UNIVERSITY OF AUCKLAND
Waipapa Taumata Rau
NEW ZEALAND

Covid-19 Modelling Aotearoa

End of contract report to Manatū Hauora

Contents

Introduction

Professor Michael Plank and Dr Dion O'Neale, Programme Leaders

Looking back over the last three and half years, it is truly incredible to see the breadth and sheer volume of mathematical and computational modelling work that has been done by the dedicated group of researchers at Covid-19 Modelling Aotearoa (CMA). The impact of this work ranged from warning decision-makers about the scale of what we were facing in March 2020, supporting the elimination strategy and vaccine rollout through 2020-21, to informing decisions about mitigation measures and healthcare capacity planning in 2022-23.

This report primarily relates to the period covered by the most recent CMA contract with Manatū Hauora and the Department of Prime Minister and Cabinet (spanning July 2022 to June 2023) and the researchers involved during that time. However, we have also listed publications and software outputs from earlier periods where they relate to the CMA team from the most recent period.

We hope that by making these tools and reports more widely available, Aotearoa and further afield will be in a better position to respond to future outbreaks of infectious disease.

This work was only possible because people were willing to pivot their research activities and adapt to working in the pressurised and fast-moving environment of an emergency response. We feel very proud of what this team has achieved, and the support we have been able to provide to multiple aspects of New Zealand's pandemic response.

It has been an immense privilege to work alongside the talented and hard-working researchers and professional staff in CMA, as well as our dedicated colleagues in central government and the national health system. Huge thanks are due to everyone who has been involved, in big ways and small – what we've achieved would not have been possible without you.

Professor Michael Plank
University of Canterbury
Covid-19 Modelling Aotearoa
Programme Co-lead

Dr Dion O'Neale
University of Auckland
Covid-19 Modelling Aotearoa
Programme Co-lead

Victoria Lousie Smith, Research Manager

When the pandemic hit our shores in 2020, researchers from across Aotearoa sprang into action to support efforts to prevent spread and minimise harm. Our group, now collectively known as COVID-19 Modelling Aotearoa (CMA), didn't have a name then – but the drive to contribute to protecting Aotearoa from this new but very real threat brought us together.

Early on, our proposed research programme spanned a wide range of crucial areas, including modelling, ethics, phylodynamics, and communication. Our collaborative network quickly expanded to include over 80 individuals from more than 12 different organisations.

As the demands of the pandemic response evolved, so too did CMA. Our programme adapted to home in on infectious disease modelling, providing detailed insights into a range of important aspects, such as potential viral spread, variants of concern and vaccination uptake.

However, just like so many communities in Aotearoa during the pandemic, one constant remained throughout our journey: the tremendous dedication, effort and energy invested by every member of CMA over the course of our more than 3-year programme. For many of us, this commitment meant putting aside all other research pursuits, family time and sleep to fulfil urgent and critical work. It required adapting to new ways of working, delivering rapid and frequent reports to diverse audiences, effectively communicating complex data and issues to the public, working double-time and balancing multiple roles, and acquiring new knowledge and skillsets in tight timeframes.

I would sincerely like to acknowledge and thank the many researchers, students, professionals and collaborators who contributed tirelessly throughout the programme, whose mahi not only demonstrates the resilience of our communities but also exemplifies the real-world impact of our scientific endeavours.

Victoria Lousie Smith
University of Auckland
Covid-19 Modelling Aotearoa Research Manager

Associate Professor Matthew Parry, Peer Review Lead

The plan for a peer review panel was first proposed on March 31, 2020 by Shaun Hendy. With COVID-19 modelling being carried out by his team increasingly underpinning ongoing advice to Government, Shaun realised that it was important to obtain independent review of the modelling. Since events were taking place too quickly for a formal peer review process, the proposal was for the formation of a diverse group of experts to provide rapid, as-required reviews. Matthew Parry, a principal investigator at Te Pūnaha Matatini, was approached to chair the panel. By April 7, 2020, the panel had been assembled for a funding application to MBIE, and the first review appeared on April 8, 2020.

In addition to a focus on technical modelling issues, the importance of equity issues was also identified from the outset. For example, "what questions should modelling be addressing?" were also considered in-scope. Indeed, the very first report identified the need for an age-structured model of Covid transmission, as well as querying whether parametric uncertainty had been adequately accounted for in model predictions.

To answer the variety of questions posed of it, the panel originally comprised Samik Datta (epidemiology and modelling), Nigel French (epidemiology and modelling), Markus Luczak-Roesch (modelling and computing), Melissa McLeod (Māori health and public health), Anja Mizdrak (public health), and Fraser Morgan (agent-based modelling). The members were approached based on contacts within Te Pūnaha Matatini or on the recommendation of members of the COVID-19 Technical Advisory Group. The inclusion of Fraser was in recognition, even in April 2020, that an agent-based model or network model would likely be required.

In 2022, Samik moved to the modelling team, and the panel was expanded to include Amanda Kvalsvig (public health), Linda Martis (data science), Patricia Priest (epidemiology) and Ben Ritchie (data science). The panel also co-opted Thomas Lumley (survey statistics), Patrick Walsh (economics) and Maksym Polyakov (economics) for one-off advice.

Each review was initiated by a draft report sent from the modelling team, usually with a timeline attached. The report was then sent on to the panel members and a Zoom meeting scheduled. After the meeting, the chair typed up the notes and shared the review simultaneously with panel members and the modelling team as "living document". This enabled more immediate feedback and, when necessary, further discussion with the modelling team.

As the timeline below indicates, the peer review panel was not called upon uniformly in time. Not surprisingly, peak activity typically coincided with outbreaks or new variants of concern.

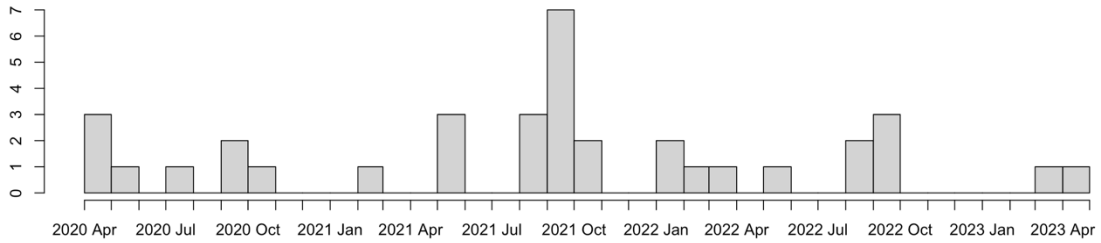

Figure 1. Number count of peer review panel reports in time

Ultimately, 36 reports were written by the peer review panel from April 2020 through to April 2023 – with a 37th snuck in after the end of the contract! Topics reviewed included the effect of different alert levels, elimination strategies, transmission within MIQ facilities, the effect of vaccination, variants of concern, and the impact of changes to isolation policies. One of the final reviews noted: “Working back from change in transmission to investigate scenarios of what caused the change is very nice. The approach taken is logical but it’s clearly challenging to draw strong conclusions for policy because of lack of validation data to narrow down the possibilities. It would be worthwhile to add a few bullet points about key information gaps and what would be needed to address them. Articulating this data need would make a strong argument for research explicitly designed to address information gaps, so future modelling can benefit.”

Associate Professor Matthew Parry
University of Otago
Covid-19 Modelling Aotearoa
Peer Review Lead

Our People

Management

- Professor Michael Plank, Programme Co-Lead, University of Canterbury
- Dr Dion O'Neale, Programme Co-Lead, University of Auckland
- Victoria Louise Smith, Research Manager, University of Auckland
- Kylie Stewart, Communications Manager, Independent
- Matthew Mullin, Research Coordinator, University of Auckland

Compartment-based modelling

- Professor Michael Plank, Project Lead, University of Canterbury
- Dr Audrey Lustig, Manaaki Whenua
- Dr Samik Datta, NIWA
- Dr Oliver Maclaren, University of Auckland
- Dr Giorgia Vattiato, University of Canterbury
- Dr Leighton Watson, University of Canterbury

Network- and individual-based modelling

- Dr Dion O'Neale, Project co-lead, University of Auckland
- Dr Emily Harvey, Project co-lead, Market Economics
- Joshua Looker, University of Auckland
- Dr Gray Manicom, University of Auckland
- Frankie Patten-Elliot, University of Auckland
- Ella Priest-Forsyth, Market Economics
- Kylie Stewart, Independent
- Joel Trent, University of Auckland
- Dr Steven Turnbull, University of Auckland
- David Wu, University of Auckland

Mobility Modelling

- Aaron Cutter, Project Lead, Finity
- Jevon Fullbrook, Finity
- Emma Vitz, Finity
- Tyler Dent, Finity

Epidemiology and Public Health

- Professor Trish Priest, University of Otago
- Distinguished Professor Nigel French, Massey University

Software automation and code review

- Pieta Brown, Precision Driven Health
- Ning Hua, Precision Driven Health
- Rachel Owens, Precision Driven Health
- Dr Kevin Ross, Precision Driven Health

Peer review

- Associate Professor Matthew Parry, Peer Review Lead, University of Otago
- Distinguished Professor Nigel French, Massey University
- Dr Amanda Kvalsvig, University of Otago
- Associate Professor Markus Luczak-Roesch, Victoria University of Wellington
- Dr Melissa McLeod, University of Otago
- Dr Anja Mizdrak, University of Otago
- Dr Fraser Morgan, Manaaki Whenua – Landcare Research
- Ben Richie, Nicholson Consulting

Covid-19 Modelling Aotearoa would like to acknowledge the contributions of numerous colleagues in previous iterations of the programme since 2020.

What Is Mathematical Modelling?

A mathematical model is a simplified representation of a real-world phenomenon expressed in mathematical language. In epidemiology, models are used to understand the way infectious diseases spread through populations. They combine basic principles of how a disease spreads – contact between someone who is infectious and someone who is susceptible – with characteristics of the population to estimate how many people will get infected over time.

Mathematical modelling is a powerful tool for supporting impact assessment and planning, interpreting raw epidemiological and clinical data streams, providing situational awareness, evaluating control measure effectiveness, and comparing alternative policy options. Models provide a framework to think systematically about the consequences of a range of assumptions, and test which assumptions are consistent with empirical data.

Models typically have inputs relating to:

- Characteristics of the pathogen, such as the incubation period, infectiousness, and age-specific risk of symptoms, hospitalisation or death.
- Characteristics of the population, such as the age structure, ethnicity, and the level of immunity either from vaccination or from previous infection.
- Some estimates of the rates of contact between people, including interaction patterns and social structure, and how these are affected by various public health interventions.

Some of these inputs are taken directly from real data. Others cannot be observed directly or are uncertain and so assumptions need to be made. Models are typically run for a range of different assumptions to investigate how much this affects key outcomes. Models are often developed iteratively, by comparing model outputs to new data and refining assumptions as needed. This process itself can help identify areas of uncertainty or important drivers of outcomes.

All models are a simplification of reality. They cannot capture every detail about who is interacting with whom, how that changes over time, and the myriad of variations between individuals. Instead, they try to focus on the most important factors that affect the epidemic trajectory and its impacts at the population level. Deciding which simplifications and assumptions it is appropriate to use with a particular model depends on questions that you want the model to be able to answer. Sometimes the decision about which details to include depends on whether sufficient quality data is available about that variable, and whether it is likely to be important for the outcomes that are of interest.

Models are used in different ways depending on what scientists, health officials, or policy makers are trying to understand. Models can take recent data on cases to produce a short-term prediction (typically a few weeks), which may be useful for planning health care capacity. Models can be used to make medium-term projections (typically 2-3 months) of the epidemic trajectory if conditions stay as they are, or change in some specified way like relaxing public health measures. Models can also be used to investigate longer-term scenarios. These can be useful to think about “what if” type questions, like what if a new variant with specific characteristics emerges, but by necessity these include more uncertainty.

Governments may use modelling results to help inform decisions about policy. However, models are not the only factor considered and decisions are based on a range of data, evidence, and expertise. A model on its own cannot tell you what to do, but it can help weigh up the pros and cons of alternative options.

Our models

Ordinary Differential Equation Model

A major component of Covid-19 Modelling Aotearoa's work in 2022-23 was to develop, deploy and refine a compartment-based ordinary differential equation (ODE) model of Covid-19. This model was developed from the stochastic branching process model that had been developed between March 2020 and June 2022. The new model was motivated by the need for a more computationally efficient model suited to the large case numbers experienced with the Omicron variant, with reduced need to model stochastic effects and intensive case finding and contact tracing measures that were previously important when case numbers were lower.

Like the branching process model, the ODE model is age-structured and includes vaccination status, waning of vaccine-derived and infection-derived immunity, and time-varying contact patterns. The computational efficiency of the ODE model enabled a more rigorous approach to fitting the model to data on reported cases, hospital admissions and deaths caused by Covid-19.

The branching process model had previously been used to model the impact of potential new variants of SARS-CoV-2, results which informed the Ministry of Health's Strategic Framework for COVID-19 Variants of Concern. In June 2022, whole genome sequencing data from ESR was used to estimate the growth advantage of the BA.5 variant over the previous BA.2 variant. This was a crucial model input in estimating the size of the BA.5 wave in winter 2022 [9]. Over time, additional features were added to the ODE model including rollouts of additional booster doses, policy changes such as the end of the Covid-19 Protection Framework in September 2022, reduced testing rates over time, seasonality, and the effect of antiviral medicines on fatality rates [58].

The ODE model was frequently used to give insight into the potential impact of policy changes, for example on mask use and case isolation requirements [28-30]. Estimates for the effect of alternative policy options on transmission rates were made using the network contagion model and/or the simulation model for isolation periods. The ODE model was also used to assess likely future demand for hospital-level care, particularly during winter.

Code supporting the models detailed in our published papers is available in public repositories - see individual papers for links.

Network Contagion Model

Most traditional models of disease spread, such as the compart-based models used by CMA, rely on a simplification called the "well mixed population assumption". This assumes that individuals in the model interact stochastically, essentially bumping into (and infecting each other) at random. In contrast, a contagion network model assumes that people have specific interactions with other individuals and that infections can only take place via those interactions. A network contagion model is therefore well suited to modelling demographic effects (e.g. relationships between ethnicity and household size or industry sector for workers) and can explicitly represent the contexts where infections take place (e.g. infections acquired at home vs at work, school, or in the community). This additional complexity and more accurate representation of a population comes at the prices of greater computational cost and model complexity.

CMA developed an Aotearoa-specific network contagion model (NCM) in order to be able to better address equity concerns from disease spread and to better model the effect of specific scenarios such as changes to case isolation or contact quarantine rules where spread within dwellings affects disease dynamics.

The network: At the heart of the network contagion model is a detailed interaction network of approximately 5 million individuals in Aotearoa New Zealand. Each individual has the demographic characteristics of age, sex, ethnicity, and geographic location (Statistical Area - SA2) of usual-residence. Each individual also has a vaccination history. Individuals in the network are linked to specific group nodes or interaction contexts. These consist of dwellings, workplaces, educational institutions, and "community" events which cover all remaining interactions (e.g. sports, religious, social, & shopping interactions).

Dwellings are derived from Census data and reproduce the size and composition (age and ethnicity structure) observed in each SA2. Individuals in dwellings are linked to education and/or workplace nodes using education and workforce status and commuting data from census.

Workplaces and schools, within each SA2, reproduce age, ethnicity, and sex composition based on school roll and tax records. Schools are split into early childhood education, primary, and secondary. Workplaces have attributes of industry sector (level 1 ANZSIC06) and whether or not they have workers operating on site at various Alert Levels or Covid-19 Protection Framework (CPF) settings.

Community events have composition and size distributions drawn from the social networks literature, including factors such as ethnicity assortativity. Individuals attend events that are either short-range (near where they live, work, or study) or long-range (outside of their Territorial Authority, TA, of usual-residence). Patterns of long-range connections are determined for each SA2 using anonymised electronic transaction data from 2019 and 2020.

The contagion: Infection on the interaction network spreads via a stochastic contagion process. Infected individuals can, at random, transmit infection to those individuals to whom they are connected in the interaction network. If the transmission is successful, the new individual moves into an exposed state. Pathogen-specific parameters control the amount of time that infected individuals spend in the various disease progression states and the rate at which state transitions, including rate of infection, occur. These states include exposed, infectious (including asymptomatic), hospitalized, recovered, among others.

Most of the disease states can take the form of being *unconfirmed*, *confirmed,* and *quarantined* (or isolating). Subsequent state transitions depend on an individual's current state. E.g. individuals who are

isolating can only infect susceptible individuals from the same dwelling; individuals can only become hospitalized, or enter critical care, if their infection is symptomatic.

Disease transmission probabilities are affected by individual attributes including the vaccination status of individuals. Each individual is assigned a vaccination history with this record being derived from individual vaccination data according to age, ethnicity, and location (SA2).

The model: The model explicitly represents processes such as testing, tracing, and isolating, allowing these to be adjusted to reproduce specific Test, Trace, and Isolate (TTI) policies.

Individuals in the model seek testing at specified rates depending on whether or not they have symptoms, or are a known contact of a confirmed case. Test return rates are calibrated to published testing data.

Contact tracing processes in the model can be specified to follow different tracing processes and policies (with different parameters) for different interaction contexts. This can, for example, represent a policy where workplace contacts are only advised to seek a test if symptomatic, but interactions via another context are contacted by health officials and required to test and or isolate. Similarly, different isolation policies can be represented explicitly for different exposure contexts.

In addition to vaccination status, a range of non-pharmaceutical interventions can be represented, either directly or by proxy through additional processes. E.g. mask requirements reducing transmission in workplaces or schools at different CPF settings; closing specific interaction contexts (e.g. different industry sectors, schools); or restricting certain interaction contexts to only individuals with a specified vaccination status (e.g. vaccine pass requirements in hospitality settings).

Benefits of a network contagion model: Accurate network contagion models have significant extra complexity and overhead, compared with traditional contagion models. However, they have a number of features that make them attractive.

Most importantly, infection spread on networks has been shown to naturally capture contagion dynamics much more accurately than traditional well mixed models. One reason for this is that network models automatically capture the effects of *local saturation*. In a well-mixed model, the number of people an infected person transmits the disease to is determined by the proportion of the overall population that is susceptible at that point in time. In contrast, individuals in a network model can only infect those susceptible individuals that they interact with during the period when they are infectious. For example, if all the contacts of an infectious individual in a network model have already been infected, that individual will not lead to any further infections, even if a large number of susceptible non-contacts exist in the overall population. This means that network models can separately capture the effects of individuals changing their interaction patterns, alongside the effect of other transmission reduction measures.

Network contagion models are well suited to capturing the effect of heterogeneity, both for individuals and in the effect of disease reduction interventions. As an example, simulations that apply a blanket transmission reduction of 50% to all workplaces display very different dynamics to simulations that apply a complete transmission reduction to 50% of workplaces and no reduction to the remaining 50%. When the former may show a reproduction number below 1 with infections dropping, the latter will show a reproduction number appreciably greater than 1, with infections growing.

A contagion network model is also able to capture effects that arise due to the correlation of factors. For example, several effects that increase transmission risk are known to be correlated. E.g. lower paid

workers are less likely to be able to work from home, less likely to be able to isolate effectively, and more likely to live in larger households.

While any model is only as good as its assumptions and its input data, network models of disease contagion give the opportunity to simulate detailed scenarios. This is due not only to their natural suitability for including specific attributes of individuals, their interaction patterns, and the nature of theory interaction contexts, but also their ability to allow for detailed mechanistic processes (such as TTI policies and NPIs) that can take place on interaction networks.

Other Covid-19 Modelling Aotearoa Models

FluTracking Analysis and Dashboard

During the elimination phase of the COVID-19 pandemic response, researchers at Covid-19 Modelling Aotearoa developed a statistical package for estimating the incidence of respiratory illnesses such as influenza, colds, and COVID-19 from the Flutracking participatory surveillance survey. Outputs from this analysis were initially used to estimate the number of tests needed for effective symptomatic testing coverage and for calculating the probability of detecting a community case of COVID-19 as symptomatic test-seeking behaviour from week to week.

With the move from an elimination strategy to a suppression approach, the outputs of the Flutracking analysis became an important source of information about the rates of spread of respiratory illness in Aotearoa. With increasingly uncertain case ascertainment rates, respiratory symptom incidence rates provided a useful sense check for plausible bounds on changing infection numbers over time, in different regions and age groups.

The CMA team also developed a public facing dashboard for communicating symptom incidence rates, including uncertainty estimates that responded to changing reporting rates. With help from Orion/PDH this dashboard has been re-published as SIICC - Symptom Incidence of Influenza, Cold, and Covid (https://siicc.covid19modelling.ac.nz).

Analysis of the Flutracking data required developing tools including de-biasing response data, population re-weighting, and calculating confidence intervals. The code for these has been published as a free-to-use, open-source software library. Methods from this library have since been adopted by ESR for their regular reporting of Flutracking survey results.

Stochastic Model for Isolation and Quarantine Testing

Investigators in CMA developed a stochastic simulation tool for calculating the likely effects of different policies for case isolation and contact quarantine.

Given a specific scenario for case isolation, or contact quarantine rules, these simulations were used to estimate metrics such as the average number of hours when a case would be infectious in the community post-release, the average hours of excess isolation when cases would be required to isolate beyond the end of their infectious period, and the proportion of infected contacts who would be detected. The CMA team used surveys of the evolving international literature on viral load for SARS-CoV-2 infections, and sensitivity of rapid antigen tests to accurately parameterise the evolution of infectivity for cases and the probability of testing positive on an antigen test.

Working in collaboration with analysts at NZ MoH, CMA researchers used case confirmation data from household contacts to infer test timing and to evaluate the efficacy of different quarantine policies with realistic parameterisation of the behaviour of contacts.

Simulation of different case isolation policy options was used to provide advice on how isolation policies could be chosen to balance cost or inconvenience against the risk of increasing infections in the community. These scenarios included quantifying the benefits of “test-to-release” for ending isolation policies and the effect of changing the start of the isolation period from symptom onset to test report date. See [37] for more details.

In addition to calculating the direct impact of policies, the stochastic simulation of isolation and quarantine library was used to calculate the necessary inputs for models such as CMAs ODE model for onward transmission of COVID-19 in order to estimate the future impact on case numbers from changes in case isolation policy. The code developed by CMA has been published as a fully documented and free to use open-source library `MitigatingIsolationAndQuarantine.jl` (https://cma-public-projects.gitlab.io/MitigatingIsolationAndQuarantine.jl/).

The Aotearoa Co-Incidence Network

Covid-19 Modelling Aotearoa researchers took advantage of Aotearoa’s unique linked data resource - the Integrated Data Infrastructure (IDI) - combined with novel network science approaches to build a tool that can estimate regions of high transmission risk based on interaction through work and education, without running contagion calculations. The Aotearoa Co-incidence Network, or ACN, uses administrative data for employment and education to build a network where households are linked if a member from each household is co-incident at the same workplace or education institution. These links between dwelling with co-incident individuals are then aggregated up to the SA2 spatial units (about the size of a suburb) before the resulting network of interactions between areas is analysed with a number of network science tools to infer measures like transmission risk and the geographic boundaries of connected communities.

By partnering with the GeoHealth Lab at the University of Canterbury, CMA researchers were able to publish a tool with interactive maps where estimated transmission risk could be viewed alongside areas with the highest vulnerability to severe consequences from a Covid-19 infection.

The ACN was subsequently extended, in joint work with analysts at the Ministry of Health, to include measles vaccination coverage. The resulting tool was used internally at MoH in responding to the emergence of measles in Aotearoa in the first half of 2023.

The source code for both the data analysis (to be run inside the IDI) and the visualisation tool (to produce interactive maps) have been made publicly available as an open source GitLab repository - see the software section of this report for details.

Wastewater Surveillance Modelling

Covid-19 Modelling Aotearoa researchers developed a new method for interpreting wastewater surveillance data in conjunction with data on reported cases of Covid-19. This method produces estimates of the time-varying reproduction number and relative changes in the case ascertainment rate over time. ESR funded additional work to operationalise this model on data from their wastewater sampling program and incorporate the results into their wastewater surveillance reporting to the Ministry of Health. See [26] for more details.

Te Whatu Ora Covid-19 Dashboard

Between February 2022 and June 2023, Covid-19 Modelling Aotearoa supplied results from the branching process model and later the ordinary differential equation model, which Te Whatu Ora (formerly TAS) displayed in a Power BI dashboard for DHB health planners. This allowed dashboard Covid19modelling.ac.nz

users to explore different scenarios for the future impact of Covid-19, for example showing the effect of different levels of behavioural change, variant impact, or seasonality. Model outputs for reported cases, hospital occupancy, and deaths were shown alongside data, which was updated in real-time. Te Whatu Ora disaggregated results from CMA's national model to allow dashboard users to see information stratified by age and ethnicity, either nationally or in a selected Health Region or District. The results were accompanied by a description of the modelling assumptions, interpretation and limitations, co-designed by CMA and Te Whatu Ora. This was supported by verbal briefings to dashboard users by CMA researchers. Dashboard content was updated periodically to reflect changes in the epidemiological situation and updates to the model, for example to include the effect of reinfections, new variants and policy changes.

Covid-19 Forecasting Model

Covid-19 Modelling Aotearoa researchers developed a model to produce near-term forecasts (up to 3 weeks ahead) of Covid-19 cases and hospitalisations. This model is designed to be run in real time and be responsive to the latest trends in surveillance data. The model produces a quantitative forecast with associated uncertainty ranges to support healthcare planning. This is a different type of modelling approach to the ODE model, which is typically used for longer-term scenario analysis and comparison of alternative policy options. The forecasting model is more empirically driven and less mechanistic, meaning that it requires fewer assumptions and parameter estimates than the ODE model, but the results are only valid over a short time horizon.

The forecasting model has been operationalised in partnership with Precision Driven Health and Te Whatu Ora and provides weekly forecasts on real time data updates.

Modelling Collaborations

Finity – Transmission Risk and Mobility Model

Through the University of Auckland, CMA contracted Finity Consulting Pty Ltd (Finity) to provide short term, geographically and demographically granular forecasts of COVID-19 infections and hospitalisations based on near real time mobility patterns in New Zealand. To meet this need, Finity produced a probabilistic model that combined a synthetic population dataset and mobile movement data to inform future spread of COVID- 19.

CMA researchers from the University of Auckland provided a synthetic population dataset, with one record for each individual in New Zealand. The dataset included:

- Household information
- Personal characteristics; Age/Gender/Ethnicity
- Employment status, type and location
- Education status and location

The model estimates future weeks' cases and hospitalisations based on:

- Reported recent cases in the community, these are persons likely to infect or have already infected others they have interacted with
- Vaccination status and historical case history of individuals
- Transmission risk by location of infection outlined below

Transmission Location	Effects Parameterised
Home	Number of people sharing a household, risk of others within the household having COVID-19
Work	Location and type of work
School	Size of the school and risk of others within the same class having COVID-19
Community	Informed by device level mobile movement data which was merged with the population dataset. If an individual either lives in or visits an area highly frequented by likely affected persons.

Severity of infection parameters by age, gender and ethnicity were incorporated in projections of hospitalisation and death resulting from COVID-19.

The model was initially set with a number of model parameter values based on first-principles and literature review. A series of hyper parameter tunings were also run regularly to ensure that the models continued to reflect recent experience and therefore remain accurate for forth-coming weeks, but also to describe the changes in environment being observed.

The insights can be used to inform a variety of responses including estimating granular geographic case growth predictions, scenario testing movement restrictions, hospital capacity planning, population movement restrictions and compliance therewith and vaccination prioritisation.

Due to delays in the purchasing of the mobility data (Finity did not receive the mobile data until March of 2023), the mobility model was not used during the acute phases of the pandemic. In order to maximise the utility of the data and model developed, Finity presented COVID-19 use cases that were implemented for the New South Wales Ministry of Health and Victoria Department of Health in Australia and alternative use cases.

Orion Health Subcontract for Dashboard Automation

For the period 1 July 2022 to 30 June 2023, Orion Health subcontracted to the University of Auckland to provide model automation services under the COVID-19 Modelling Aotearoa (CMA) contract with the Department of Prime Minister and Cabinet (and later Te Whatu Ora) for real-time fitting and projection of epidemic dynamics including new infections, cases, hospitalisations and deaths at the national level.

Orion Health's services were to involve:

- Leading the Orion Health team of Data Scientists
- Operationalising regular reporting of stable contagion model algorithms
- Performing routine data analysis as it relates to ongoing reporting

Specific contributions of the Orion Health team under this subcontract are summarised below.

Symptom Incidence of Influenza, Cold and COVID-19 (SIICC) Dashboard

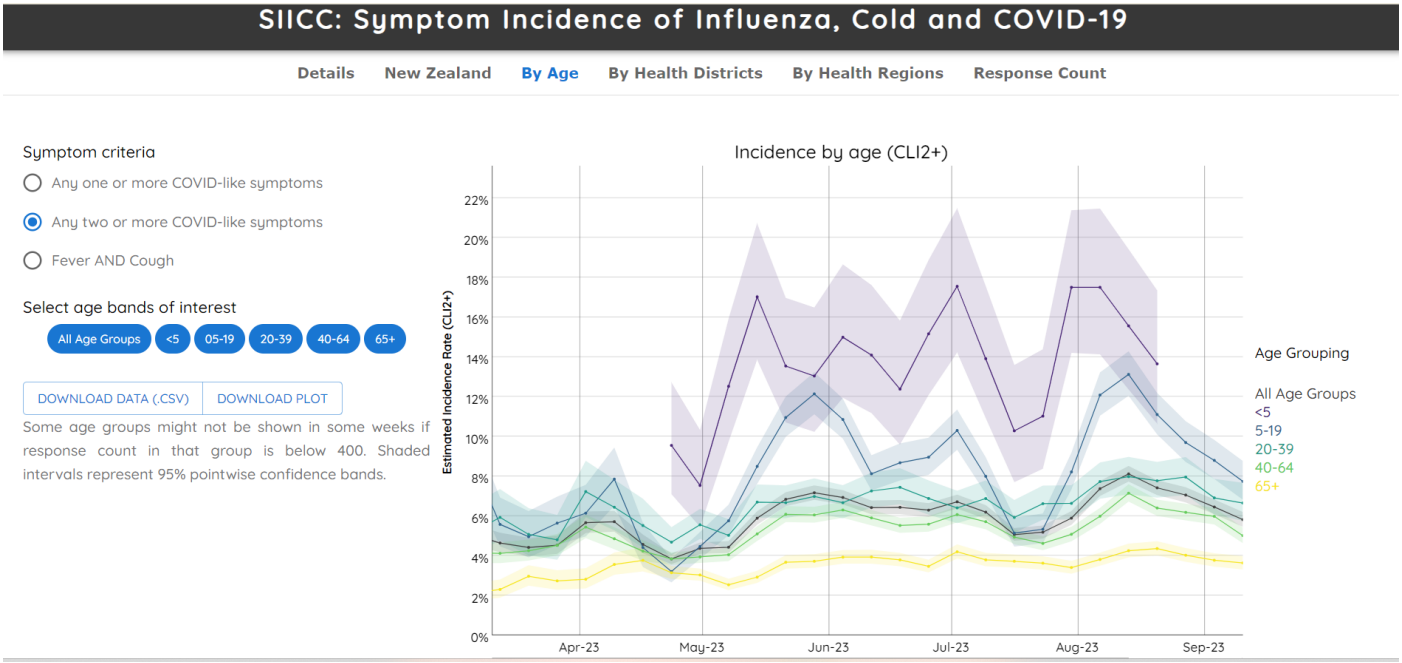

Figure 2: Screenshot of the SIICC dashboard

The flutracker dashboard was a Shiny app developed by CMA to visualise flu survey data. Orion Health refactored the analysis code for this dashboard, created a React front-end for performance and

scalability purposes, and deployed the dashboard on AWS. This dashboard is now called "Symptom Incidence of Influenza, Cold and COVID-19" or "SIICC" and can be viewed on the CMA website

ODE Model

Orion Health initially investigated automating the ODE model however it was decided that this model would not be suitable for a high level of automation due to a requirement for oversight of scenario generation and outputs.

Instead, Orion Health conducted a peer review of the model code base, has documented this model, and has provided suggestions for code refactoring.

Covid Forecasting Model

The Covid Forecasting Model (CFM) provides nearer term forecasts for infections, hospitalisations, and deaths. Orion Health was contacted in late May 2023 by James Harris (from TAS, now Te Whatu Ora) with a request to automate this model so that model outputs were available over the winter months. Orion Health is in the process of completing this automation, hosted on AWS.

Research Highlights

1. The Aotearoa Co-incidence Network

Harvey, Emily P, Matt Hobbs, Joshua Looker, Dion R J O'Neale, and Steven Martin Turnbull. "Exploring COVID-19 Transmission Risk and Vulnerability Through the Aotearoa Co-Incidence Network (ACN)." Technical Report. Covid-19 Modelling Aotearoa, February 9, 2021.

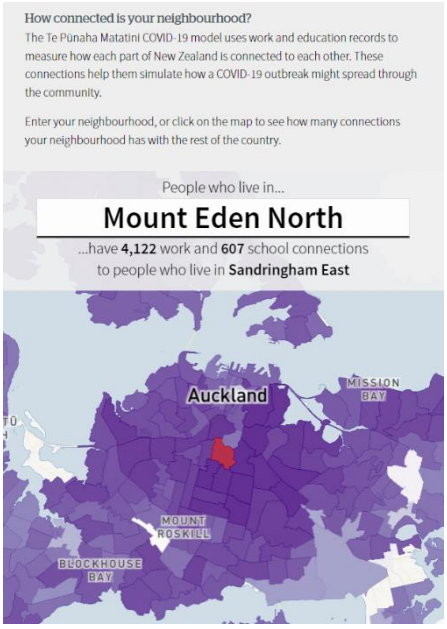

Figure 3: Screenshot from the NZ Herald, using our app to visualise transmission risk.

This research used data from Aotearoa New Zealand's Integrated Data Infrastructure (IDI) to create a co-incidence network of workplace employment and school enrolment. The Aotearoa Co-incidence Network (ACN) provided a highly insightful tool to explore the manner in which the regions of Aotearoa New Zealand are connected to each other through co-incidence of individuals at workplaces and schools.

We showed how analysis of the network could be used to inform the (then) strategy of mitigating existing outbreaks ("stamp-it-out") by revealing those sets of areas between which an outbreak is likely to spread most quickly. We also showed how analysis of the network structure can reveal spatially limited communities which can inform regional responses to disease outbreak (i.e., regional based interventions) should they need to occur, as well as specific areas of high transmission risk — both of these results could be used to aid a "prepare-for-it" strategy. Finally, we cross-referenced our findings with data on disease vulnerabilities (i.e., long-term health conditions, ethnicity, and deprivation) to highlight specific areas with a combination of high risk of contagious disease transmission and elevated vulnerability to such diseases.

We published an open-source library for the code and worked with MoH analysts to help them extend the code in the IDI to include early childhood education centres in the education interactions and to combine the co-incidence network with vaccination data. This went on to be used by Ministry of Health analysts in early 2023 as part of the response to the discovery of community cases of measles. A web-based app allowed for visualisation and exploration of transmission risk and vulnerability and was presented as a useful tool for decision and policy makers to inform more equitable responses to diseases such as COVID-19. It was also used to publicly communicate risk.

"*Pick a neighbourhood in any New Zealand town or city, and then drop a single, hypothetical case of Covid-19 into it. Imagine that, from this one point, you could watch the coronavirus snake out into local schools, or into places where the adults living in that neighbourhood are likely to travel to and work.*

Imagine that each of those connections goes on to create tens of thousands of new ones, which in turn create millions, as the outbreak spirals into a dense, spaghetti-like web of infection. Imagine that we could watch how this mind-bogglingly complex picture unfolds in real-time - and observe it dramatically change when we simulated a lockdown, or threw in the added power of testing and tracing.

This is just what scientists can now do, using a model so sophisticated and weighty that it requires a supercomputer to load and run." – Jamie Morton, NZ Herald. September 6 2021.

2. Modelling the Impact of the Omicron BA.5 Subvariant in New Zealand

Lustig, Audrey, Giorgia Vattiato, Oliver Maclaren, Leighton M. Watson, Samik Datta, and Michael J. Plank. "Modelling the Impact of the Omicron BA.5 Subvariant in New Zealand." *Journal of The Royal Society Interface* 20, no. 199 (February 2023): 20220698.

Data and Matlab code to reproduce the analysis are available at https://github.com/michaelplanknz/modelling-ba5-in-nz

Supplementary materials

New Zealand experienced a wave of the Omicron variant of SARS-CoV-2 in early 2022, which occurred against a backdrop of high two-dose vaccination rates, ongoing roll-out of boosters and paediatric doses, and negligible levels of prior infection.

New Omicron subvariants have subsequently emerged with a significant growth advantage over the previously dominant BA.2. We investigated a mathematical model that included waning of vaccine-derived and infection-derived immunity, as well as the impact of the BA.5 subvariant which began spreading in New Zealand in May 2022. The model was used to provide scenarios to the New Zealand Government with differing levels of BA.5 growth advantage, helping to inform policy response and healthcare system preparedness during the winter period.

In all scenarios investigated, the projected peak in new infections during the BA.5 wave was smaller than in the first Omicron wave in March 2022. However, results indicated that the peak hospital occupancy was likely to be higher than in March 2022, primarily due to a shift in the age distribution of infections to older groups. We compare model results with subsequent epidemiological data and show that the model provided a good projection of cases, hospitalizations and deaths during the BA.5 wave.

3. Case Isolation Policy Modelling

O'Neale, Dion R J, Emily P Harvey, and Ella Priest-Forsyth. "Quantifying the Effect of a Change in Case Isolation Settings." Covid-19 Modelling Aotearoa, April 20, 2023.

Harvey, Emily P, Joshua Looker, Dion R J O'Neale, Michael Plank, Ella Priest, and Joel Trent. "Quantifying the Impact of Isolation Period and the Use of Rapid Antigen Tests for Confirmed COVID-19 Cases." Covid-19 Modelling Aotearoa, August 15, 2022.

Isolating confirmed cases while infectious is an important way of reducing transmission of infectious diseases. The infectious period of most diseases varies between people, therefore matching this period to an ideal isolation period is difficult. Doing so requires balancing the impact that isolation has on individuals and the community with the risk of avoidable onward infections if people are released from isolation while still infectious. Rapid antigen tests (RATs) have been suggested as a way to help identify cases who are still infectious and to better target isolation requirements. We extended the approach used by the UKHSA to investigate the impact of different isolation periods and test-to-release conditions for SARS-CoV-2.

We produced two reports which quantified a range of output metrics including hours infectious in the community and hours of excess isolation for different case isolation policies, including with the use of test-to-release (TTR). We found that we could use TTR to make people safe and require less cost and disruption to the economy from excess isolation.

We published the code for these simulations, making it possible for anyone easily compare and evaluate different case isolation policy options. This ensured that calculations were transparent, assumptions were clear, and the research was reproducible. The work resulted in significant media interest. Newsroom's Marc Daalder wrote an article about different isolation options and their consequences. It included interactive visualisations of model results, built from our publicly released code, to illustrate different scenarios covered in the article.

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Software

- **The Populated Aotearoa Interaction Network (PAIN)** - an extensive software library written in R and Python for processing demographic data from a range of sources and using the resulting synthetic population to build a bipartite interaction network for Aotearoa (or sub-regions). PAIN and CoBiN together comprise the Network Contagion Model described above. PAIN requires inputs of a number of custom data tables in order to characterise the approx 5 million individuals in Aotearoa along with their interaction contexts (dwellings, workplaces, schools, and "community" events). A version of the library suitable for public release is in progress. Access to the non-public code repository has been provided to analysts at NZ MoH.
- **Contagion on a Bipartite Network (CoBiN)** - a library written in the Python programming language for simulating disease spread on a bipartite network, where individuals are linked to explicit interactions contexts. Requires a network built from the PAIN software as input, though sample networks are included with the code via a figshare link.
    - code: https://gitlab.com/cma-public-projects/cobin
    - documentation: https://cma-public-projects.gitlab.io/cobin/
- **Stochastic Simulations for Managing Isolation & Quarantine** - a package written in the Julia programming language for fast stochastic simulation of the direct impact of different case isolation and contact quarantine scenarios, including test-to-release. Calibrated to international literature for viral load and test sensitivity and to case data from Aotearoa for contact testing behaviour.
    - code: https://gitlab.com/cma-public-projects/MitigatingIsolationAndQuarantine.jl
    - documentation: https://cma-public-projects.gitlab.io/MitigatingIsolationAndQuarantine.jl/
- **Flutracking** - a library of analytic tools for calculating robust incidence rates for respiratory disease in Aotearoa from weekly Flutracking survey data. Includes methods to adjust for response bias, population re-weighting, and calculating confidence intervals. Code is written in the R programming language; an older version of the public dash-board, using R Shiny is available.
    - dashboard: (https://siicc.covid19modelling.ac.nz/)
    - analytic tools & code: https://gitlab.com/cma-public-projects/flutracking-methods-article
- **The Aotearoa Co-incidence Network (ACN)** - this repository consists of code (R and SQL) that can be run inside the Statistics NZ Integrated Data Infrastructure (IDI) to produce a table of counts for the number of connections between area units when dwellings are linked through an interaction at a shared school or workplace. The repository also includes code (written in R) for analysis and visualisation of the aggregated data after extraction from the IDI. This includes methods for estimating transmission risk and its correlation with age and vulnerability.
    - interactive visualisation: https://stur600.shinyapps.io/aotearoa-coincidence-network/

- analytic tools & code: https://gitlab.com/cma-public-projects/aotearoa-connection-network/

Covid-19 Modelling in the Media

Our researchers are sought-after and trusted experts. Over the full course of the programme, they've collectively fielded well over a thousand media requests, resulting in quotes across a vast range of local and international media including RNZ, NZ Herald, Stuff.co.nz, The Project, NewstalkZB, 1 News, NewsHub, Newsroom, The Guardian, The BBC, Te Hiku Media, and assorted regional newspapers. They have also written widely syndicated articles for The Conversation and The Spinoff which have seen a readership in the hundreds of thousands. Our team has raised the profile of mathematical modelling, and has worked hard to communicate our findings with the public, to help Aotearoa better understand disease spread and how to keep themselves safer.

Editorial highlights

Plank, M., Shearer, F., McCaw, J., Wood, J. With COVID now endemic, modelling suggests targeted protection will be more effective than blanket measures. *The Conversation*, August 24 2023.

Baker, M., Welch, D., & **O'Neale, D.** With COVID on the rise again, here are some simple steps to help us socialise safely during the holidays. *The Conversation,* December 20, 2022.

Plank, M., Geoghegan, J., Welch, D. With most mandatory public health measures gone, is New Zealand well prepared for the next COVID wave? *The Conversation*, September 15 2022.

Plank, M., **Lustig, A.**, **Welch, D.**, **Vattiato, G**. A new Omicron wave is upon New Zealand, with older people now most at risk – here's what to expect. The Conversation, July 7 2023.

Plank, M., **O'Neale, D., & Harvey, E.** As New Zealand relaxes restrictions, here's what we can still do to limit COVID infections. *The Conversation*. March 23, 2022.

O'Neale, D. NZ's confirmed COVID case numbers are rising fast, but total infections are likely much higher – here's why. *The Conversation.* February 25, 2022.

O'Neale, D., Harvey, E., Sporle, A., & Turnbull, S. As Aucklanders anticipate holiday trips, Māori leaders ask people to stay away from regions with lower vaccination rates. *The Conversation*. November 30, 2021.

O'Neale, D., Harvey, E., Sporle, A., & Turnbull, S. How to lower your Covid risk these summer holidays. *The Spinoff*, November 30, 2021.

O'Neale, D., Harvey, E., Gilmour, J., & Turnbull, S. New Zealanders are super-connected. When restrictions lift in Auckland, it won't take much to amplify Delta's spread. *The Conversation,* October 26, 2021.

O'Neale, D., Harvey, E., Gilmour, J., & Turnbull, S. We built a model that shows how small rule changes can fuel deltas spread. *The Spinoff,* October 26, 2021.