Technical report: modelling the potential spread of COVID-19 during the August 2021 outbreak

Nicholas Steyn, Shaun Hendy, Michael Plank, Rachelle Binny

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Executive summary

1. We consider the epidemic course for the August 2021 cluster, detected on 17 August in Auckland, following the shift to Alert Level 4 restrictions in New Zealand using a stochastic branching process model.
2. Assuming $R_0 = 6$ for the Delta variant, we estimated on 20 August that the total number of people infected prior to the move to Alert Level 4 on 17 August was 104 (interquartile range 43 – 211) at low testing rates or 71 (interquartile range 30 – 143) at high testing rates. Results from wastewater testing and/or establishing the introduction date as 7 August reduce these estimates.
3. Subsequent case detection shows that the outbreak size was in fact close to or larger than the upper end of these ranges.
4. We note that the effects of Alert Level 4 on transmission are not expected to become evident in case numbers for 7-10 days following the change in Alert Level.
5. However, in order to simulate the epidemic course, we consider low, central, and high transmission scenarios for the effect of Alert Level 4.
6. Modelled average daily case numbers decline to less than 10 around mid-September in the low transmission scenario and by early October in the central scenario. At this point, supported by effective contact tracing, elimination would be within reach.
7. In the high transmission scenario, daily case numbers continue to grow in the short term and the outbreak is contained by a combination of ongoing Alert Level 4 restrictions and the rollout of the vaccination programme.
8. In the central and the high transmission scenarios, an accelerated vaccination programme could reduce the time needed at Alert Level 4 but the benefit of this is only felt in the medium term (months).
9. If an untraced outbreak has been seeded into a region outside Auckland, it would take until around 2 September to reach a high level of confidence that this has been detected via either symptomatic testing or wastewater testing. High testing rates and/or a strong effect of Alert Level 4 in reducing transmission will improve this.

Introduction

On 17 August 2021 a case of COVID-19 was identified in Auckland, ending an extended period with no community transmission of SARS-CoV-2. This was subsequently confirmed to be the Delta variant of SARS-CoV-2. In response, the government moved the entire country to Alert Level 4 – the most stringent form of restrictions. It is uncertain at present how large the outbreak could be, how far it has spread and how effective the response will be in controlling the outbreak.

The purpose of this technical report is to describe mathematical modelling that was used in the days following detection of the outbreak to provide situational awareness and inform the government's high-level outbreak response. We present initial estimates for the number of people infected at the time the outbreak was first detected and outline plausible scenarios for the outbreak dynamics in the following weeks. We also describe a method for assessing the risk of hidden outbreaks in parts of New Zealand with no detected cases, based on community testing rates and the results of wastewater testing.

Methods

A modified version of the age-structured stochastic branching process model for COVID-19 transmission with vaccination [1] was implemented. The proportion of each age group that has received one or two doses of the vaccine is time-varying based on vaccinations already administered, as well as data on future bookings. Population age structure and vaccination coverage are based on data from the Auckland metro region (Supplementary Table S1). For simplicity, the vaccine coverage prior to detection on 17 August was assumed to be fixed at 17 August levels; this assumption has a negligible effect on model outputs. Vaccine effectiveness parameters are as in Steyn et al (2021), with the additional assumption that one dose of the vaccine provides 23% protection against infection (relative to 70% protection after two doses). All vaccine doses are assumed to take effect two weeks after being administered.

Infected individuals are categorised as either clinical or subclinical, with the clinical fraction increasing with age (see Table 1b). Subclinical individuals are assumed to be 50% as infectious as clinical individuals. Clinical individuals are assigned a symptom onset time which is gamma distributed from infection time with mean 5.5 days and s.d. 3.3 days [2]. In the absence of interventions, we assume generation times are drawn from a Weibull distribution with mean 5.0 days and s.d. 1.9 days [3]. There is at present conflicting evidence in the literature as to whether the Delta variant of SARS-CoV-2 has a shorter mean generation time or mean incubation period than older variants [4-8]. Generation times in particular are difficult to empirically measure because this requires the infection times of both cases in a transmission pair. If infection times are unavailable but symptom onset dates are known, the serial interval can be used as a proxy for generation time. However, serial interval measurements contain more noise as they depend on both individuals' incubation periods. In addition, for both generation times and serial intervals, realised values are affected by control interventions such as test, trace and isolate measures. If the mean generation time is shorter than assumed in this model, the inferred value of the pre-outbreak reproduction number would be smaller, but the effectiveness of case isolation and contact tracing measures would be reduced. Further modelling work will address this in more detail.

Outbreaks are seeded by introducing one case on an unspecified date, with the day of the first positive test result then defined to be 17 August. Unless otherwise stated, no other restrictions are placed on outbreaks. Prior to detection of the outbreak, we assume the probability that a symptomatic individual seeks a test is p_{detect} with a mean time of 4 days from symptom onset to return of test result.

Once an outbreak is detected, we assume the probability of case detection for all infected individuals (clinical and subclinical) increases to 80%. This is the overall case ascertainment rate from all forms of case detection including symptom-triggered testing and contact tracing, and incorporating the effects of imperfect test sensitivity. This reflects the fact that once the contact tracing system is acting, case ascertainment is typically very high, e.g.

approximately 95% of cases in New Zealand's last significant outbreak (August 2020) had an epidemiological link identified. Case detection is assumed to occur with an exponentially distributed delay with mean of 4 days from the onset date, or pseudo-onset date for subclinical individuals. In reality, some close contacts are scheduled for testing on day 5 and day 12 after exposure; however we do not attempt to model the contact tracing process at this level of detail. The shape of the distribution is consistent with onset to reporting times from the August 2020 outbreak. Any cases with a new detection time that is prior to the outbreak detection are instead assigned detection times uniformly randomly within the week following detection. All cases are assumed to be immediately isolated on detection with no further transmission. The estimated reduction in R from these measures is 16.5%. Parameter values are shown in Supplementary Table 1.

Given the lag from infection to testing, the effect of Alert Level 4 (AL4) on reported case numbers will not be seen until around 7-10 days after restrictions were introduced. Until then, it is uncertain what the effective reproduction number under the current Alert Level 4 restrictions may be. In April 2020, during an outbreak caused by multiple introductions of the wildtype variant of SARS-CoV-2, we estimated R_{eff} to be between 0.4 and 0.6 during AL4. However, in New South Wales, a current lockdown is struggling to contain their outbreak, with R_{eff} above 1.

For simplicity, we assume that vaccination, case isolation, and Alert Level restrictions act independently to provide multiplicative reductions in R_{eff}. We assume that Alert Level 4 reduces the effective reproduction number to R_{AL4}. This is modelled as a relative reduction in transmission of R_{AL4}/R_c due to Alert Level 4 restrictions, where R_c is the effective reproduction number under the combined effect of vaccination at 17 August coverage levels and case isolation measures. We assume that, rather than a step change, the effect of Alert Level 4 reductions is to decrease transmission linearly over a period of 5 days starting on 17 August. Therefore the relative effect of Alert Level 4 restrictions on transmission at time t is characterised by $C(t) = 1 - \alpha(t)(1 - R_{AL4}/R_c)$, where $\alpha(t)$ is equal to 0 before 18 August, equal to 1 from 23 August onwards, and linearly increases from 0 to 1 between these dates. This 5-day transition period models a gradual reduction in transmission due to Alert Level restrictions and could include effects such as saturation of household transmission and people travelling home after the lockdown was announced. The ongoing vaccination programme continues to reduce the effective reproduction number over time; R_{AL4} should be interpreted as the effective reproduction number under Alert Level 4 restrictions and at 17 August vaccine coverage levels.

Given the uncertainty in R_{eff} for the Delta variant under Alert Level 4 conditions, we model spread under Alert Level 4 at three values of R_{AL4}: 0.5, 0.8, and 1.1. We refer to these three values as the low, central and high transmission scenarios respectively. These scenarios represent our best estimate of the plausible range of the effectiveness of Alert Level 4 for the Delta variant. However, it is possible that R_{eff} could be outside this range. Once more data is available, it will be possible to use daily reported cases to estimate the effect of the Alert Level restrictions on transmission via parameter inference.

Note that the model does not explicitly identify household contacts and does not distinguish between household transmission and transmission in other settings. This is partly because we lack quality data on the transmission setting both for the current outbreak and for previous New Zealand outbreaks. The results presented in this report have been used for situational

awareness and policy advice alongside other information streams, including a more finely resolved model based on an explicit contact network.

Results

Size at Detection

Note: the estimates for size at detection reported in this section were made based on information available up to 20 August and have not been subsequently updated.

We consider the size at detection under four values for pre-AL4 R_0 and two values of symptomatic testing in Auckland (estimated from pre-detection testing rates and Flutracking data in the Auckland metro area). Table 1 gives the median and interquartile range for the size of the outbreak at detection, and Table 2 gives the median and interquartile range for the time from exposure of the first community case until detection.

Wastewater testing in Auckland was negative on 11 August. We initially assumed that wastewater testing would have a limit of detection of N = 1, 5, or 10 active infections (at least 3 days from infection). Filtering out simulations that would theoretically return a positive wastewater result gives Tables 3 and 4. These simulations assume $R_0 = 6.0$ and $p_{detect} = 0.123$.

Finally, there is a strong genomic link to a case from New South Wales that entered New Zealand on 7 August. 14.5% of our simulations (with $R_0 = 6.0$ and $p_{detect} = 0.123$) have a seed time on or after this date. These simulations have a median outbreak size at detection of 35 (IQR 15, 70) and median seed date was 8 August (IQR 7 August, 9 August).

Size at Detection	$p_{detect} = 0.123$	$p_{detect} = 0.185$
$R_0 = 4$	64 (26, 127)	42 (18, 86)
$R_0 = 5$	85 (34, 168)	56 (25, 112)
$R_0 = 6$	104 (43, 211)	71 (30, 143)
$R_0 = 7$	131 (54, 259)	87 (37, 177)

Table 1. Median and interquartile range of size of outbreak at detection. Results are from 10,000 simulations where at least one case was detected.

Time to Detection	$p_{detect} = 0.123$	$p_{detect} = 0.185$
$R_0 = 4$	17 (13, 21)	15 (12, 19)
$R_0 = 5$	16 (12, 20)	14 (11, 18)
$R_0 = 6$	15 (12, 19)	14 (11, 17)
$R_0 = 7$	15 (12, 18)	14 (11, 17)

Table 2. Median and interquartile range of time from exposure of initial community case until detection. Results are from 10,000 simulations where at least one case was detected.

	N = 1	N = 5	N = 10
All simulations		104 (43, 211)	
Filtered	33 (14, 68)	56 (24, 105)	76 (34, 142)
% simulations that meet criterion	21%	56%	78%

Table 3. Median and interquartile range of size of outbreak at detection assuming that wastewater testing (with a lower limit of detection of N = 1, 5, or 10 active infections at least 3 days after infection) of samples taken on 11 August was negative. Results are from 10,000 simulations where at least one case was detected.

	N = 1	N = 5	N = 10
All simulations		15 (12, 19)	
Filtered	10 (9, 11)	12, (10, 15)	14 (11, 17)

Table 4. Median and interquartile range of time to detection assuming that wastewater testing (with a lower limit of detection of N = 1, 5, or 10 active infections at least 3 days after infection) of samples taken on 11 August was negative. Results are from 10,000 simulations where at least one case was detected.

Outbreak scenarios

As at 25 August, the total number of reported cases in the outbreak has risen to 210, the vast majority of which were likely infected prior to the first positive test result on 17 August. To capture this outbreak size, we run simulations with a higher initial value of $R_0 = 8$ and a lower probability of testing $P_{detect} = 0.06$ prior to the outbreak being detected. Note that these parameter values do not necessarily apply to the population as a whole, but may be more representative of the specific groups and settings within which the outbreak was spreading during its early stages, i.e. predominantly young age groups with high contact rates and significant superspreading. With these parameters, the median number of people infected when the outbreak is first detected is 312 (IQR 126 – 624). Results are taken from 1,000 simulations where at least one case was detected.

Figure 1 gives the median and interquartile range for the number of daily infections that occur between 10 August (one week prior to detection) and 1 October (six weeks following detection) for the low ($R_{AL4} = 0.5$), central ($R_{AL4} = 0.8$) and high ($R_{AL4} = 1.1$) transmission scenarios. Figures 2-4 show the median and IQR for the daily and cumulative number of reported cases, which depends on the lag from infection to reporting. These Figures also include a counterfactual scenario where there was no strong Alert Level response. We modelled this as a 25% reduction in transmission following 17 August, in addition to the same vaccination and case isolation measures as in the main scenarios, leading to $R_{eff} = 4.2$ (red curves in Figures 2-4). The results in Figures 2-4 suggest that, in the immediate near-term, it may be difficult to discern from case numbers alone whether we sit closer to the low transmission or the high transmission scenario. Once more data is available, we will perform parameter inference to estimate the effect of the Alert Level restrictions on transmission.

These results show that in the low transmission scenario, where Alert Level 4 is highly effective (90% reduction in transmission), average daily reported case numbers could decline to less than 10 by mid-September. In the central scenario, cases decline more slowly and it takes until early October for average daily case numbers to fall to less than 10. At this stage, contact tracing and quarantine would make a strong contribution to the chance of achieving elimination. In the high transmission scenario, the case numbers continue to grow in the medium term (see below for effects of vaccine roll-out).

There is further uncertainty not captured in this modelling. Three key areas that need to be kept in mind when considering these results are:

1. Further information on case numbers over the coming days will help provide certainty over the size of the outbreak and this data could increase or decrease the estimated timeframes required to reduce average daily case numbers to a given level.
2. We assume vaccines are evenly distributed within age-groups. In reality vaccination is likely clustered, so some communities will experience lower-than-modelled transmission, while others will experience greater-than-modelled transmission. If the outbreak enters a community with low vaccine coverage and/or high contact rates, it could spread more rapidly than predicted by the model. The more community transmission there is, the higher the risk this could occur.
3. We do not explicitly model essential workers or household structure. While the model includes individual heterogeneity in transmission rates (e.g. to allow for the occurrence of superspreading), we may understate the effect of this heterogeneity as potential superspreaders during lockdown (e.g. supermarket workers) are more likely to have contact with other potential superspreaders.

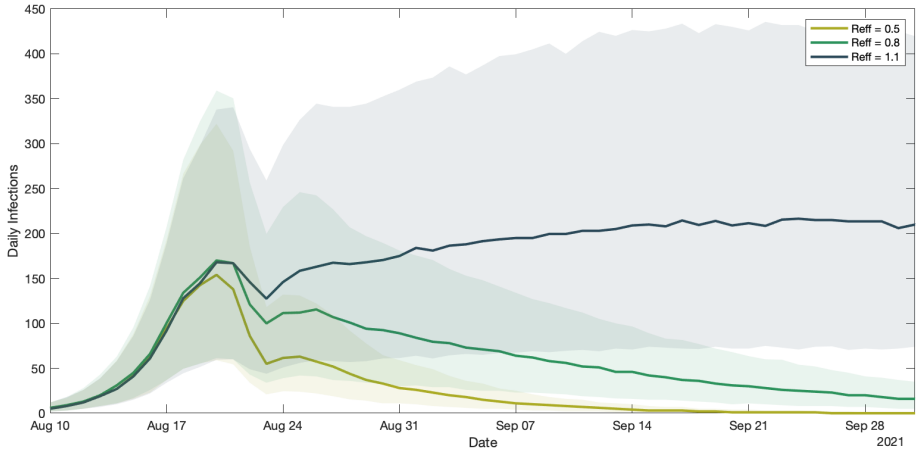

Figure 1. Median daily new infections under a low transmission scenario, central scenario, and high transmission scenario. Shaded areas represent the interquartile range. Note this implies that 50% of scenarios lie *outside* the shaded region, reflecting the high variability in infection numbers in small outbreaks. Results are from 1,000 simulations where at least one case was detected.

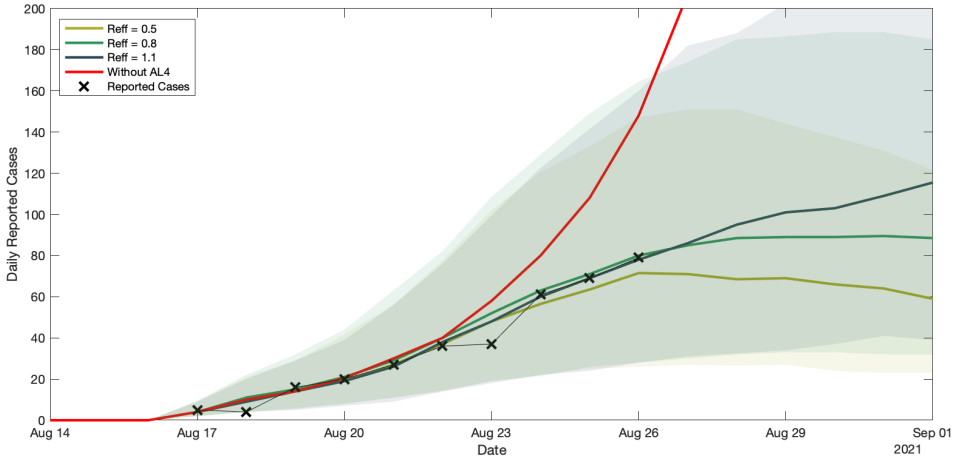

Figure 2. Daily reported cases until 1 September under a low transmission scenario, central scenario, and high transmission scenario. Lines represent the median and shaded area represents the IQR. Note this implies that 50% of scenarios lie *outside* the shaded region – reflecting the high variability in case numbers in small outbreaks. Red curve shows the median in a counterfactual scenario with no strong Alert Level response. Results are from 1,000 simulations where at least one case was detected. Note: reported daily case data covers the period from midnight to midnight each day and differs from the number of cases reported in the Ministry of Health's 1pm media releases.

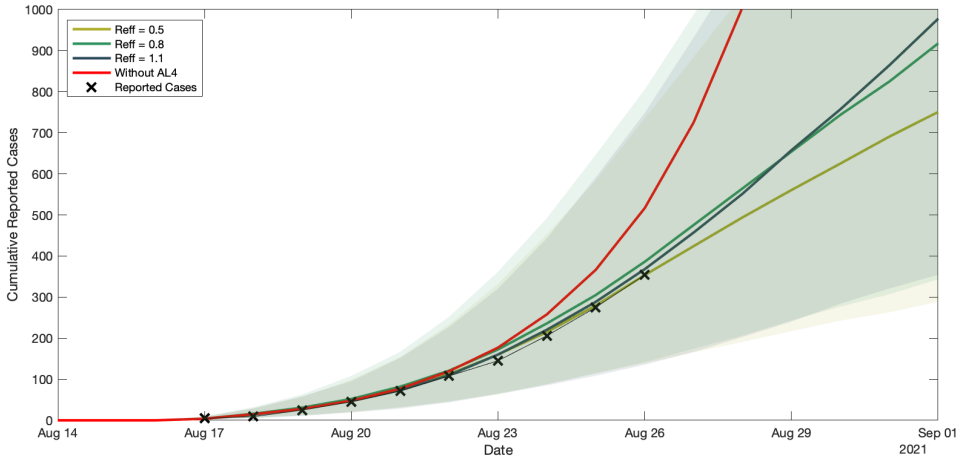

Figure 3. Cumulative reported cases until 1 September under a low transmission scenario, central scenario, and high transmission scenario. Red curve shows the median in a counterfactual scenario with no strong Alert Level response. Results are from 1,000 simulations where at least one case was detected.

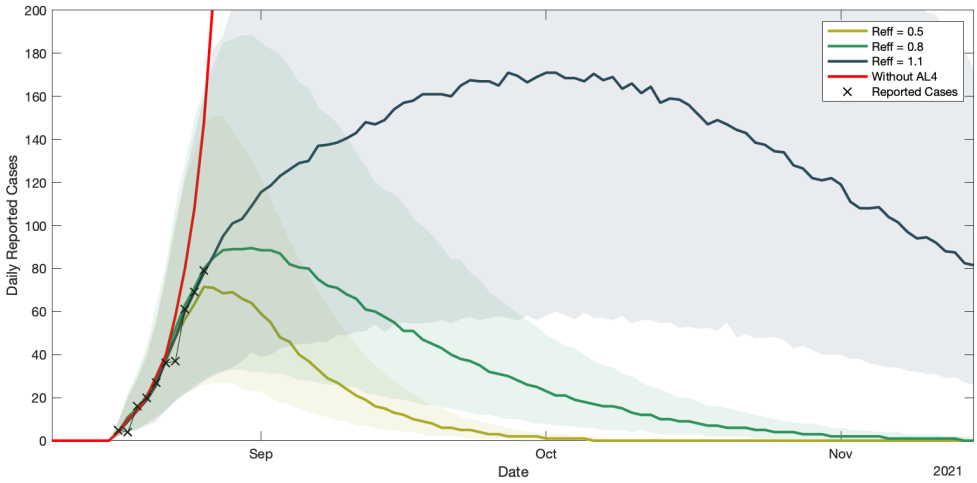

Figure 4. Daily reported cases until mid-November under a low transmission scenario, central scenario, and high transmission scenario. Red curve shows the median in a counterfactual scenario with no strong Alert Level response. Results are from 1,000 simulations where at least one case was detected. Note: reported daily case data covers the period from midnight to midnight each day and differs from the number of cases reported in the Ministry of Health's 1pm media releases.

Effect of vaccination

The modelled vaccine effect from 1 September onwards relies on vaccination appointment bookings data. This could underestimate the number of vaccinations administered if additional capacity is available for this period. To test the effect of increasing vaccination rates we reproduce the high transmission ($R_{AL4} = 1.1$) scenario when actual doses are twice and four times the levels currently booked. This adjustment is made within each age-group, until the group is fully vaccinated. As bookings increase in younger individuals the vaccine provides a greater reduction in transmission at the population level. This allows us to investigate the potential to use targeted vaccination as part of a set of measures to control the outbreak.

Figure 5 shows the relative reduction in the reproduction number as a result of increasing levels of vaccine coverage, under these different vaccination rate scenarios. Other control measures, including case isolation, contact tracing and alert level restrictions, are assumed to provide an additional multiplicative reduction in transmission independent of the level of vaccine coverage.

Figure 6 reproduces the high transmission ($R_{AL4} = 1.1$) scenarios from Figure 1 over a longer time frame. These results show that the effect from any substantial increase in vaccination rates, relative to data on vaccination bookings as at 18 August, is not seen until early October. This assumes that Alert Level 4 restrictions maintain their effectiveness over this entire period, which may not be plausible.

These results show that, even under a highly optimistic scenario where vaccination rates can be increased to four times higher than the rates suggested by existing bookings, increasing

vaccine coverage only provides significant benefits for controlling the current outbreak in the medium to long term.

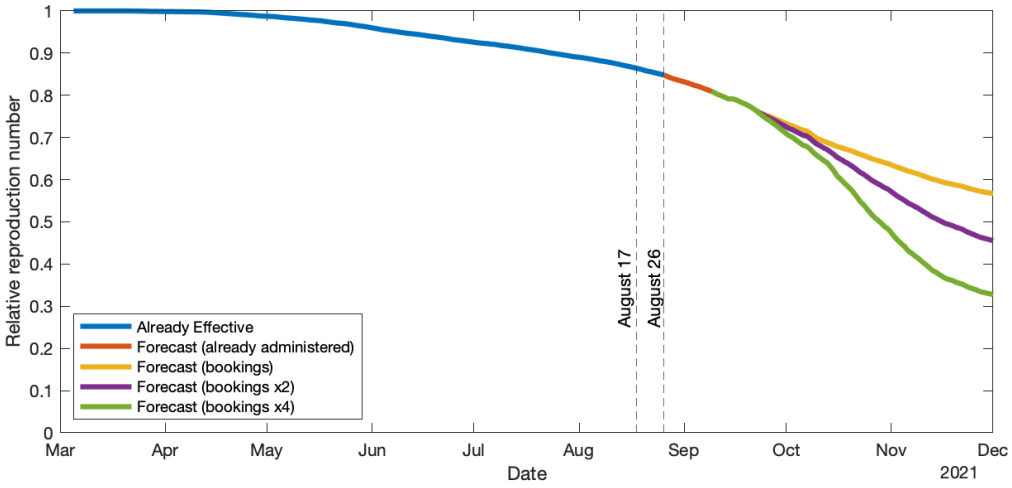

Figure 5. Estimated reduction in the model reproduction number as a result of increasing vaccine coverage levels over time. Results show the ratio of the reproduction number with vaccine coverage levels on a given date to the reproduction number with no vaccination.

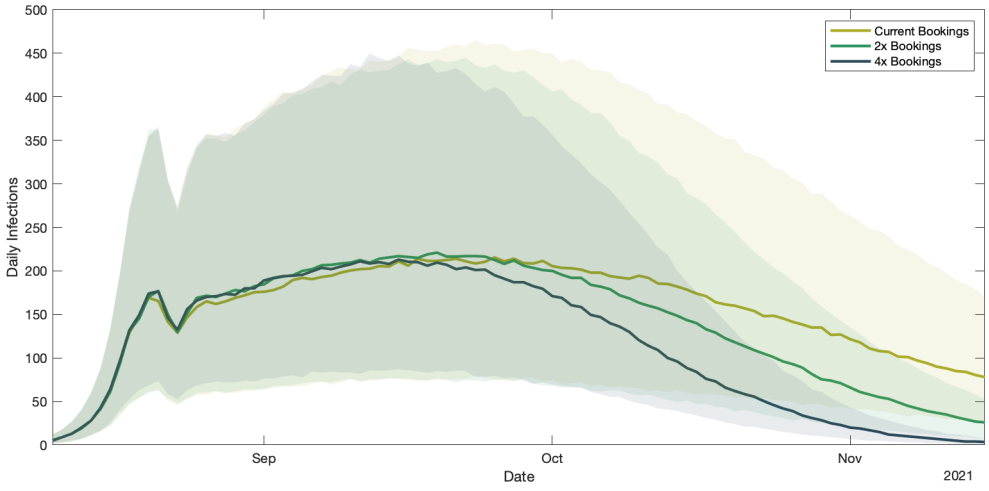

Figure 6. Daily new infections under the high transmission scenario ($R_{AL4} = 1.1$) for three different projected vaccination rates. Results are from 1,000 simulations where at least one case was detected.

Detecting outbreaks outside of Auckland

Recalibrating the model with the national age structure and vaccination coverage, we consider the probability that, if an outbreak was seeded outside Auckland, the outbreak would still be active and undetected at a given time. We assume that an outbreak outside Auckland was seeded with a single case randomly between 8 August and 20 August (to allow for the 17-20 August period when people were allowed to travel home). An outbreak is considered active if it is within 14 days from the infection time of the most recent case. Testing is assumed to detect 5% of symptomatic infected individuals prior to Alert Level 4 (based on data on testing rates and Flutracking data outside the Auckland region). After the outbreak in Auckland is detected, we assume the probability of detecting a symptomatic individual is higher, reflecting the nationwide increase in testing, and we test a range of values from 0.1 to 0.9.

Prior to Alert Level 4, the reproduction number outside of Auckland is assumed to be 6.0. There is insufficient data to estimate the reproduction number outside of Auckland during Alert Level 4. We assumed a reproduction number of 1.0, which is an agnostic assumption meaning that outbreaks that have been seeded do not either grow or decline rapidly, but will tend to continue with relatively stable case numbers over time.

Figure 7 shows the probability that, if a case was seeded outside Auckland, the outbreak will have either gone extinct or been detected by time t. This only considers detection via testing of symptomatic cases and should be interpreted as the probability of detecting an outbreak that would otherwise be missed by contact tracing. Furthermore, this work does not consider the likelihood of outbreaks having been seeded in different regions, which will depend on travel rates and the size of the outbreak in Auckland over time.

We also consider the additional information from regular wastewater testing. Based on the preliminary results on the sensitivity of wastewater testing [9], we make the following modelling assumptions:

1. Wastewater samples are collected regularly with a given sampling interval from a catchment with a population size $N_{catchment}$.
2. Based on the “infectious cases” (model 2) of [9], we assume that the probability of a positive result depends on the number of active cases in the catchment, as shown in Table 5. Cases are defined to be active from 3 days prior until 9 days after symptom onset (or pseudo-onset in subclinical individuals).
3. There is a fixed lag of 3 days from the sample being taken to the result being returned.
4. The results from successive samples in the same catchment are assumed to be independent random variables. Under this assumption, increasing the frequency of wastewater sampling would increase the probability an active outbreak would be detected. However, when samples are taken close together in time, this assumption would become invalid. Therefore we do not investigate sampling intervals shorter than 4 days.

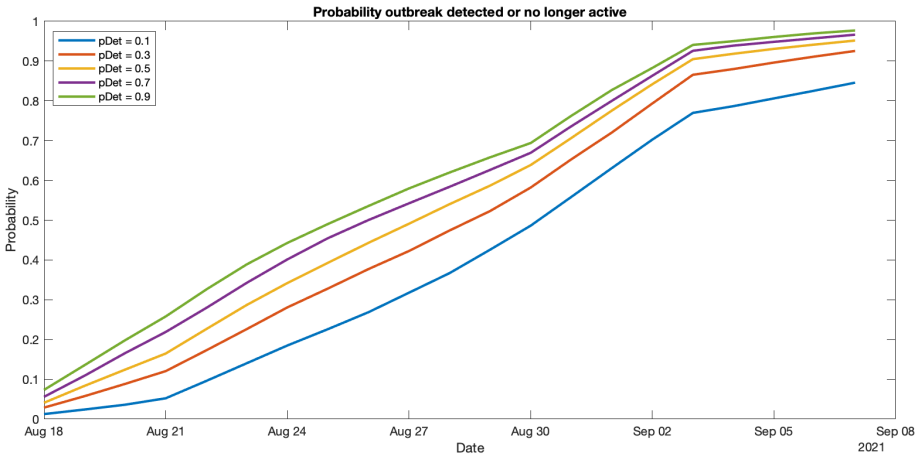

Figure 7. Probability that an outbreak outside of Auckland is either detected or no longer active, assuming a single seed case between 8 August and 20 August, and for different values of the probability a symptomatic individual is detected (p_{det}). No wastewater testing is assumed. Results are from 10,000 simulations.

Catchment sizes for sites currently sampled outside of the Auckland region range from 1,000 (Reefton) to 368,000 (Christchurch), with the majority of sites in the 10,000 – 100,000 range. Figure 8 shows results of the combined symptomatic testing and wastewater testing model for different combinations of the symptomatic testing probability $p_{test,outbreak}$ and catchment size $N_{catchment}$, and with a fixed sampling interval of 4 days. These results show that negative wastewater testing results can over time substantially increase confidence that any outbreak would have been detected. If in addition, Alert Level 4 is found to have a strong effect in reducing case numbers, this would increase confidence that any undetected outbreak would have gone extinct.

Number of active cases per 100,000 people in catchment	Probability of detection
1	0.19
5	0.28
10	0.41
20	0.69
40	0.96

Table 5. Assumed probability of a positive wastewater test result depending the number of active cases per 100,000 people in the catchment being sampled. Based on results of [9].

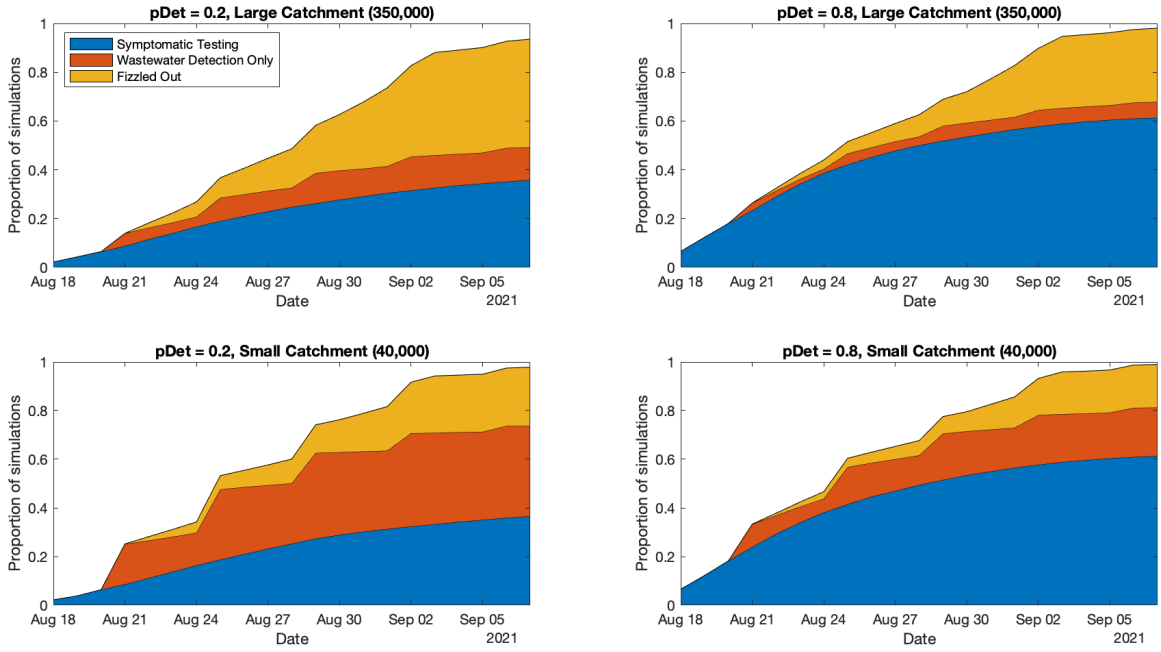

Figure 8. The proportion of seed cases that are detected by symptomatic testing, wastewater detection, or have gone extinct by the given date. Results are shown for two catchment sizes that roughly represent Christchurch (large) and Queenstown (small), and two symptomatic detection rates of $p_{det} = 0.2$ and $p_{det} = 0.8$. Results are from 10,000 simulations.

Parameter	Value
Basic reproduction number in the absence of control	$R_0 = 6$ or 8
Incubation period	Mean 5.5 days, s.d. 3.3 days
Generation interval	Mean 5.0 days, s.d. 1.9 days
Relative infectiousness of subclinical individuals	$\tau = 0.5$
Heterogeneity in individual reproduction number	$k = 0.5$
Vaccine effectiveness:	
- against infection (one dose)	$e_{I,1} = 0.23$
- against infection (two doses)	$e_{I,2} = 0.7$
- against transmission in breakthrough infection (two doses)	$e_T = 0.5$
Probability of a community case being tested:	
- before an outbreak is first detected (clinical cases only)	$p_{detect} = 0.123$ or 0.06
- after an outbreak is detected (clinical and subclinical)	$p_{test,outbreak} = 0.8$
Mean time from symptom onset to test result	4 days

Age-specific parameters																
Age (yrs)	0-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75+
Pr(clinical) (%)	54.4	55.5	57.7	59.9	62.0	64.0	65.9	67.7	69.5	71.2	72.7	74.2	75.5	76.8	78.0	80.1
Susceptibility*	0.46	0.46	0.45	0.56	0.80	0.93	0.97	0.98	0.94	0.93	0.94	0.97	1.00	0.98	0.90	0.86
% of popn**	6.2	6.6	6.5	6.3	7.3	8.5	8.3	7.5	6.5	6.6	6.3	6.0	5.0	4.0	3.3	5.1
1 dose (%)**	0.0	0.0	0.0	4.2	5.9	6.8	8.1	9.9	14	14	16	16	22	22	23	21
2 doses (%)**	0.0	0.0	0.0	3.9	9.7	12	13	13	14	15	19	25	31	49	55	57

Supplementary Table 1. Parameter values used in the model. *Susceptibility for age group i is stated relative to susceptibility for age 60-64 years. **Representing the Auckland metro region population as at 3 August 2021, the doses which are assumed effective on 17 August 2021.

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