

Contribution of mathematical modelling to COVID-19 response strategies in regional and remote Australian Aboriginal and Torres Strait Islander communities

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The health and science communities recognised early on in the SARS-CoV-2 pandemic that Aboriginal and Torres Strait Islander Australians were likely to be at high risk of COVID-19 infection and severe outcomes, due to high rates of comorbidities associated with severe outcomes [1,2], and multiple factors predisposing to increased SARS-CoV-2 transmission [2,3,4]. In March 2020, the Australian Government convened [the Aboriginal and Torres Strait Islander Advisory Group on COVID-19 \(IAG\)](#), co-chaired by the Department of Health and the National Aboriginal Community Controlled Health Organisation. The role of the IAG was to develop and deliver a National Management Plan to protect Aboriginal and Torres Strait Islander communities. Our research groups—located at the Doherty Institute, the Kirby Institute and La Trobe University—were commissioned to carry out modelling, under the guidance of the IAG, to help inform aspects of this plan related to regional and remote communities.

Our prior research and existing modelling frameworks enabled us to quickly begin the process of responding to the questions of interest to the IAG which included:

- How important is a timely response to the first identified case of COVID-19?
- Who should be quarantined and/or tested in communities?
- How important is it to test people when they are in quarantine and prior to exit from quarantine?
- Is there a role for community-wide lockdown in initial containment?

Together, we repurposed a stochastic, individual-based modelling framework which had previously been developed at the Kirby Institute to examine the dynamics of sexually transmitted infections in remote communities [5]. Within this framework, we incorporated a model of population mobility and household structure relevant to disease spread via close contact in remote communities. This model was originally developed at La Trobe University and the Doherty Institute as part of a research program focused on understanding the drivers of high prevalence of Group A *Streptococcus* disease in these communities [4]. We also integrated a COVID-19-specific disease transmission model and the effects of various public health responses. Throughout this model building process, we regularly engaged with the IAG and representatives from other peak bodies and public health units to iteratively refine details and assumptions (described in [Box 1](#) and [Figure 1](#)).

To address the questions of interest to the IAG, we used the model to simulate and analyse a number of outbreak response scenarios. We designed the scenarios in consultation with public health service providers working closely with communities (with options varying by jurisdiction and community). These included:

- Case isolation, with or without an exit test, and with various expected delays between case identification and response;

- Case isolation and quarantining the contacts of a case (based on different definitions of contacts), with or without exit tests, and with or without tests on entry to quarantine;
- Case isolation and population lockdown (entire community quarantined), with or without exit tests, and with various levels of assumed compliance to lockdown.

Box 1. Brief model summary.

The individual-based, computational model we designed simulated the “silent” introduction of SARS-CoV-2 into a remote community of either 100, 500, 1000 or 3500 people, the subsequent transmission of SARS-CoV-2 within the community, and the public health response. The model explicitly represented the infection status of each community member, as well as their age and place of residence within the community, which were tracked and updated daily. Community members were assumed to have close family connections across multiple dwellings in the community (their so-called “extended household”), between which their time at home was distributed, and within which they were at higher transmission risk compared to individuals staying in different dwellings (Figure 1a). Infected community members were further classified according to whether or not they would present to healthcare services for testing (if symptoms developed and were recognized, and fear/stigma did not prevent individuals from presenting, Figure 1b). At the time we developed our model, there had been no SARS-CoV-2 transmission in Australian Aboriginal and Torres Strait Islander communities. Therefore, our model was parameterized based on the experience of SARS-CoV-2 in other populations [6], but accounting for the expected increase in transmission due to enhanced mixing anticipated in interconnected and overcrowded households [2,3].

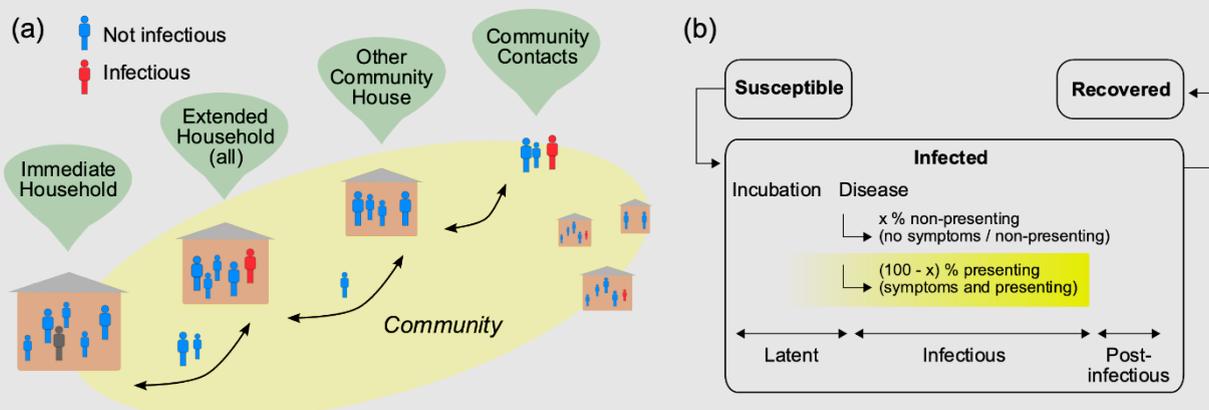


Figure 1. Schematic representation of the individual-based model. The model simulates the “silent” introduction of SARS-CoV-2 into a remote community, the subsequent transmission of SARS-CoV-2, and the public health response. Here we illustrate the structure of the (a) population model; and (b) disease model.

To gain an understanding of the range of possible epidemic outcomes, we used our model to run 100 simulations of each outbreak response scenario (defined by a set of parameters controlling the transmission of SARS-CoV-2, the public health response, and the assumed response of community members to the response). For different response scenarios, we compared and reported the median and interquartile range of several model outputs of interest, including the percentage of the community who were infected at the peak of the outbreak (peak infection prevalence) and by the end of the outbreak (the attack rate), the number of cases identified versus the number of cumulative infections over time, the total number of person-days community members were in quarantine for, and the number of tests performed.

We sought regular feedback on the response scenarios considered, and our interpretation and communication of model outputs. This ensured we were always addressing relevant questions and faithfully relaying our findings (summarised in [Box 2](#) and [Figure 2](#)).

Our work informed both the *CDNA National Guidance for remote Aboriginal and Torres Strait Islander Communities for COVID-19* [7] and the *Australian Health Sector Emergency Response Plan for Novel Coronavirus (COVID-19)* [8]. We have since submitted a publication for peer-review

describing our work, currently available as a pre-print [9]. We also worked together with the IAG to develop a plain-language document containing key messages for health services [10], and a plain-language presentation [11] containing key messages for Health service decision makers and community leaders to consider when deciding how a remote community will respond to a COVID-19 outbreak.

To date, efforts to protect Australian Aboriginal and Torres Strait Islander peoples from COVID-19 are working – there have been no incursions of SARS-CoV-2 into remote Australian Aboriginal and Torres Strait Islander communities, and the incidence of locally-acquired cases among all Australian Aboriginal and Torres Strait Islander peoples is six-times lower than the Australia-wide incidence [12].

Box 2. Brief summary of findings.

Our analysis indicated that without an effective public health response, an introduction of SARS-CoV-2 into a regional or remote Australian Aboriginal and Torres Strait Islander community would likely result in rapid spread. Furthermore, multiple secondary cases would likely be present in a community by the time the first case is identified, indicating that capacity for early case detection and a prompt response would be crucial in constraining an outbreak. A response involving case isolation and quarantining of close contacts of cases defined by extended household membership was found to significantly reduce peak infection prevalence compared to the non-response scenario, but subsequent waves of infection consistently led to unacceptably high attack rates in excess of 80% in modelled scenarios. Rapidly initiating an additional 14-day, community-wide lockdown of non-quarantined households could reduce the attack rate to less than 10%, but only if compliance with the lockdown was at least 80% (Figure 2).

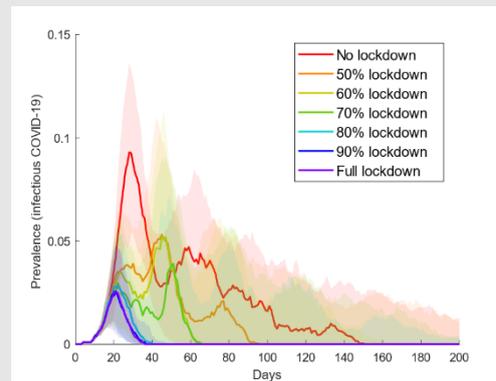


Figure 2. Impact of initiating a 14-day lockdown in addition to case isolation and quarantining of contacts with entry and exit testing on epidemic control. Epidemic curves for a community of 1000 individuals with various levels of individual compliance with community lockdown [9].

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