1140]

Table 3. Cumulative Cases (confirmed cases and total cases) at day 60 and 150 post-detection. Results shown are *median [lower quartile, upper quartile]*.

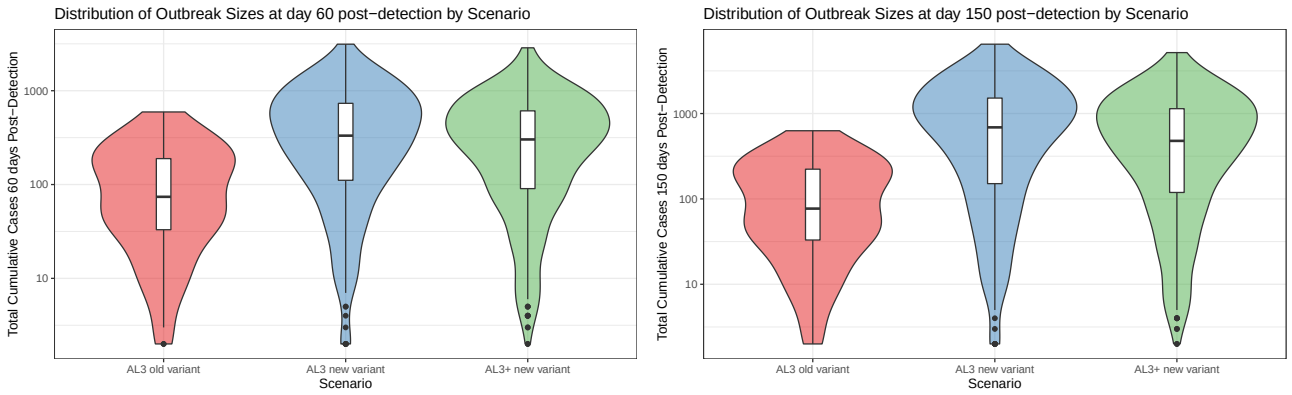

Figure 8. Distribution of Total Cumulative Cases at day 60 and day 150 by Variant and Intervention. This plot shows the distribution of the total cumulative number of cases (i.e. both confirmed cases and unknown cases) at day 60 and day 150 after detection **on a log scale**. Note: the scale of the y-axis differs between the two times. Density plots indicate the lower quartile, median, upper quartile, and distribution of cumulative cases across the set of simulations for each variant and intervention level.

As expected, the outbreak dynamics are influenced by the initial size of the outbreak. At 60 days post-detection, with AL3 (respectively AL3+), outbreaks of the new variant with a size at detection in the range 2–10 had a median of 25 (resp. 20) total cases compared with a median of 229 (resp. 108) for outbreaks with a size at detection in the range of 11-20. Table 4 reports

cumulative number of total and 'known' cases at 60 days post-detection, while Figure 9 shows the distribution of the total cumulative outbreak sizes at 60 days post-detection for a range of different initial outbreak sizes.

Scenario	Cases	Size of outbreak at detection				
		2-10	11-20	21-50	51-100	101+
AL3 old variant	Confirmed	8 [4, 12]	26 [22, 29]	74.5 [41, 111]	145 [131, 193]	327 [327, 327]
	Total	14 [7, 26]	48 [43, 62]	140 [80, 203]	281 [256, 419]	629 [629, 629]
AL3 new variant	Confirmed	16 [7, 39]	122 [47, 254]	351 [164, 575]	784 [580, 1242]	1580 [1228, 2015]
	Total	25 [10, 71]	229 [86, 506]	653 [286, 1057]	1437 [1033, 2348]	2813 [2179, 3675]
AL3+ new variant	Confirmed	13 [6, 24]	62.5 [42, 145]	240.5 [151, 412]	613 [402, 887]	1231 [881, 1648]
	Total	20 [7, 44]	108 [68, 260]	432.5 [250, 740]	1131 [745, 1602]	2214 [1577, 2960]

Table 4. Cumulative Cases (confirmed cases and total cases) at day 150 post-detection for different initial outbreak sizes at detection and interventions. Results shown are *median [lower quartile, upper quartile]*.

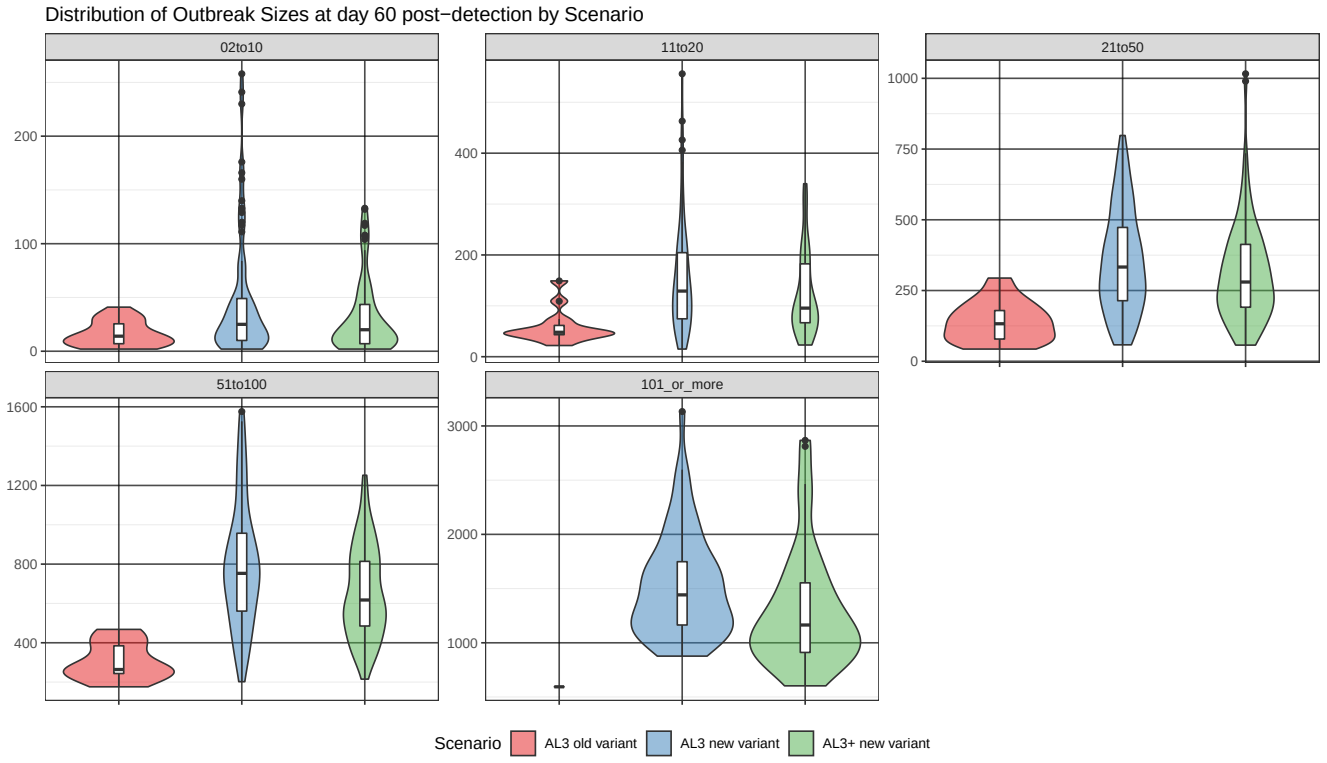

Figure 9. Distribution of Total Cumulative Cases at day 60 by Scenario and Outbreak Size at Initial Detection. This plot shows the distribution of the total cumulative number of cases (i.e. both confirmed cases and unknown cases) at 60 days after detection. Results are split by outbreak size at initial detection (five sub-figures) and across the scenarios of AL3, and AL3+. 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.

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

New confirmed cases

While Alert Level 3 (including with contact tracing improvements) might be insufficient for elimination of an outbreak of the new variants of COVID-19, it is capable of suppressing such outbreaks. This leads to long time periods with low numbers of new daily cases, as long as Alert Level 3 continues to operate effectively/ Looking at Figure 10, we see that under AL3 there are up to 30 new confirmed cases per day, but that most days have fewer than five new confirmed cases. This is a lower bound on the total number of new cases as it does not include new infections that are undetected (c.f. Figure 7).

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. This is within the official limits of the NCTS which are 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)[13].

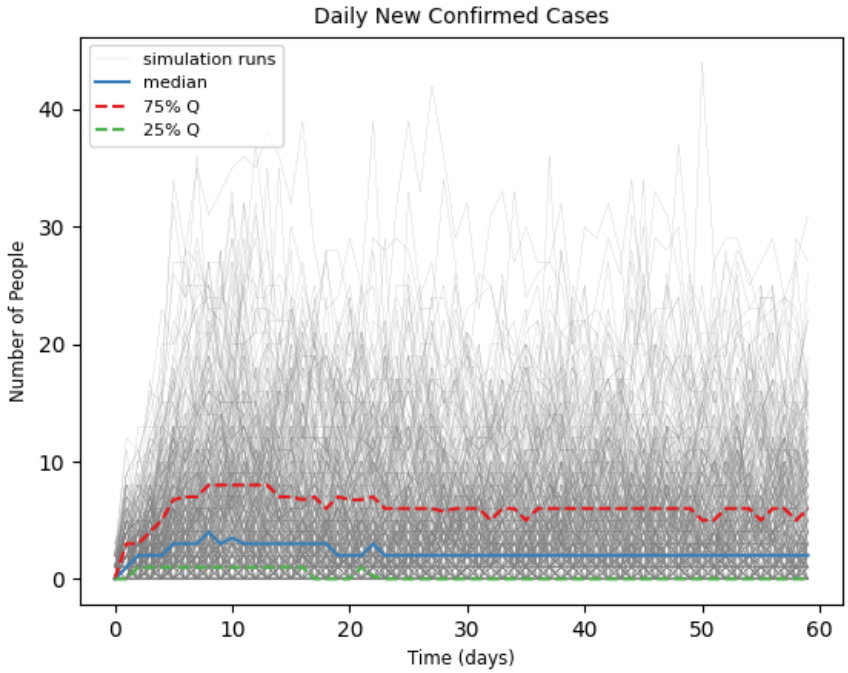

Figure 10. Daily new confirmed cases through time for an outbreak of a new variant, for 60 days post-detection, under Alert Level 3.

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 Tamaki Makaurau where the capacity for COVID-positive cases is 222 beds[14].

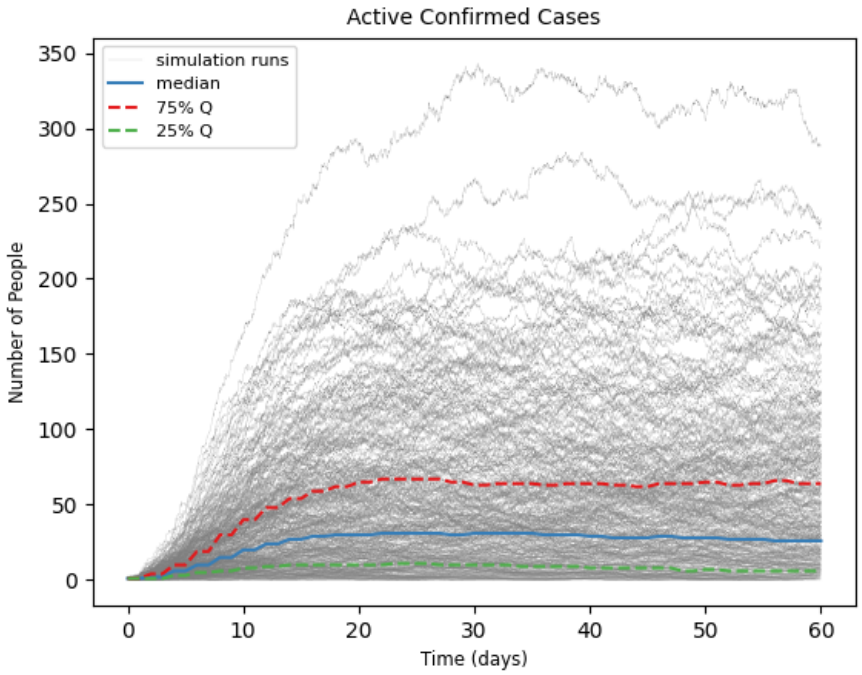

Figure 11. Number of active confirmed community cases in managed isolation (MIQ) through time for an outbreak of a new variant, for 60 days post-detection, under Alert Level 3.

Looking at the number of active confirmed cases (Figure 11) it can be seen that although many outbreaks only require fewer than 50 beds at a time, there are still a number of outbreaks where this number might reach beyond the capacity of this facility. In addition, much of the space may be required for new cases within the MIQ facilities from incoming travellers, or for active cases that have since recovered in MIQ but require an additional 72 hours symptom free before release[15].

Close contacts to identify and contact

We plot the number of close contacts identified and successfully contacted each day in Figure 12. 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 42 for the new variant under AL3 (see Table 5). With greater outbreak sizes at detection, the peak number of people in isolation increases. Outbreaks of size 11-20 had a peak number of around 120 isolations, while outbreaks sizes of 100 or more had around 450 isolations. The number of isolations is reduced under AL3+, with it being around 29 for outbreaks of size 2-10 at detection, around 100 for outbreaks of size 11-20, and around 416 for outbreaks over 100.

Scenario	Size of outbreak at detection				
	2-10	11-20	21-50	51-100	101+
AL3 old variant	19 [9, 45]	47 [34, 83]	91.5 [68, 122]	157 [120, 192]	294 [294, 294]
AL3 new variant	42 [16, 73]	120 [72, 163]	174 [130, 231]	278 [225, 365]	448 [370, 521]
AL3+ new variant	29 [13, 63]	99.5 [59, 127]	161 [112, 205]	264.5 [216, 329]	416 [357, 483]

Table 5. 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.

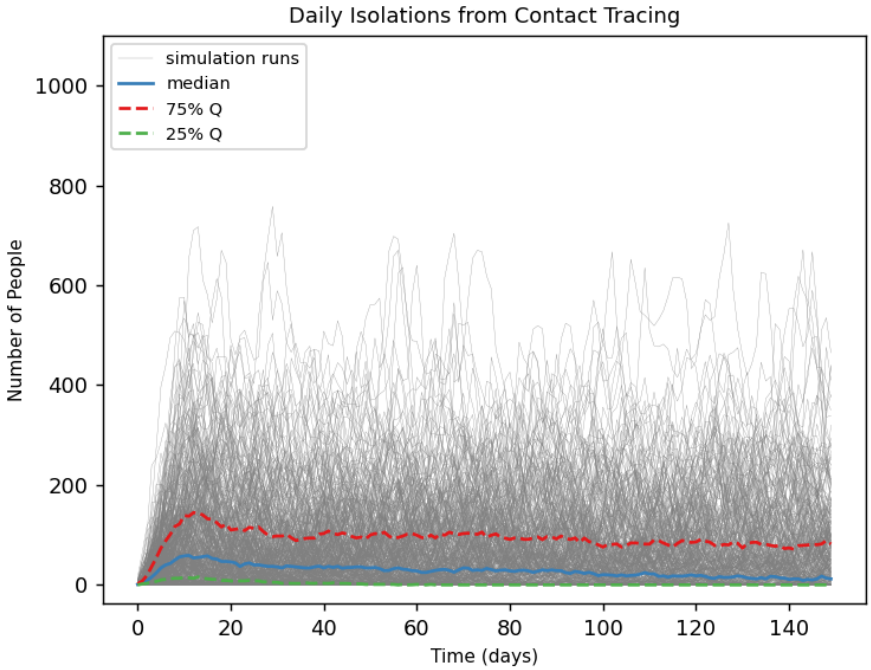

Figure 12. Number of close contacts successfully identified and contacted each day for an outbreak of a new variant, for 150 days post-detection under Alert Level 3.

Considering that the mean number of calls to reach a close contact is 1.9[13], contact tracing at this rate would be within the NITC ready capacity of 10,000 calls per day with scalable capacity of up to 20,000 calls per day[13]. While the peak capacity of the NITC is likely to be sufficient to deal with the expected number of new daily cases from even a large initial outbreak under Alert Level 3, the fact that AL3 produces suppression behaviour rather than elimination means that this high capacity would have to be maintained for a number of months with no decrease in efficiency or effectiveness if the outbreak were to remain suppressed. Furthermore, this does not take into consideration the calls that would need to be made to people other than the initial call to a close contact, including the repeat follow up calls to close contacts to support them to isolate and monitor their health, calls to confirmed cases to perform case interviews, calls to businesses or other exposure locations to identify potential close or casual contacts.

Sustained response

Because the Alert Level 3 measures are not enough to rapidly eliminate an outbreak, the contact tracing and isolating response will need to keep performing at a high level for months. We see from Figure 12 that at 150 days post-detection, for the many simulations there are still over 100 close contacts to contact and isolate each day. Related to that, since close contacts must stay in isolation for 14 days, at any time there are a large number of people in self-isolation who need to be supported and monitored. Figure 13 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 11) we can get an idea of the level of resourcing required.

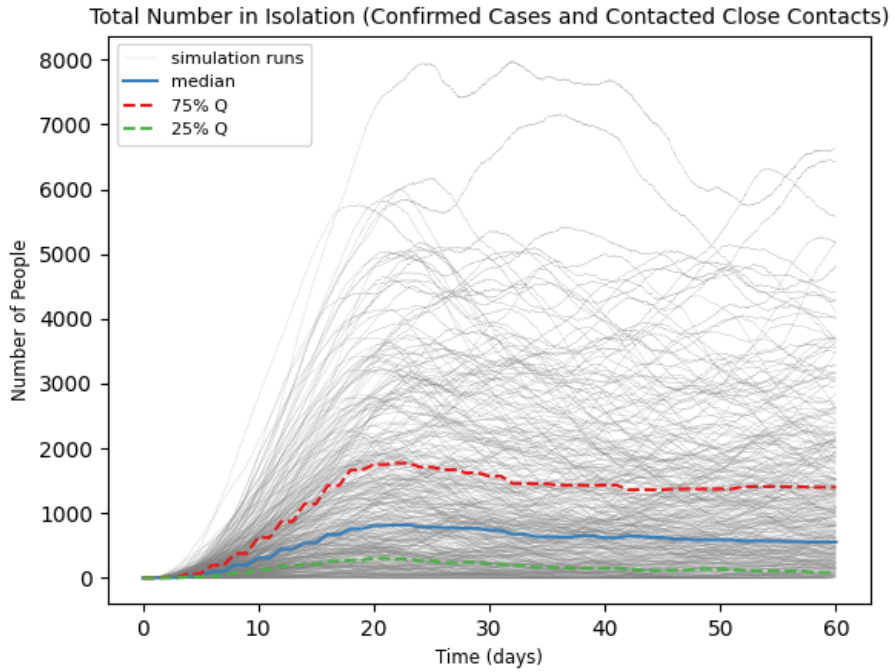

Figure 13. Number of people currently in isolation (both confirmed cases and close contacts in self isolation) through time for an outbreak of a new variant, for 60 days post-detection, under Alert Level 3.

Scenario	Size of outbreak at detection				
	2-10	11-20	21-50	51-100	101+
AL3 old variant	104 [38, 214]	395.5 [334, 710]	1266.5 [755, 1831]	2401 [2096, 3821]	5660 [5660, 5660]
AL3 new variant	239 [86, 599]	2252 [783.5, 5132]	6526 [2898, 11495]	14523 [10669, 23892]	29457 [22013, 36178]
AL3+ new variant	200.5 [70, 540]	1119 [650, 3078]	4604 [2540, 8245]	12432 [7884, 17496]	24003 [16718, 31549]

Table 6. Total cumulative number of isolations from contact tracing in the first 200 days post the first infection for different initial outbreak sizes at detection and interventions. Results shown are *median [lower quartile, upper quartile]* unless otherwise stated.

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, etc). The community interactions also include long-range travel within Aotearoa New Zealand, based on cellphone movement data[16].

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 the chances 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[17] to simulate our main 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[18] and is now standard in the network contagion literature[19].

Although our main dynamics are Markovian and compatible with the standard Gillespie algorithm, we incorporate additional realism by allowing for delay processes, particularly in our tracing dynamics. We do this by having Markovian 'initiation' dynamics but delayed 'completion' times, with arbitrary distributions allowed for completion times. Delay processes can be handled in an exact manner using an extension of the standard direct Gillespie method[20,21], and we follow this approach here.

Key assumptions

Full model details are described elsewhere[8], 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.[22].
- 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[23,24]. 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)[8], but also affects the chance 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.
- 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.

Some differences to note:

- Our 'casual contacts' category encompass both the 'casual contacts' and the newly defined 'casual plus contacts' categories created by the Ministry of Health, in that the casual contacts in our model all did have contact with a confirmed case which carried a risk of transmission. Casual contacts in our model are encouraged to get a test regardless of symptoms, but are not self-isolating until they receive a negative test result
- Symptomatic cases are not self-isolating at the onset of symptoms in our model. They only change behaviour (and transmission risk) when they receive their test result, unless they are already self-isolating because they are a close contact of a confirmed case
- We only do first degree contact tracing, we do not for example trace close contacts of close contacts.
- Confirmed cases leave MIQ once they recover and are no longer infectious. This can be before 14 days has passed.

Initial conditions

In order to create initial conditions for the more transmissible, new variant for AL3 and AL3+ scenarios, we set 500 simulations running using parameters for our best estimate of a 'Baseline Alert Level 1'[6] to simulate infection spread prior to detection of the first case. This includes a β parameter that corresponds to a 50% increase in COVID-19 infectivity, relative to older variants. Once the first infected case is detected and confirmed we turn on the Alert Level 3 (or AL3+) simulation parameters described above.

We follow a similar procedure for 100 additional simulations, using a β parameter that corresponds to the infectivity of older variants of COVID-19 used in previous reports[6–8]. These lower infectivity simulations are used to give context and allow straightforward comparison for the more transimissible variant.

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[25]. We assume a test positivity rate of 80%[26], 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[25] 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.

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

Even though the transmission settings in the simulation are identical for the increased transmissibility AL3 and the AL3+ 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, we compare the distribution of outbreak sizes at detection for the simulation runs that are used for the AL3 and AL3+ scenarios. See Table 7 and Figure 14.

Outbreak sizes at detection for the older variant are expected to be smaller due to its lower transmissibility. Hence, initial conditions at the point when the the AL3/AL3+ interventions are applied will differ for the two variants. Differences in the outbreak size at detection for the two variants are reported and discussed in the Pre-detection phase section, in addition to being included in Figure 14 below.

Scenario	All runs	Distribution of different initial outbreak sizes (new variant)				
		2–10 (n)	11–20 (n)	21–50 (n)	51–100 (n)	101+ (n)
AL3	34 [14,66] (441)	6 [4, 8] (79)	15 [12, 18] (75)	34 [27, 40.5] (135)	68 [59, 82] (97)	134 [111,155] (55)
AL3+	34 [16,63] (442)	5 [4, 8] (78)	16.5 [13, 18] (68)	33 [27, 41] (141)	67 [59,83] (106)	120 [111,146] (49)

Table 7. Distribution of initial outbreak sizes within each size band for the simulations from the pre-detection phase of the AL3 and AL3+ scenarios with the higher transmissibility variant and the AL3 scenario 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.

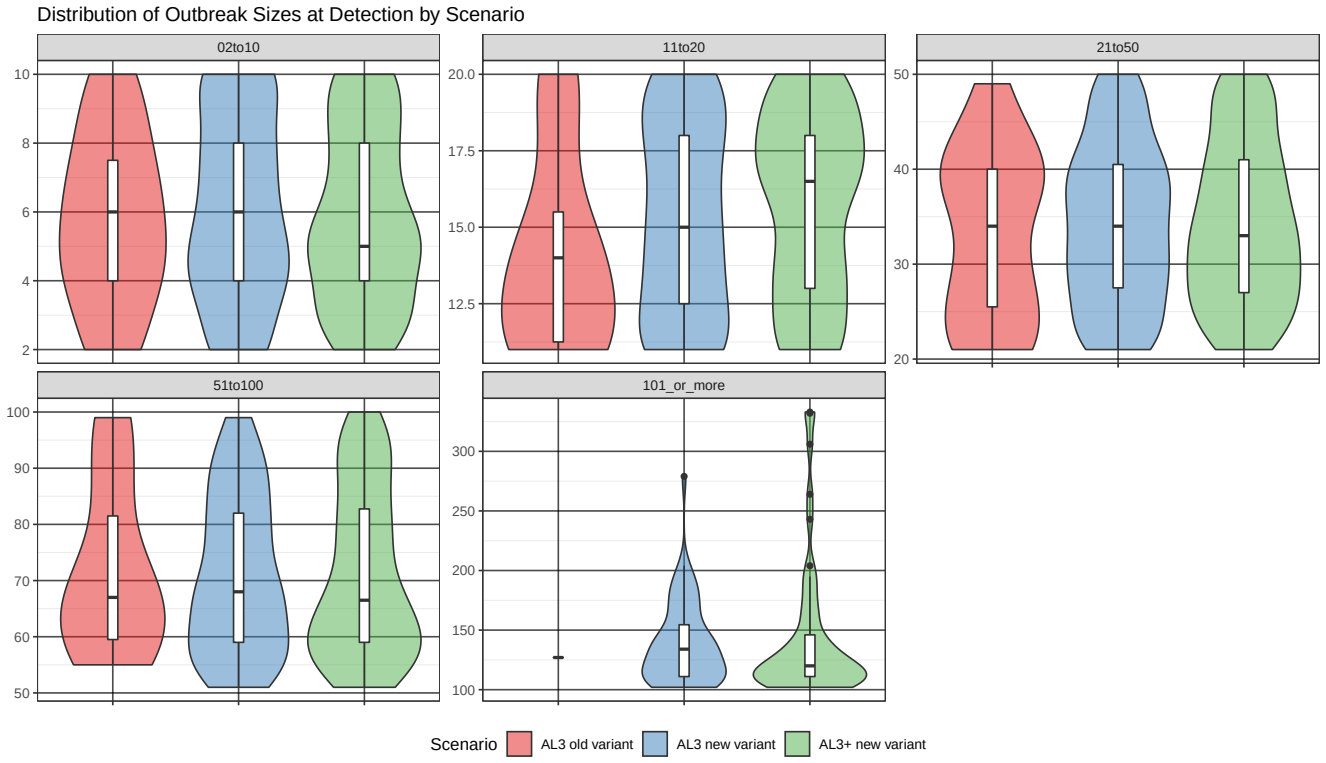

Figure 14. Distribution of Initial Outbreak Sizes, by Scenario and Variant. This plot shows the distribution of initial outbreak sizes for AL3, and AL3+ scenarios with the new variant — these use identical simulation conditions. We also show the distribution of initial outbreak sizes for the less transmissible, older variant. The distributions of the initial outbreak sizes used for the simulations are comparable across intervention scenarios for each variant, but not between the two different variants.

Discussion

The results presented here show that **COVID-19 variants with increased transmission rates considerably impact the ability of non-pharmaceutical interventions to eliminate a community outbreak**. For old variants, Alert Level 3 led to elimination within 200 days post-detection in nearly all cases, regardless of the outbreak size at detection. In contrast, **for the new variant, elimination within 200 days is much less likely in general, and is strongly dependent on the size of the outbreak at first detection**. Our estimates for R_{eff} (based on post-processing our simulations) for the new variant are close to 1 under both AL3 and AL3+, indicating either suppression behaviour or that some simulations that do not eliminate within 200 days may be heading to elimination over a longer time period. However, this requires AL3/AL3+ measures to be sustained for periods of time that may place heavy burdens both on the population and contact tracing systems.

Only around 40% of all simulations of the new variant under AL3 led to elimination within 200 days, and improved contract tracing (AL3+) only had a very small (though statistically detectable) effect on this. There was no statistically discernible effect on elimination probability when controlling for outbreak size at detection. **For small outbreaks (2-10 cases at detection) of the new variant, AL3/AL3+ led to elimination within 200 days in around 90% of the simulations, but this dropped off significantly with outbreak size at detection: for outbreaks detected at size 51–100 the probability of elimination within 200 days falls to around 10%. For intermediate size outbreaks (11-50 cases at detection) the probability of elimination under AL3/AL3+ was around 50%**. Even for those simulations that did eliminate the new variant within 200 days, this often took a long time: for example, only about 12% of new variant runs reached elimination within 60 days of detection under AL3 interventions.

One key message from these results, echoing those of our previous reports, is that the smaller an outbreak is when interventions such as AL3 are first applied, the higher the probability of elimination and the smaller the total outbreak size. However, this effect is even more pronounced for new variants: **the effectiveness of Alert Level 3 at achieving elimination is greatly reduced unless the outbreak is caught very early**. While AL3 is likely sufficient to eliminate either outbreaks of old variants or very small outbreaks of new variants, **AL3 cannot guarantee the elimination of larger outbreaks of new variants with high confidence.** Furthermore, even when elimination of a new variant can be achieved under AL3/AL3+ interventions, this may take a significant time.

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