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Summary of Advice to Cabinet on Auckland's August 2020 COVID-19 Outbreak

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Executive Summary

- The effective reproduction number R_{eff} measures the potential for COVID-19 to spread. If $R_{eff} > 1$, new daily cases are likely to increase over time, if $R_{eff} < 1$ new daily cases will decrease over time.
- For the Auckland August outbreak, R_{eff} was found to be between 2.1 and 2.5 before Auckland moved to Level 3 on August 12 and between 0.6 and 0.8 during Level 3.
- This was a higher value for R_{eff} in August pre-lockdown compared to that seen pre-lockdown in the March/April outbreak. This may be due to a combination of factors, including Level 1 conditions (no gathering size restrictions, etc.), different behaviour of cases associated with international travel in March/April, higher transmission rates in winter, and differences between the communities affected.
- Highly effective contact tracing and case isolation played an important role in keeping R_{eff} below 1 in Alert Level 3 and 2.5/2.
- We estimated that it was highly likely that the Auckland August cluster was eliminated by October 5 before Auckland returned to Alert Level 1 on October 7. However, in scenarios that did not lead to elimination, case numbers grew rapidly in the absence of Alert Level 3 restrictions.
- We estimated that the likelihood of undetected cases linked to this outbreak occurring outside the Auckland region was initially quite high, but that by mid-September the likelihood of this was falling and was less than 10%.

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Abstract

In August 2020, New Zealand's run of more than 100 days with no detected cases of COVID-19 in the community came to an end. On August 11 a case of COVID-19 was diagnosed in an Auckland resident with no known links to the border, suggesting that there was a potentially large outbreak in progress. In response, Auckland was subject to a regional Alert Level 3 controls from August 12, while the rest of the country was moved to Level 2 and travel in and out of the Auckland region was restricted. This paper describes the modelling methods used to advise Cabinet in its decisions concerning the de-escalation of Alert Level restrictions during the period from August through to October. Indeed, on October 7, Auckland returned to Alert Level 1, having successfully contained and most probably eliminated the 'Auckland August cluster'. We provide estimates of the effective reproduction number, the probability of elimination, the effectiveness of contact tracing, and the likelihood of spread of the cluster beyond Auckland during this period.

Introduction

On 11 August 2020, a South Auckland resident was diagnosed with COVID-19 after developing symptoms five days earlier. As this case had no known links to the border, this suggested that there was a potentially large outbreak in progress. Initial investigations linked the outbreak to a cold-store facility in Mt Wellington, but at the time of writing (October 12) there have been no links established to the border. With the potential for a large outbreak, Auckland was subject to a regional Alert Level 3 restriction from August 12, while the rest of the country was subject to Level 2, and travel into and out of the Auckland region was restricted. Indeed, at the current time, the 'Auckland August cluster' is known to involve a further 178 cases, that are either epidemiologically or phylogenetically linked to the August 11 index case.

The Auckland August outbreak exhibited some important differences to the March/April outbreak. Spread primarily occurred via workplace, community, and household contacts in Auckland, without widespread seeding from international arrivals, which was the key feature of New Zealand's first outbreak. Although the outbreak was Auckland-wide, it was concentrated in South Auckland amongst Pacific communities that value multi-generational living but which lack access to suitable housing. This results in overcrowded living situations and provides conditions where COVID-19 may be expected to spread more rapidly. There was certainly potential for a significant epidemic in a community that had been previously identified as being at higher risk of serious consequences from the disease (Steyn 2020).

This paper describes the modelling methods used to advise Cabinet in its decisions concerning the relaxation of Alert Level restrictions during the period from August through to October. Advice was provided to inform the Cabinet decisions on the de-escalation of controls across the country on August 28, September 4, September 14, September 21, and October 1. Indeed, on October 7, Auckland returned to Alert Level 1, having successfully contained and most probably eliminated what was known as the 'Auckland August cluster'. Here, we provide estimates of the effective reproduction number, the probability of elimination, the effectiveness of contact tracing, and the likelihood of spread of the cluster beyond Auckland during this period. We use case data that was available up until late September to compute these estimates.

Effective reproduction number

We use three different methods for estimating the effective reproduction number R_{eff} , all using data on confirmed and probable cases of COVID-19 in New Zealand linked to the Auckland August outbreak (i.e. excluding cases with a recent history of international travel or links to the border). The effective reproduction number R_{eff} measures the potential for COVID-19 to spread. If $R_{eff} > 1$, new daily cases are likely to increase over time, if $R_{eff} < 1$ new daily cases will decrease over time.

Method 1. Reconstruction of the epidemiological tree. We perform Monte Carlo reconstructions of the epidemiological transmission tree using contact tracing data on the index case and serial interval distribution (James et al., 2020; Lauer et al., 2020). From a reconstructed tree, we can directly estimate the number of secondary infections attributed to each case. We calculate R_{eff} by averaging these

across all cases with symptom onset dates in the relevant time period. For recent dates this method is expected to underestimate R_{eff} as secondary infections have not yet been detected.

Method 2. Fitting a model for the spread of COVID-19. We fit the stochastic branching process model calibrated to New Zealand conditions (see Appendix for details) to daily reported case counts.

Method 3. EpiNow2 – an open source method for estimating R_{eff} from daily reported case counts (Abbott et al., 2020). EpiNow2 produces daily estimates and confidence intervals for R_{eff} . We averaged these estimates over the relevant time periods, weighting by the number of new daily cases. Caution is needed in interpreting these results because of the lag from infection time to reporting time. Results are shown in Table 1 for the pre- and post-lockdown period of the first and second outbreaks.

	Before lockdown	During lockdown (AL3-4)	After lockdown (AL2-2.5)
March-April outbreak	M1: 1.21 [1.19, 1.23] M2: 1.80 [1.44, 1.94] M3: 2.2 [1.42, 3.37]	M1: 0.54 [0.53, 0.55] M2: 0.35 [0.28, 0.44] M3: 0.47 [0.16, 1.41]	N/A
August-September outbreak	M1: 2.48 [2.27, 2.67] M2: 2.15 M3: 1.64 [1.44, 1.81]*	M1: 0.60 [0.55, 0.65] M2: 0.73 M3: 0.74 [0.52, 0.88]	M1: 0.50 (0.47, 0.54)** M2: 0.58 M3: 0.60 [0.35, 0.83]

Table 1. Estimates for the effective reproduction number R_{eff} for the two outbreaks before and during lockdown using three different methods M1-M3. Results for the first outbreak for M2 have been previously reported in (Binny et al., 2020).

* Results from M3 for the pre-lockdown August period are unreliable because they are weighted by case reporting dates, which are all 11 Aug or later because transmission prior to this time was undetected.

As shown in Table 1, for the Auckland August outbreak, R_{eff} was between 2.1 and 2.5 before Auckland moved to Level 3 on August 12, between 0.6 and 0.8 during Level 3. It has remained comparably low (~ 0.7) during Level 2.5. Thus, the Alert Level response was successful in reducing R_{eff} below 1 and containing the Auckland August outbreak. It appears that highly effective contact tracing and small case numbers reduced R_{eff} even further below 1 in Alert Level 2.5/2.

The higher value for pre-lockdown R_{eff} in August compared to the March/April outbreak may be due to a combination of factors, including Level 1 conditions (no gathering size restrictions, etc.), different behaviour of cases associated with international travel in March/April, higher transmission rates in winter, and higher rates of multi-generational living in affected Auckland communities.

Probability of elimination

Using the stochastic model (see Appendix) we can calculate the probability this outbreak will be eliminated by any particular date providing Alert Level 2.5/2 is maintained (note that we assume that R_{eff} at Level 2 in Auckland is the same as that estimated for Level 2.5). Using the fitted R_{eff} values of Table 1 this is estimated to be approximately 58% by October 5. That is, 58% of scenarios where Alert Levels are maintained have no cases reported after October 5. Table 2 shows the results of this calculation as well as the probability of elimination by October 14 and 31. This estimate does not use additional information on the number or type of cases currently being reported, i.e. recent low case numbers or predominantly close contacts who may already be in quarantine.

Date	5 October 2020	14 October 2020	31 October 2020
P(elimination)	84%	92%	98%

Table 2. Probability of elimination by a given date, using the first method, which does not account for current case numbers.

A second method for estimating the probability elimination is to consider the specific level of recent case reporting. This method is more useful in the final stages of an outbreak when the “average”

disease outbreak is no longer relevant. Using the same model output we consider any simulation with a run of consecutive days with no reported cases. We then calculate the probability that no further new cases will be reported (Figure 1). From September 13 to 25, there were no new reported symptomatic cases linked to the Auckland August cluster. These results show that with 17 consecutive days of zero symptomatic cases, the probability of no more symptomatic cases being reported is almost 100%.

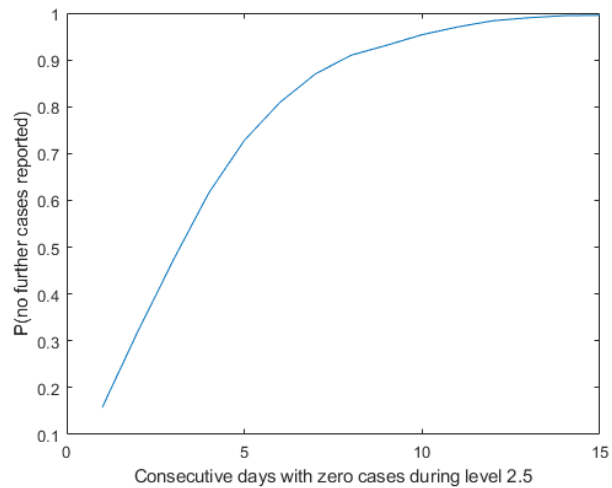


Figure 1. The probability of elimination after a run of zero case days using the second method where we consider the proportion of simulations that eliminate after a run of consecutive days with no reported cases.

Contact tracing performance

We used ESR’s EpiSurv dataset to calculate the contact tracing metrics reported in James et al 2020, namely the proportion of cases quarantined within 4 days of the index case being quarantined (Q2Q) and the probability a case was quarantined before symptom onset (QB4O). When quarantine dates were not available the isolation date was used. Assuming case isolation and quarantine are 100% effective we used the infection kernel of (Ferretti et al., 2020) to calculate the reduction in transmission due to quarantine or isolation of each case. Cases were classified as either “Contact” or “Sought Healthcare” according to the How Discovered field in EpiSurv. Daily values are smoothed using a weekly average. The results are shown in Figure 2 and Table 3 below. The metrics suggest that contact tracing performance is as effective as during the March/April outbreak, despite the lower Alert Level settings. Its contribution to reducing R_{eff} is estimated to be as high as 30-60% during Alert Level 2.5.

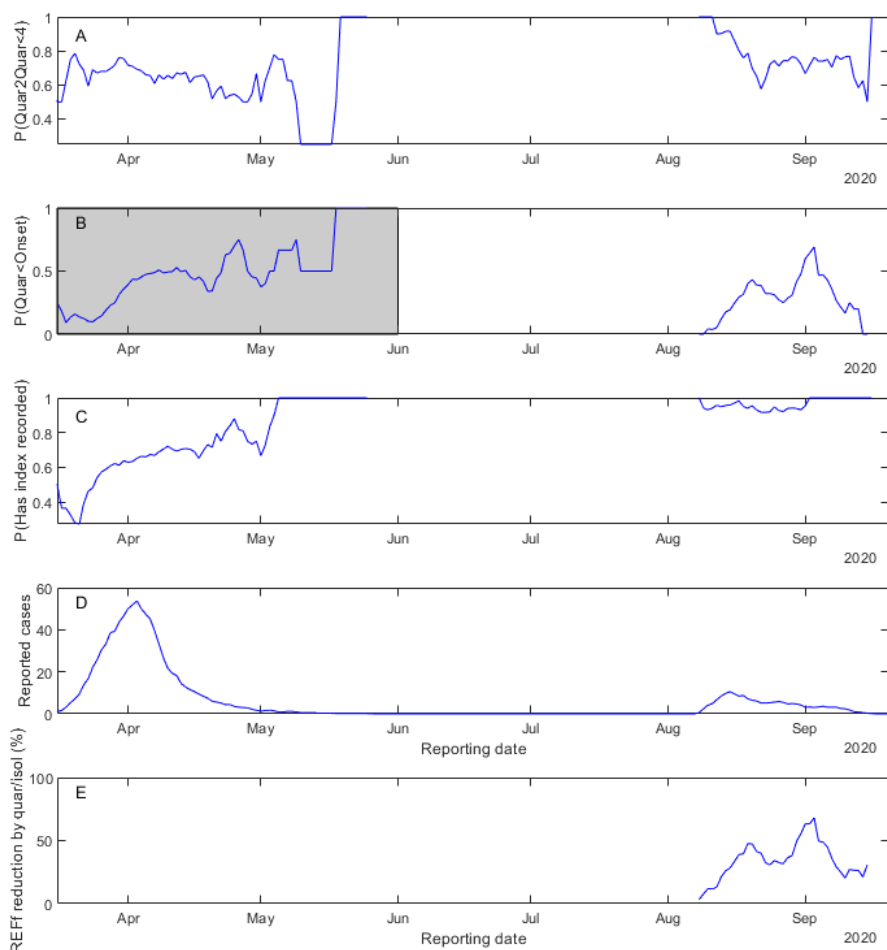


Figure 2. Daily estimates of contact tracing metrics by date of case reporting. A) The probability a secondary case is quarantined or isolated within 4 days of the index case being quarantined or isolated. B) The probability a case is isolated or quarantined before symptom onset. C) The probability a case has an index case recorded. D) The number of cases reported each day. E) The estimated reduction in transmission due to early quarantine and isolation through contact tracing. All values are smoothed over a 7 day window. The grey box identifies unreliable information from the March-April outbreak. Metrics computed for the last week should be treated with caution because of lags in data entry.

Metric	1 st April – 30 th April	30 th August – 13 th Sept
Number of cases (domestic only)	573	42
Cases with index recorded	68%	100%
Recorded as “Contact”	76%	98%
Quarantine date recorded	27%	50%
E(time from onset to test)	Sought Healthcare – 8.3 days Contact – 6.7 days	Sought Healthcare – 4.1 days* Contact – 4 days
Index Quar to Case Quar < 4 days	66%	73%
Quar or Isol before Onset	46%	42%

Table 3. Comparison of contact tracing metrics between the March-April outbreak (for the month of April) and the August outbreak for the first two weeks of September. *Average for August 14th – Sept 14th.

Likelihood of active undetected cases outside the Auckland region

Using travel data on flights and road transport in and out of the Auckland region and the stochastic model, Figure 3 shows the probability that there is more than one active case outside of Auckland linked to the Auckland August cluster given that none have yet been detected. Here we have assumed that the mean length of stay of travellers from Auckland is three days and we assume that the chances of travel are homogenous across the Auckland population. As with the first method for calculating the probability of elimination, these results are for an “average” outbreak and do not take into account the recent run of zero case days linked to the Auckland August cluster.

The probability of active cases outside Auckland is very high (~0.5) before the move to Alert Level 3, but falls once this is put in place from August 12. It rises again in September as travel restrictions ease, but then declines as case numbers in Auckland also decline. Nonetheless, there is a lot of uncertainty in these results due to uncertainty in estimates of travel volumes (Table 4) and the length of stay distribution for inter-regional travel.

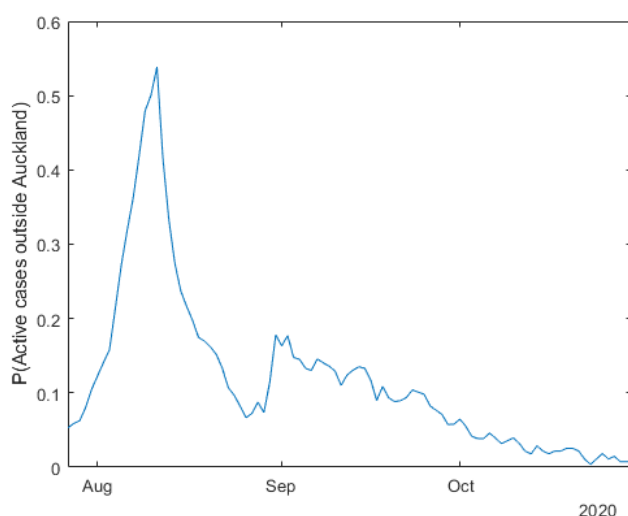


Figure 3. Probability there are active undetected cases outside of the Auckland region linked to the Auckland August cluster given that none have been detected.

Additional travel model assumptions:

- Assumed travel volumes shown in Table 4 below.
- Each resident of region A has equal probability of travelling to region B each day.
- When people travel to a different region, length of stay is one day plus an exponentially distributed variable such that $LOS - 1 \sim Exp(\mu - 1)$ with $\mu = 3$ days.
- Populations within each region are assumed to be well mixed
- Proportion of clinical cases detected (after Aug 11th): 90% (Auckland region), 50% (elsewhere)
- Mean time from symptom onset to testing (after Aug 11th): 3 days (Auckland region), 6 days (elsewhere).

	Number of people travelling per day		
	Before 12 Aug	12 Aug to 30 Aug	From 31 Aug
Auckland -> rest of NI	10000	2000	9000
Auckland -> SI	3000	400	2200

Table 4. The volume of travellers from Auckland to the South Island are estimated from Air New Zealand daily passenger counts before versus after 12 August. Travellers from Auckland to the rest of North Island estimated from Air New Zealand daily passenger counts plus 25% of telemetry data for Wellsford and Rosehill to exclude commuting and other short trips at low risk of transmission. Road traffic was assumed to drop to 20% of pre-lockdown levels during Alert Level 3.

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Appendix: Model Details

We use a continuous-time branching process to model the number of infections similar to that of (Plank et al., 2020), with a single initial seed case representing an incursion from a border facility. Key model assumptions are:

- Infected individuals are grouped into two categories: (i) those who show clinical symptoms at some point during their infection; and (ii) those who are subclinical. Each new infection is randomly assigned as subclinical with probability $p_{sub} = 0.33$ and clinical with probability $1 - p_{sub}$, independent of who infected them. Once assigned as clinical or subclinical, individuals remain in this category for the duration of their infectious period.
- In the absence of self-isolation measures (see below), each infected individual i causes a randomly generated number $N_i \sim Poisson(R_i)$ of new infections. For clinical individuals, $E(R_i) = R_{clin}$ and for subclinical individuals, $E(R_i) = R_{sub}$, which is assumed to be 50% of R_{clin} (Davies et al., 2020).
- Individual heterogeneity R_i is drawn from a Gamma distribution (Lloyd-Smith, Schreiber, Kopp, & Getz, 2005) with as given above and dispersion, or superspreading, parameter k .
- The time between an individual becoming infected and infecting another individual, the generation time T_G , follows a Weibull distribution (W) with mean and median equal to 5.0 days and standard deviation of 1.9 days (Ferretti et al., 2020). The infection times of all N_i secondary infections from individual i are independent, identically distributed random variables from this distribution (see Figure 1).
- Clinical individuals have an initial period during which they are either asymptomatic or have sufficiently mild symptoms that they have not self-isolated. At the end of this period, once they have developed more serious symptoms, they have a probability p_{detect} of being detected, reported and isolated and their infectiousness reduces zero. Individuals that are not detected are not reported nor isolated.
- Subclinical individuals do not get isolated and are not reported.
- All individuals are assumed to be no longer infectious 30 days after being infected. This is an upper limit for computational convenience; in practice, individuals have very low infectiousness after about 12 days because of the shape of the generation time distribution (Fig. 1).
- The time T_{iso} between infection and isolation the sum of two random variables T_1 and T_2 . T_1 represents the incubation period (time from infection to onset of symptoms) and has a gamma distribution with mean 5.5 days and shape parameter 5.8 (Lauer et al., 2020). T_2 represents the time from onset to isolation and is gamma distributed with standard deviation 80% of the mean value (cf NZ case data).
- Cases are isolated and reported on the same day.
- The model does not explicitly include a latent period or pre-symptomatic period. However, the shape of the Weibull generation time distribution (Figure 1) captures these phases, giving a low probability of a short generation time between infections and with 90% of infections occurring between 2.0 days and 8.4 days after infection.
- The model is simulated using a time step of $\delta t = 1$ day. At each step, infectious individual i produces a Poisson distributed number of secondary infections with mean

$$\lambda_i = R_i F(t - T_{i,i} - T_{iso,i}) \int_t^{t+\delta t} W(\tau - T_{i,i}) d\tau \quad (1)$$

where $R_i \in \{R_{clin}, R_{sub}\}$ is the individual's mean number of secondary infections, $T_{i,i}$ is time individual i became infected, $T_{iso,i}$ is the delay from becoming infected to being isolated, and $F(t)$ is a function describing the reduction in infectiousness due to isolation:

$$F(s) = \begin{cases} 1 & s < 0 \\ 0 & s > 0 \end{cases} \quad (2)$$

- The model was initialised with a single seed case representing an incursion from border facilities. The first day a case is detected and isolated is labelled Aug 11th.

- At the first time a case is isolated and detected, this may not be the seed case, the alert level is changed to level 3. This results in changes to R_{clin} , R_{sub} , k , p_{detect} and T_2 (onset to isolation time). Individual values for previously infected individuals are recalculated at this time. Any update value of T_2 that results in an individual having already been isolated are corrected to allow the individual to isolate and report at the time of the alert level change.
- The same method is applied to the alert level lowering 18 days later.
- The model was run for 3000 simulations. All simulation runs that did not result in a detected outbreak were discarded.
- Model fitting was done using reported case counts of symptomatic cases in the New Auckland cluster between August 10th and October 5th 2020, minimising the least squares error over the three values of R_{clin} .
- R_{eff} estimates were found by averaging across all individuals in all simulations with a symptom onset date during the appropriate period.

Parameter	Value	Source
Distribution of generation times	<i>Weibull</i> (5.67, 2.83)	(Ferretti et al., 2020)
Distribution of exposure to onset (days)	$T_1 \sim \Gamma(5.8, 0.95)$	(Lauer et al., 2020)
Distribution of onset to isolation (days) (from data)	$T_2 \sim Exp(.)$	(Davies et al., 2020)
Relative infectiousness of subclinical cases	$R_{sub}/R_{clin} = 50\%$	
Proportion of subclinical infections	$p_{sub} = 33\%$	(Davies et al., 2020)
Basic reproduction number (no case isolation or control)	$R_0 = p_{sub}R_{sub} + (1 - p_{sub})R_{clin}$	(Davies et al., 2020)
Parameter values for Alert Levels 1-3		
Reproduction number for clinical infections (no case isolation or control)	$R_{clin} = 3.3, 0.95, 0.9$	Fitted to data
Superspreading dispersion parameter	$k = 0.4, 0.7, 0.7$	Estimated from NZ April case data
Probability of case detection	$p_{detect} = 0.1, 0.9, 0.9$	Estimated
Expected onset to isolation (days)	$E(T_2) = 6, 3, 3$	Estimated from NZ April case data

Table A1. The parameters used in the model and their source.