Appendix – ODD Protocol

This Appendix is organised according to guidelines from the Overview, Design concepts and Details (ODD) protocol for describing Individual and Agent-Based Models (ABMs). Commented code for the model can be viewed in the associated Github repository: https://github.com/JTHooker/COVIDModel.

It should be noted that the model as presented in this paper and described in this ODD protocol describes a limited set of total functions available in the full model located in the repository.

1. Purpose and patterns

The purpose of this model is to explain and predict the consequences and impact of social policy actions taken by Governments in response to the SARS-CoV-2 outbreak over time. The model has been specifically calibrated and targeted to consider conditions in Australia and New Zealand after being initially calibrated to Wuhan, China. It could be reasonably adapted by other countries or regions wishing to use it for their own purposes or intervention planning.

The patterns observable in the model relate to disease progression through an simulated society as a result of either unmitigated spread or in response to social / physical distancing measures, prophylactic technical or equipment adoption measures (e.g., track and tracing apps, mask-wearing, school attendance policies), and other related economic and social restrictions enacted and/or lifted over time.

As much as being able to realistically model the quantitative outcomes of policy decisions (e.g., infections, deaths, ICU demand, likely elimination timeframes, etc.) the model is constructed as a means of understanding estimated patterns of disease progression and qualitative differences in outcomes across 3 domains – health (physical and mental), economic and social over time.

We are conducting this work from the perspective of optimising the performance of health systems (Murray & Frenk, 2000; World Health Organization, 2000). This means optimising strategies that balance three elements:

1. Population health (e.g., does this strategy protect health?)
2. Financial sustainability of the system and society (e.g., does it cost individuals or society a reasonable amount of money?), and
3. Responsiveness of the system to non-medical aspects (e.g., will the social restrictions and requirements of the strategy be acceptable to the population (e.g., social distancing), etc.)

The current manuscript explores only elements related to the first factor, population health.

The model is not static. It is built in modules enabling additional questions and functions to be included as it evolves or as policy-makers might want to explore additional policy scenarios. The software platform used is Netlogo version 6.1.0 (Wilensky, 2019).

2. Entities, state variables and scales

The model is built on a 60 x 80, 4800 parcel-sized area ‘patches’ that wrap both horizontally and vertically (i.e., the world contains no borders – it is toroidal) (see below). The area in the model is not represented beyond representation of locations, neighbours (i.e., someone can be located in the same place as someone else and they can assess characteristics of neighbours on adjoining locations), and relative distance.

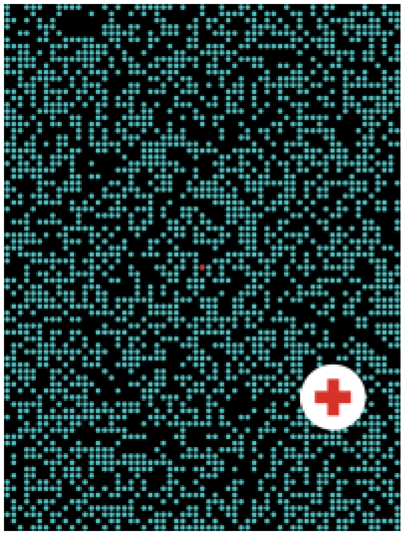


Figure 1.The model environment at time 0 featuring 2499 blue uninfected people and 1 infected person.

Time is scaled to 1 day per model time-step. Patterns of interest are generally observable between day 0 and 400.

The world is initially populated by 2500 agents, representing a small community of 2500 people. 2499 of these people are initially colored blue, representing people who are uninfected with SARS-CoV-2, but still susceptible. At least one person (located in the middle of the image, above) is colored red, indicating they have contracted COVID-19 and could potentially pass it to other people they contact. This person represents case 0. The number of initially infected cases can be adjusted by the model user in response to local evidence or to create more stability in the initial model stages and more chances of the disease ‘catching on’ in the population. For example, in calibrating the model to Wuhan, China, and recognising that Wuhan represented an example that had already occurred (i.e., it was not realistic to model scenarios where the index case did not infect other people) we initiated the model with a mean of 86 cases, consistent with Wu, Leung, and Leung (2020).

The model is stochastic. As (or if) infections spread throughout the community, the model scales up over 4 further stages beyond the initial 2500 person community by a factor of 10 to represent the interaction of 25,000 people, then 250,000, then 2,500,000, then a maximum of 25 million (5 stages total).

The 5 scales are labeled 0 through 4. As the scale moves out, each ‘dot’ in the model represents one unit of measurement at each scale. First 1 person, then 10, then 100, then 1000, and finally 10,000. This scaling function serves multiple purposes. Firstly, it enables greater fidelity at the early and late stages of infection when there are just a few infected individuals in a small community and policies and suppression efforts are targeted at individual outbreaks or clusters. This is also the stage (e.g., low levels of infections per day of 0 to 20) that Australia and New Zealand have spent most of their time within since the beginning of the epidemic. As the scale increases, the potential movement radius of agents progressively scales down to represent geographic and social barriers that exist between populations and communities that exist in Australia and New Zealand who live in distant locations

This scaling feature distinguishes the function of the model from standard SEIR representations that assume perfect diffusion through a population and do not incorporate geographic disparities. Agents in this model assume rapid diffusion through the smallest represented community (e.g., 2500 people), but this is markedly slowed at the maximum scale.

The second purpose of the scaling function is to reduce the computing power required to run the model when infection rates are highest, or in unmitigated scenarios where the majority of the 25,000,000 population are infected. Instead of needing to represent the entire population of individuals (e.g., 25,000,000 for Australia), the total number of agents in the model does not change, however the number of people that each agent in the model represents does, aligning the scale of interest with the likely scale of public interest and public health policy decision-making at the time. For example, in the early and late stages of infection in Australia and New Zealand, individual cases, locations and circumstances, were (are) identified and described. However, as daily infections reach(ed) 300 per day at the infection's peak around late March (or as they reach many tens of thousands in other countries), the scale of pattern description and interest similarly scales up; the circumstances of individual cases are no longer policy-relevant. At the tail-end of the epidemic curve, we have returned to a scale of interest that identifies individual cases and locations again. Similarly, the model scales down again at this point to reflect this changed focus.

This function has a practical utility in that any public health authority could take this model, tune it to their own circumstances, and run it on a regular desk-top computer, without the need for high-performance computing power. This places the model, which is offered free to download by anyone, in the hands of potential users across the globe and stands in contrast to other large-scale, 1:1 models (Chang, Harding, Zachreson, Cliff, & Prokopenko, 2020).

Each person agent has a set of individual characteristics, the combination of which are unique to them. These include personal / epidemiological, psychological, and economic characteristics. Only those health variables pertinent to the currently presented model are listed below:

2.1. Personal / Epidemiological variables

- **Infection status** – red = infected, blue = susceptible, yellow = recovered.
- **timeNow** – an integer variable counting the number of days since an infected person first contracted COVID-19.
- **IllnessPeriod** – a float variable assigned to each individual specifying the total number of days they are infected for pending infection. This follows a log-normal distribution with mean of 20.8 days and sd of 1.
- **inICU** – a boolean variable noting whether the person has been moved to ICU or not.
- **R_{eff}** –The effective reproduction number i.e., the mean count of other people the person has infected on the last day of their infectious period.
- **requireICU** – A boolean value indicating the requirement of the person to be admitted to ICU if they become ill with COVID-19.
- **ageRange** – The age-bracket of the person, calibrated to the current Australian census data
- **incubationPd** – The incubation period of the disease for this person before showing symptoms, calibrated to a median of 5.1 days (Lauer et al., 2020) and a log-normally distributed standard deviation of 1.5 days (se 2.25).
- **dailyRisk** – The risk of death per person per day after contracting the disease based on age and international case fatality risk estimates – this can be adjusted as new evidence come to hand.
- **riskofDeath** – The overall risk of death for this person based on their age-profile having experienced the disease – calibrated to international data.

- **Pace** – The speed at which the person moves around the environment – higher speeds result in more contacts with others. By default, this is set to 1, meaning that at each time-step, the person moves one space in the environment.
- **Heading** – The direction of travel of the person at the current time-step. This is calculated in degrees from the agent's current heading. 0 degrees means that the person is moving straight ahead, 90 degrees means they are moving 90 degrees to the right of their current heading, and 180 degrees means they move backwards (and then move backwards, again, returning to their original position). The heading variable can be used to create communities and control interaction between and across communities. For example, if everyone has a heading of 90, then everyone moves in a small, 2 x 2 square and only interacts with other people who overlap in that square, slowing interaction and infection spread. Conversely, if everyone has a heading of 0 or close to 0, this creates a great deal of diffusion and interaction between people in the environment.
- **contacts** – The count (integer) of other people in the environment that the person has interacted with in the past day as they move around the environment – more than one person can be located in one place at once.
- **essentialWorkerFlag** – a boolean variable that determines if the person is an essential worker or not (set to 30% of working-aged people in Australia and 20% in New Zealand) randomly distributed across people aged 18-69. Essential workers are less able to restrict their movement in the model to avoid other people.
- **personalVirulence** – an integer variable ranging from 0 to 100 (flat distribution) that determines the maximum infectious potential an infected person can have if they become infected.
- **currentVirulence** – a float variable that is calculated at each time-step should the person become infected that determines the infectiousness of the person at that time-step. This is a triangular distribution that increases monotonically from day zero to peak infectiousness at the cessation of the incubation period, returning to zero at the end of the illness period.
- **householdUnit** – an integer variable describing an individual household unit that each person belongs to.

2.2. Health care resources

- The model contains one **Hospital Agent**. This does not indicate that only 1 hospital exists, but represents the capacity of the country's hospital system. Capacity of the Hospital is represented by the number of white pixels it occupies in the model, which is controlled by the 'Hospital_Beds_In_Australia' input variable. By default, this is set to a value of 65,000 for the full 25 million. Sick patients who require hospitalisation can be sent there as long as there is spare capacity in the system. Otherwise, they stay in the community.
- **ICU beds** are present in the model. Because of their small numbers, they are not 'owned' by the Hospital, but instead presented as a global variable set by the **'ICU_Beds_in_Australia'** input variable. By default, this is set to 7000 beds, which is an approximation of current expanded capacity of Australian hospitals, but can be altered through user input / calibrated to alternative estimates. A percentage of people who contract COVID-19 (set by the '**ICU_Required**' input variable) will require ICU after their incubation period has elapsed, with these numbers monitored as a global '**Require_ICU**' count updated each day and plotted against the available ICU Beds. The default setting is that 5% of COVID-19 cases will require ICU. Again, this can be adjusted by the user in response to their own country circumstances or emerging evidence.

2.3. Global variables

The model also includes 'global variables', whose values interact with, and influence the behaviour of agents in the model. These variables primarily represent either a) policy settings or initialisation parameters available to the model user (the observer), or b) summarised population-level variables calculated from combinations of agent outputs (e.g., total infection rates, Reff values, etc.). They include:

- A boolean switch that turns dependent physical distancing policies (see below) ‘on’ or ‘off’.
- A boolean switch that turns **case_Isolation** policies ‘on’ or ‘off’.
- A **PPA** input that controls a **proportion_People_Avoid** setting for determining the percentage of people who Socially Distance when the policy is enacted (e.g., 85%).
- A **PTA** input that controls a **proportion_Time_Avoid** setting for determining the percentage of *time* that people who Socially Distance *actually* Socially Distance for (e.g., 85%).
- Settings for determining the efficiency of **track_and_Trace** measures to identify people for **quarantine** after the lapse of their incubation period – set between 0% likelihood of being identified per day of post-incubation infection and 100%.* This is set to 20% likelihood of identification per day by default, a mean of 3 days post incubation for identification and potential Quarantine.
- Settings for controlling the proportion of people who comply with case isolation through the **compliance_with_Isolation** setting.
- A **Global_Transmissability** setting that controls the likelihood of transmission between an infectious person and a susceptible person per close contact. This can be altered in conjunction with the number of contacts per day to calibrate the R_0 in the early stages of the model.
- An illness period setting that enables the user to set the mean **illness duration** from the first day of infection. By default, **this is set to 15 days**, with a log-normal distributed standard deviation of .99 days but can be altered by the user.
- A **superspreaders** setting set as an integer between 0 to 100 that controls the dispersion of infected people in the environment moving suddenly from one location to another, increasing dispersion among susceptible people throughout the society by placing infected people into populations of susceptible people. At each time-step a random number between 0 and 100 is drawn that is compared to the superspreaders setting. If this random integer is less than the superspreaders setting, a number of agents, controlled by the ‘diffusion adjustment’ setting (below) are dispersed to random locations.
- A **diffusion adjustment** setting that controls the number of people dispersed in the population as part of the superspreaders setting, above. This is an integer value between 0 and 10.
- A **tracking** variable enables a function that traces people in the community who are infected through manual means – this is a stochastic process with the likelihood of being tracked variable on any particular day set at a default of 25%.
- An **age_Isolation** setting enables the user to set an age-range over which social distancing and case isolation measures apply (e.g., a policy of isolating people over 70 years-old).
- The **assignAppEss** switch determines whether Essential Workers are targeted for uptake of a digital tracking and tracing phone app.
- The **residualCautionPPA** and **residualCautionPTA** (integer) variables determines what the new baseline social-distancing practice for the population is after the cessation of lockdown (e.g., 20% of people (PPA) may still attempt to practice social distancing 20% of the time (PTA)).
- A **scale** variable (ordinal) that indicates the scale at which the population dynamics should be interpreted.
- A **casesToday** (integer) counter that tracks the number of new cases who have reached day 6 of their infection.
- An **OS_Import_Switch** (Boolean) variable that enables the OS_Import function to be used (below).
- An **OS_Import_Proportion** variable (float) that determines the proportion of cases that are acquired through overseas travel prior to lockdown.
- An **OS_Import_Post_Proportion** variable (float) that determines the proportion of cases that are acquired through overseas travel post lockdown.

- A **PolicyTrigger** switch (Boolean) that acts as a master switch to turn sets of other policies on at given time points.
- A **TriggerDay** input variable (integer) indicating the model step on which policies should be enacted.
- A **LockdownOff** switch (Boolean) that acts as a master switch to turn sets of other policies off at given time points.
- A **TimeLockDownOff** input variable (integer) indicating the model step on which policies should be lifted.
- A **RiskofDeath** (float) variable determining the risk of death of an individual should they contract COVID-19 based on their age.

Variables available but not used in current implementation*

- An **eWAppUptake*** input slider determines the proportion of essential workers that are assigned a digital tracking and tracing app if the AssignAppEss switch (see above) is set to true
- A **schoolsPolicyActive*** switch (Boolean) sets in motion the return of students to school. This switch turns on the schoolsPolicy switch at a time determined by the model user (see below)
- The **schoolsPolicy*** (Boolean) switch sends children 18 years and under who are students (see **studentFlag*** variable) back to school. Under these conditions, students can interact with one another and with people from their own family unit but continue to observe other social distancing practices consistent with lockdown conditions.
- A **masksPolicy*** (Boolean) switch assigns masks to the population at a proportion equal to the **mask_Wearing*** global variable out of 100.
- The **mask_Efficacy*** variable (integer) determines how effective the deployed masks are in reducing infection between individuals.
- The **app_Uptake*** (integer) input slider determines what proportion of the population takes up digital tracking and tracing technology (e.g., phone Apps)
- The **link_switch*** (Boolean) variable enables a function to create links between infected individuals and their contacts
- The **TTIncrease*** (integer) input variable determines the increase in efficiency that electronic tracking and tracing apps have over manual tracing methods.
- The **freewheel*** (Boolean) switch enables the user more flexibility for interacting with the model in a live environment – timed policies are only enacted when the Freewheel variable is set to false.

Users will note that more functions and updates to agents and entities are available in the full model than are or manipulated in the presented model (e.g., mask-wearing, student status, etc.). We describe these additional functions, however, to give the reader an understanding of the flexibility and utility of the model from a public health policy perspective.

2.4. Location variables

Model patches (i.e., areas in the environment) have the following variables:

- A **utilisation** variable (Boolean) that determines whether the area is classified as empty of people or occupied.
- A **destination** variable (Boolean) that indicates whether the area is a location frequented by people (beta).

2.5. Policy settings and triggers

In addition to the features above, the model enables users to pre-set combinations of policies to run either in simulated real time (e.g., as a demonstration of experimentation) or as a suite of broader model runs and tests that sweep through variables in combination over hundreds, thousands (or more) model runs. This is enacted the ‘Behaviourspace’ area of Netlogo. There are billions of different policy combinations able to be selected and run in this model.

Model users can also choose the ‘Freewheel’ switch, which allows policy settings to be altered at will during an individual model run. These settings will update depending upon whether they are part of the initialisation and ‘setup’ phase of the model, or if they are calculated at each step of the model run (see ‘setup’ or ‘go’ functions in code).

For example, ‘**ageRange**’ is allocated to each person from a random draw at the model setup, so changing this variable part way through a model run will not change results. By contrast, changing the values of stochastic variables such as **‘Age Isolation’**, **‘Spatial Distance’**, **‘Compliance with Isolation’**, and other sliders or policy switches located in the model interface will update policy settings dynamically, enabling the model user to interact with settings as see their impact on outcomes immediately.

2.6. Experimentation across settings

With the ‘Freewheel’ switch set to ‘off’, the user can implement other policies at times of their choice.

For example, with ‘**Policy Trigger On**‘ set to on, the user can determine the number of days after the initial identification of Case 0, social isolation and case isolation policies come into effect by using the ‘**Trigger Day**‘ input slider. By default, this is set to 72 days to reflect the Australian Government’s implementation of social distancing policies on the 28th of March following the initial case identification on January 16th. In the New Zealand model version it is set to 53 days.

To reflect the ramping up of implementation across society, the model anticipates the date of implementation 2 weeks prior to enactment, exponentially increasing the public’s social distancing practices set by the ‘**Proportion_people_avoid**‘ and ‘**Proportion_time_avoid**‘ inputs described above until they reach the input parameter on the day of implementation. This reflects the gradual increase in restrictions between mid and late March, 2020 (Hale, Petherick, Phillips, & Webster, 2020). The same method is also used in reverse, with the date of anticipated lockdowns being unwound preluded by a gradual decay of adherence to social distancing restrictions that follows a negative power-law ***(e.g., Proportion_Time_Avoid = PTA – ((PTA * residualCautionPTA) / (timeLockdownOff – timenow))***. Residual caution among people in the model after lockdowns are eased can be manipulated through the ‘**ResidualCaution**‘ input (e.g., 20% of people still socially distance 50% of the time).

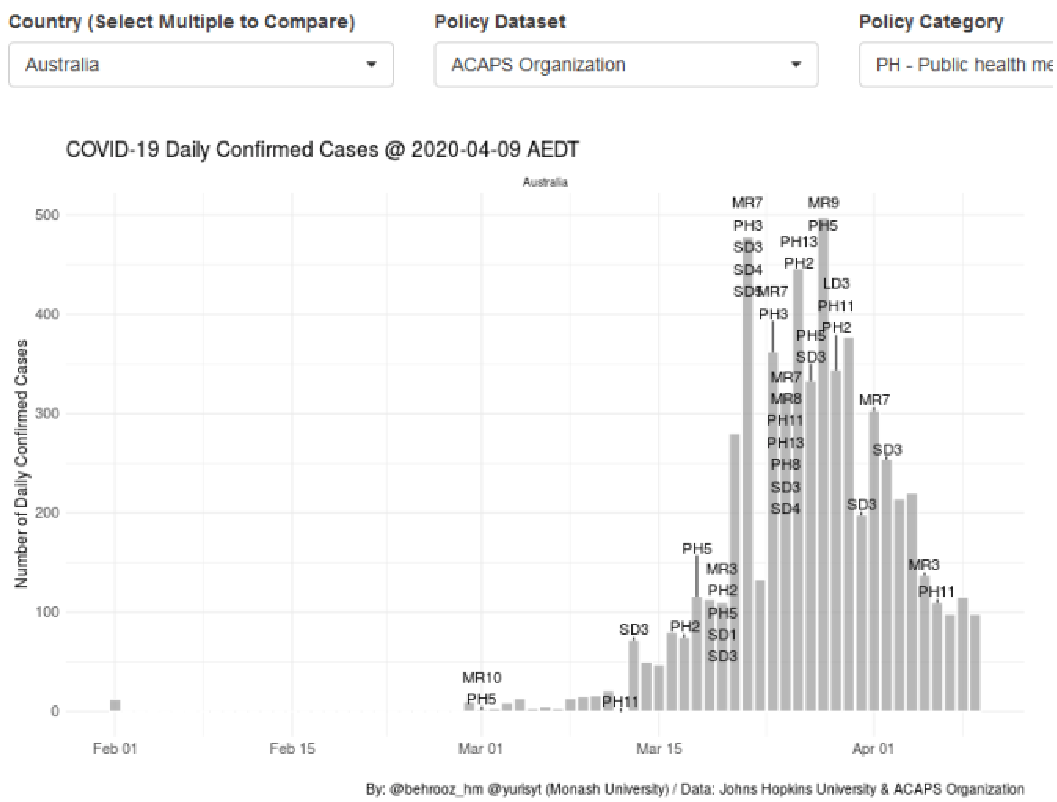


Figure 2. This chart identifies the timing and nature of public health interventions applied to Australia since the beginning of the COVID-19 pandemic https://behroozh.shinyapps.io/COVID19/ .

With the '**Lockdown_Off**' setting set to 'On', users can determine on which day they would like to ease social and economic restrictions using the '**TimeLockdownOff**' input slider. Users will notice that if they do this too quickly, the infection growth rate increases.

3. Process Overview and Scheduling

All updates in the model are serial – that is, each agent updates one at a time inside an ask function. At each time-step in the model, the following actions occur *(an action specifies (1) which entity or entities (2) execute which process or behavior that (3) changes which state variables, and (4) the order in which the entities execute the process)*:

3.1. Person-level actions and updates

- People move at a pace and to a location determined by their infection status, compliance with social distancing and isolation policies, and essential worker status. The person's location is updated.
- People make close contact with others if they are located in the same place as other people.
- Infected people who are in close contact with other people can transmit the virus to one another based on their level of personal virulence combined with their symptomatic status.
- Infection status of all people is updated.
- Infected people who are selected as super-spreaders (random-draw) are moved to a random new location.

- Tracking status of infected people is updated. Infected people can become tracked by the health system indicating they are known to have been infected and are expected to isolate.
- Infected people are sent to ~~quarantine~~ isolation if capacity exists in the hospital system, or are instructed to home-isolate if bed capacity has been reached.
- The number of days that infected people have been infected for is updated.
- Incubation status of infected people is updated.
- Recovered status of infected people is updated
- Death status of infected people is updated
- Mean contacts per day of all people are updated
- R_0 values for infected people are updated, calculated as the mean number of infections passed on by infected people on the last day of their illness period

Users will note that more functions and updates to agents and entities are available in the full model than are described here (e.g., mask-wearing, student status, etc.). The functions described above relate only to those variables of interest in the presented model.

3.2. Global actions and updates

- Model scale is updated.
- The possible radius of movement of agents is updated in response to the scale of the model.
- Time is updated (e.g., 1 time-step is scaled to 1 day).
- Deaths are updated.
- Case fatality ~~rate~~ ratio is updated.
- Total people, infections, daily infections, infection rates, and infections among specific agent populations (e.g., students, essential workers, age-brackets, etc. are updated).
- Elimination dates are updated.
- Imported case numbers are updated.
- Public health policy implementation status (e.g., ~~social~~ physical distancing, tracking and tracing, mask usage) is updated.

Users will note that more functions and updates to global variables are available in the full model than are described here (e.g., school policies, electronic tracking and tracing policy enactment, mask-wearing, etc.). The functions described above relate only to those variables described in the presented model.

3.3. Processing and scheduling rationale

Each action above takes place at each time-step (i.e., there is no scheduling of events or order hierarchy). The rationale is that each person makes a judgement about their next action based on an assessment of their disease and demographic state as well as the local environment (e.g., infected, recovered, susceptible, essential worker, compliant with ~~social~~ physical distancing, located near empty neighbours, etc.) and acts at the next time-step based on their own assessment of that state.

The exception to this rule concerns the scheduling of public health interventions under the experimental trials for individual countries and locations (e.g., Wuhan, Australia and New Zealand). Here, the model checks the current time against the scheduled time for public health policy implementation or lifting, and triggers that policy (or its removal) if the time approaches or exceeds the scheduled time.

4. Design Concepts

4.1. Basic principles

The general concept underlying this model is that infectious disease spread is driven by contact between infected and susceptible individuals in a population. This is not a new concept as many agent-based models of SEIR (susceptible, exposed, infected, and recovered) processes have been previously developed either for demonstration predictive purposes. However, this model attempts to achieve three things that prior models have found troublesome. Firstly, to create a generic model able to be used and adapted by different countries or jurisdictions. Secondly, to enable consideration of the effect of public health policy measures that alters behaviour *during* the pandemic, and therefore alters the course of disease progression. Thirdly, to do this at low computational cost.

Rather than modelling an infectious disease process that assumes behaviours are generic or homogenous, we specifically model the behaviour of individuals in response to public health interventions. This demonstrates that patterns of disease progression are possible that standard SEIR models are unable to replicate or communicate adeptly. The usefulness of this approach is that 1) it allows for hererogeneity among modelled individuals across variables of interest or importance, 2) it is more realistic than standard SEIR models whose projections in the Australian context have underestimated the effect of public health interventions, and 3) it enables governments to specifically model the potential effect of stringency and timing of public health interventions.

While SEIR models project the outcome of behaviour in terms of infection rates, deaths, and R_0 values, etc., they do not model or manipulate the behaviours that lead to these estimates, themselves. This leaves standard models able to understand the envelope of effect, but not the mechanism that drives it. In this model we reverse that hierarchy, firstly creating a behavioural model within a simulated society, and then seeding that society with an infectious disease characteristic of SARS-CoV-2.

4.2. Emergence

The behaviour of agents in the model is driven by imposed stochastic processes at the individual level, however, system-level patterns emerge that mimic and extend those expected in typical SEIR representations. Importantly, these system-level patterns differ markedly in response to the imposition and lifting of modelled public health interventions and are hence the patterns of interest for the model user.

For example, when run under an unmitigated scenario, interactions at the individual level translate into a bell-shaped infection curve, typical of standard SEIR models. Here, the model user can observe total infections over the course of the simulation, daily infections at any point in time, current or ‘active’ infections, etc.

However, the emergent behaviour of the system generated by the micro-level interaction of agents in the model shifts in response to modelled public health interventions, altering the observed patterns of infection at the macro-level across the simulated society (see example below).

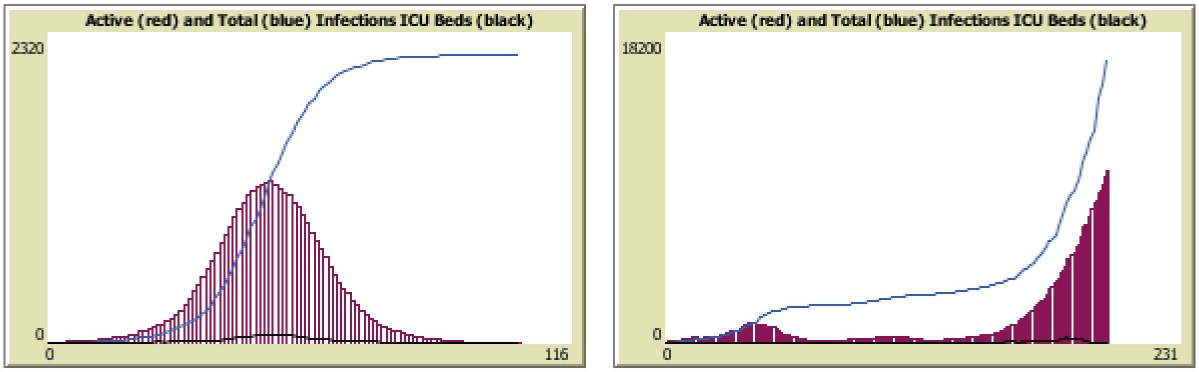


Figure 3. Differences in emergent behaviour of the macro-system in response to changes to modeled public health interventions.

Emergent, macro-level patterns are also observable in the 'geographic' location of infections at various points in disease progression across the simulated society – especially in unmitigated scenarios where distances between communities are represented by relative distance in the model.

For example, the sequence of images below shows infection patterns of a scenario representing a population of 25,000,000 people (at stage 0, stage 3, and stage 4). Apparent are geographic pockets of the population that have current infected populations (red), recovered populations (yellow), and pockets that remain susceptible (blue). Over time, the location of these areas shifts as the infection moves through the community. Noticeable, though are those areas that remain susceptible but 'protected' by sometimes surrounding recovered communities, preventing the spread of infection further.

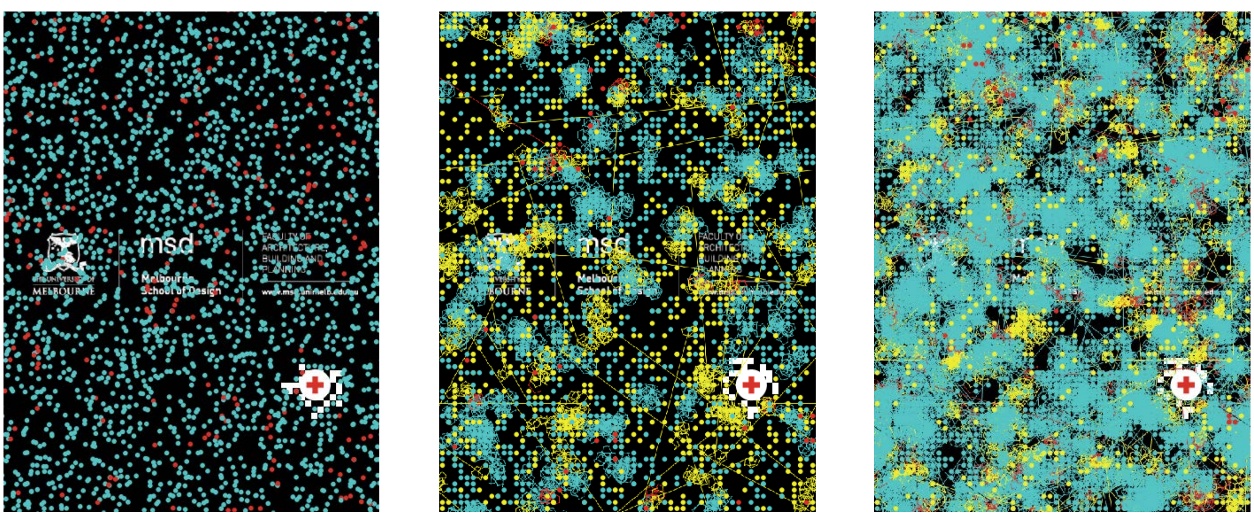


Figure 4. Emergent patterns observable from the small-scale interaction of agents in the model.

4.3. Interaction

Simulated p~~P~~eople in the model behave and make decisions in response to their perception and understanding of their environment, which includes the presence of other agents in their immediate vicinity. While agents (people) make decisions, they do not learn from experience or solve problems. The primary decision that agents make concerns when and where they move from one time-step to the next, that is, how they *move* and *avoid*.

4.3.1. Moving and transmission through direct contact

Under conditions where no public health policies related to physical distancing have been implemented, people move at a pace equivalent to 1 area unit per time-step, taking them to the next area on the grid. The heading that people move in is initially random, and at stage 0, is updated by + random 45 degrees, and – random 45 degrees on each subsequent time-step. This means that in a small initial community of 2500 people, there is a good deal of interaction among the population. People can move anywhere in the environment, except to the location of the hospital.

If a blue, susceptible person finds themselves located at the same place as a red, infected person, there is a likelihood that the infected person will pass the virus to the susceptible person. This can only happen if they are located in the same place.

The likelihood that a susceptible person will become infected when coming into close contact with an infected person is dependent upon a combination of the infected person's level of current and peak personal virulence, which is further tempered by whether the infected person is asymptomatic or not (in the full model, a mask-wearing function also controls virus spread). The higher the current and peak personal virulence of the infected person (see section 2.1, above) who is in contact with the susceptible person, the greater the likelihood that transmission will occur.

The personal virulence of each person is estimated at each time-step of their infection, reflecting a triangular distribution that that increases monotonically from day zero to peak infectiousness at the cessation of the incubation period, returning to zero at the end of the illness period. This is controlled using the following pseudo-code function:

IF I am infected and I have not completed my incubation period, THEN

> *set my current personal virulence as my maximum level multiplied by the number of days I have been infected for divided by the duration of my incubation period*

IF I am infected and I *have* completed my incubation period, THEN

> *Set my current personal virulence as my maximum level multiplied by my illness duration minus the number of days I have already been infected, divided by my illness duration minus the duration of my incubation period*

The pseudo-code for becoming infected while moving around the environment is as follows:

> *IF any other infected simuls are located here and the current personal virulence of the infected person is greater than random 100 and I am susceptible, THEN:*

set my status to infected, set my color to red, set today as the first day of my illness period

Should the infected person be asymptomatic, then their personal virulence is discounted by 1/3 as follows:

IF any other infected simuls are located here who are asymptomatic and the current personal virulence / 3 of the infected person is greater than random 100, and I am susceptible, THEN:

set my status to infected, set my color to red, set today as the first day of my illness period

Once a person is infected, they begin to make different movement decisions. While they remain untracked by the health system, they continue to move normally. However, once tracked, their pace slows to 0, reducing their interaction with other people and reducing their ability to spread infection *if* they are compliant with directions to isolate, which they are 95% of the time. This compliance input (**compliance_With_Isolation**) is adjustable (see section 2.3). When recovery has been achieved, they return to the population as a 'recovered' person and resume normal movement patterns.

4.3.2. Avoiding others (physical distancing)

When physical distancing measures are enacted, people make adjusted decisions about where they will move. Default settings for the Australian example are that 85% of people isolate 85% of the time, though these figures can be adjusted by the user (see section 2.3). This means that the model does not identify 15% of people as 'bad actors' or 85% of people as pro-social, but that at each time-step a random allocation of 85% of people will have an 85% chance of deliberately avoiding being located or moving to a location occupied by another person.

The pseudo-code for this function reads as follows:

IF physical distancing policies are enacted and I plan to avoid others and I am not an essential worker, THEN

IF there are any other people located here who are not from my own household, THEN

move away to an unoccupied location near me

ELSE

IF physical distancing policies are enacted and I plan to avoid others and I am an essential worker, THEN

IF there are any other people located here who are not from my own household and my excess exposure risk due to being an essential worker is not exceeded, THEN

move to an unoccupied location near me

ELSE

Move normally

4.3.2.1. Notes on movement differences between Australia and New Zealand

There is no robust, micro-scale adherence data for NZ and Australia in relation to physical distancing adherence. However, we assumed that it was ~~slightly~~ higher in NZ given the patterns described below.

The lockdown intensity was higher in NZ than Australia with a more restricted range of essential workers in the former (e.g., no hairdressing). Similarly, the range of permitted outings was stricter (e.g., it was not possible to buy takeaway coffee in NZ or for non-essential workers to go beyond their immediate neighbourhood). People in NZ were instructed to keep 2m apart whereas in Australia it was 1.5m. Google mobility data also suggested a tighter lockdown in NZ (e.g., overall reductions [excluding the residential category] were on 29 March 2020: 38% reduction for Australia and 73% reduction for NZ). We therefore considered the data on carbon emissions during pandemic-associated lockdown which have been studied for 69 countries (Le Quéré et al., 2020). NZ had the highest reduction in its carbon emissions (a 41.1% reduction) in these 69 countries (except for Luxembourg at 44.6%). For Australia the reduction was -28.3%. This would suggest that overall lockdown intensity in Australia was around 69% that of NZ (i.e., 28.3%/41.1%). Consequently, we have adjusted the compliance proportion up in NZ to 90%.

Further, in the revised model we assumed that it would be unrealistic for physical distancing behaviours to fully decay to pre-pandemic levels and so we have now set a lower limit of a 20% reduction from pre-pandemic levels for these reasons:

- Even in the peri-elimination phase, some people are likely to remain cautious about hand shaking or attending numerous social events etc. and may still be practicing increased hand hygiene and cough etiquette, which would be expected to remain above baseline levels.
- There might be some sustained long-term behaviour shifts e.g., having adopted online supermarket shopping, some people might persist with it for the long-term. Similarly, for more working from home, more video conferencing instead of travelling, and sustained interest in around the home activities such as gardening.

The proportion of Essential workers as a % of working age population also affected total movement patterns. There were different definitions of essential workers in NZ and Australia and the restrictions on workers changed differently overtime. For example, the Google mobility data on 29 March 2020 indicated a 59% reduction for workplaces in NZ and a 33% reduction for Australia (i.e., 56% that of NZ, consistent with emissions reduction figures, above). But data from 16 May showed the pattern was reversed: a 12% reduction in NZ and a 22% reduction in Australia. Given this complexity, we made the simplifying assumption that in the post-lockdown period, the NZ value was 2/3 that of the Australian estimation (i.e., 20%).

4.3.2.2. Notes on asymptomatic cases for Australian and NZ examples

In the updated representation, we have adjusted asymptomatic cases to 20%. These proportions are not precisely known and are subject to interpretation of symptoms / local vigilance. We used the same proportion (80%) of symptomatic cases as per a Chinese study (Bi et al., 2020) and as per an Australian modelling study (K. Lokuge et al., 2020). This value is higher than the 57% value found in an Icelandic study (Gudbjartsson et al., 2020) but this particular study did not involve long-term follow-up of the asymptomatic cases (i.e., some of the asymptomatic cases might subsequently have developed symptoms). But it is also lower than that found in another Chinese study (at 94% symptomatic) (Luo et al., 2020). A UK study of a cohort of health care workers reported that 27% of all infections were asymptomatic – but this group will be of different ages than the general population (Treibel et al., 2020).

At the time of writing, the R_{eff} value for asymptomatic cases vs symptomatic cases remains uncertain as does the infectivity per contact. We base our estimate on data from (He et al., 2020), recognizing that this, too is an early estimate. Acknowledging that evidence surrounding the infectivity of asymptomatic cases may advance, we enable this variable to be adjusted by the model user using the 'Asymptomatic_Trans' input slider.

4.3.3. Isolating infected, symptomatic, identified cases

In addition to isolating cases in the model environment, symptomatic cases that have been tracked by the system are quarantined providing there is capacity in the hospital system to do so. This isolates them from other susceptible people in the model.

The capacity of the quarantine system is adjustable by the user. For example, the user might wish to model a system where no quarantine systems are available and isolation must take place in the community.

4.3.4. Imported cases

Case records from both Australia and New Zealand prior to lockdown indicate that approximately 62% and 45% of recorded cases were imported from overseas, respectively, arriving through air or sea passenger terminals (Australian Government Department of Health, 2020; New Zealand Ministry of Health, 2020). This resulted in a more rapid increase in cases than would be expected through community transmission, alone. For NZ, the proportion of reported cases from overseas dropped from around 80% in the early stages of the pandemic prior to border closures and the beginning of more widespread community transmission. Of course, it is acknowledged that 100% of cases were imported in the very early stages.

To operationalise this, if the proportion of imported cases for each country fell below 70% of NZ's total cases prior to lockdown and 40% after, or 62% in the case of Australia, a small number (equivalent to 10% of total active cases) of susceptible people were selected at random and converted into imported cases in the lead-up to the imposed lockdown period.

When overseas cases were converted, their illness duration was brought forward to a mean of 1 day prior to the end of their individual incubation period (sd 0.5) to reflect the fact that they had acquired the disease prior to arrival and had likely spent at least 2 to 3 days in international transit. This means they arrive in a slightly advanced state of illness compared to new infections. If arriving after the lockdown period, they were also immediately tracked by the health system and required to isolate.

Other users of the model can adjust these parameters to suit their own circumstances.

4.3.5. Asymptomatic cases

The proportion of asymptomatic cases in the model can be set by the model user with the '**AsymptomaticPercentage**' input slider. In representation for Australia and New Zealand we have adjusted asymptomatic cases to 20%. These proportions are not precisely known at the time of writing and are subject to interpretation of symptoms / local vigilance. We used the same proportion (80%) of symptomatic cases as per a Chinese study (Bi et al., 2020) and as per an Australian modelling study (K. Lokuge et al., 2020). This value is higher than the 57% value found in an Icelandic study (Gudbjartsson et al., 2020) but this particular study did not involve long-term follow-up of the asymptomatic cases (i.e., some of the asymptomatic cases might subsequently have developed symptoms). But it is also lower than that found in another Chinese study (at 94% symptomatic) (Luo et al., 2020). A UK study of a cohort of health care workers reported that 27% of all infections were asymptomatic – but this group will be of different ages than the general population (Treibel et al., 2020).

Asymptomatic cases have a reduced infectiousness rate 1/3 that of symptomatic cases. This is calculated at the time of contact with other people by adjusting the effective '**personalVirulence**' factor of infected people by 2/3 as in 4.3.1, above.

4.4. Prediction

This model has been developed to predict possible *patterns* of disease trajectory more-so than the disease trajectory, itself. Therefore, we are more comfortable with the idea that the model will deliver results demonstrating directions of effect than magnitude and absolute point estimates.

We stress that the model is firstly a reasonable behavioural model focused on interaction among individuals in a society into which an infectious disease has been introduced. Therefore, the disease trajectory is a consequence of the behavioural model.

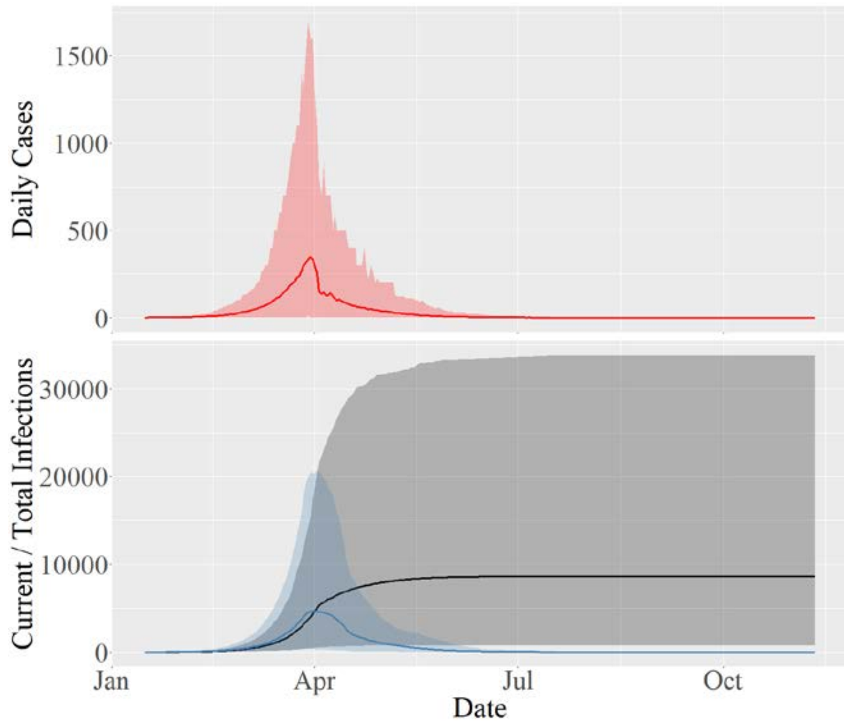
If we accept that the disease transmission mechanisms are of the nature described, (i.e., person to person transmission given close contacts) then we can use the model to project likely disease progression. This contrasts with a strict prediction exercise through 'curve-fitting' exercise that might take observed infection data and project forward without recourse to the mechanisms that underlie infection rates. In this circumstance, previous disease data may not predict future outcome data. However, unless the nature of person to person disease transmission changes dramatically, previous social behaviour will still predict the direction of future disease trajectory and progression.

This focus on representing the mechanisms that drive disease progression rather than outcomes, alone, increases the utility of the model by enabling other jurisdictions to adjust the model to reflect their own circumstances.

4.4.1. Accordance with observed data

The following charts compare the results from the model with official observed statistics from Australia and New Zealand.

4.4.1.1. Australia



a

Figure 5. Australia modelled - Estimated Australian disease progression under consistent adherence with physical distancing policies (average number of new daily (panel a) and current and cumulative (panel b) cases from 1000 simulations) with shaded areas representing 95% simulation intervals.

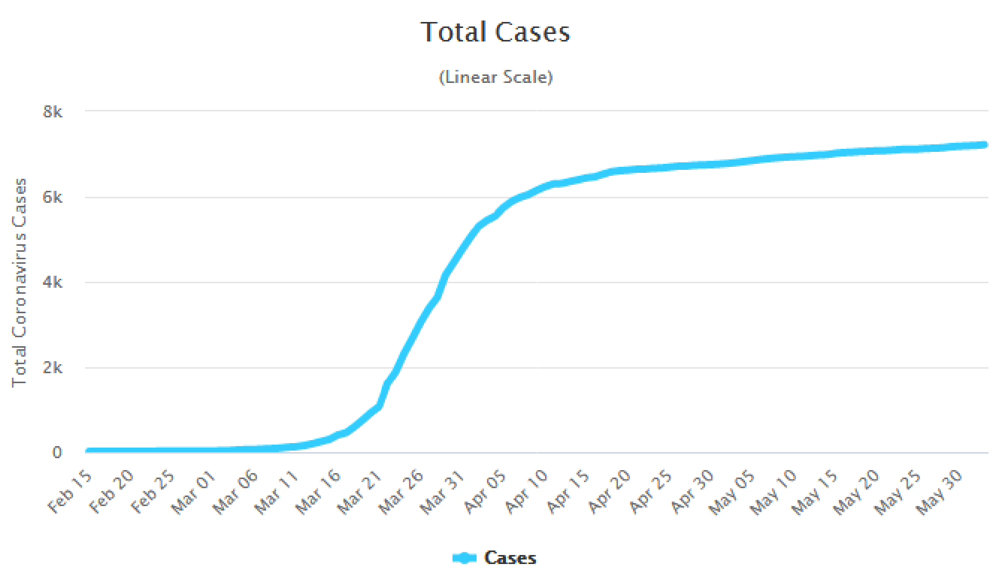


Figure 6. Australian observed total SARS-CoV-2 infections to June 3rd 2020

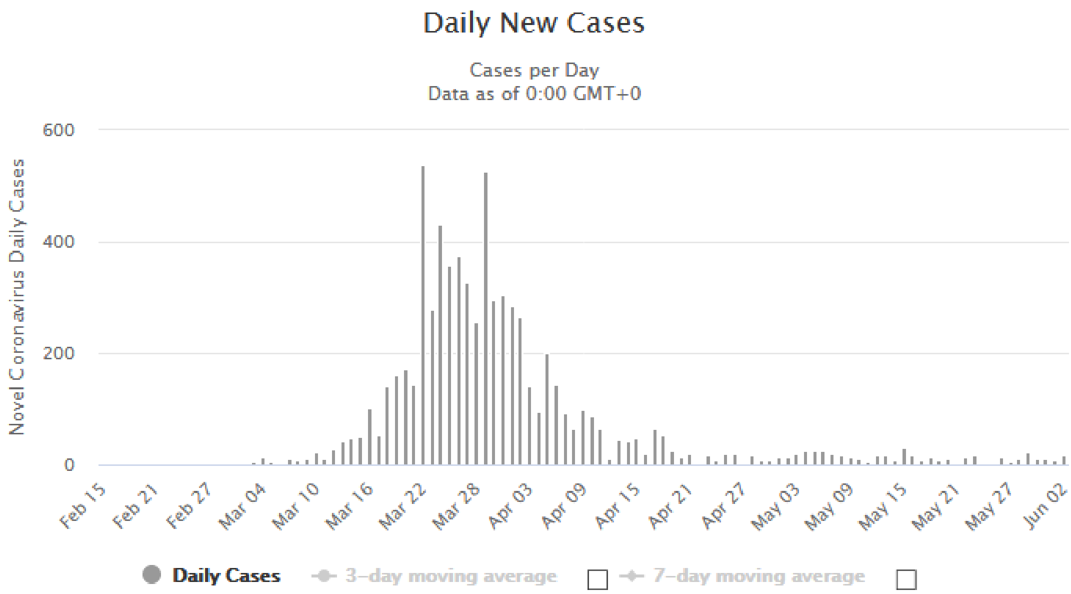


Figure 7. New SARS-CoV-2 daily cases in Australia to June 3rd, 2020,

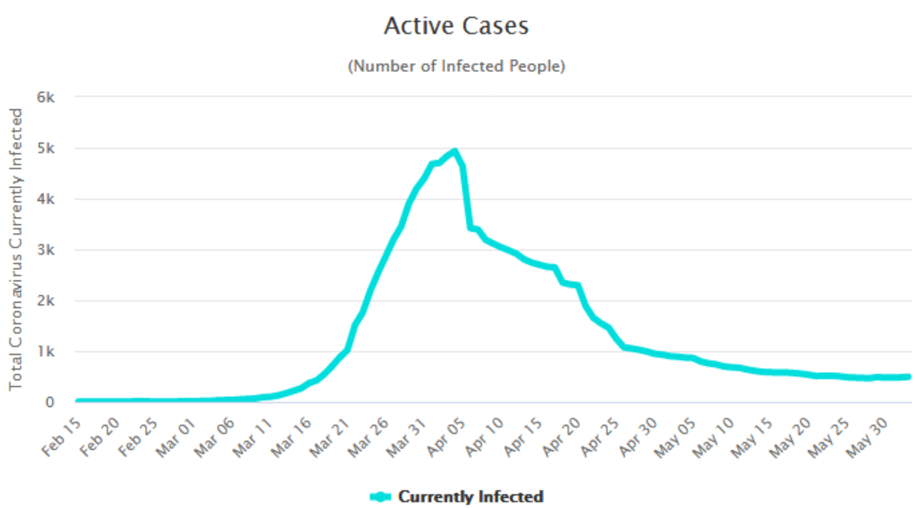


Figure 8. Active SARS-CoV-2 cases in Australia to June 3rd,2020

4.4.1.2. **New Zealand**

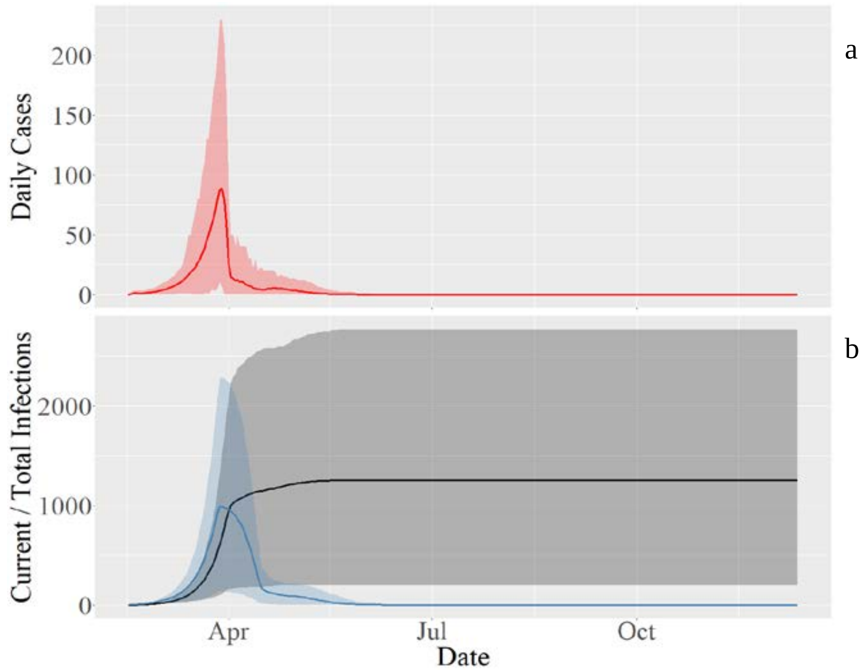


Figure 9. New Zealand modelled - Estimated New Zealand disease progression under consistent adherence with physical distancing policies (average number of daily (panel a) and current and cumulative (panel b) cases from 1000 simulations) with shaded areas representing 95% simulation intervals.

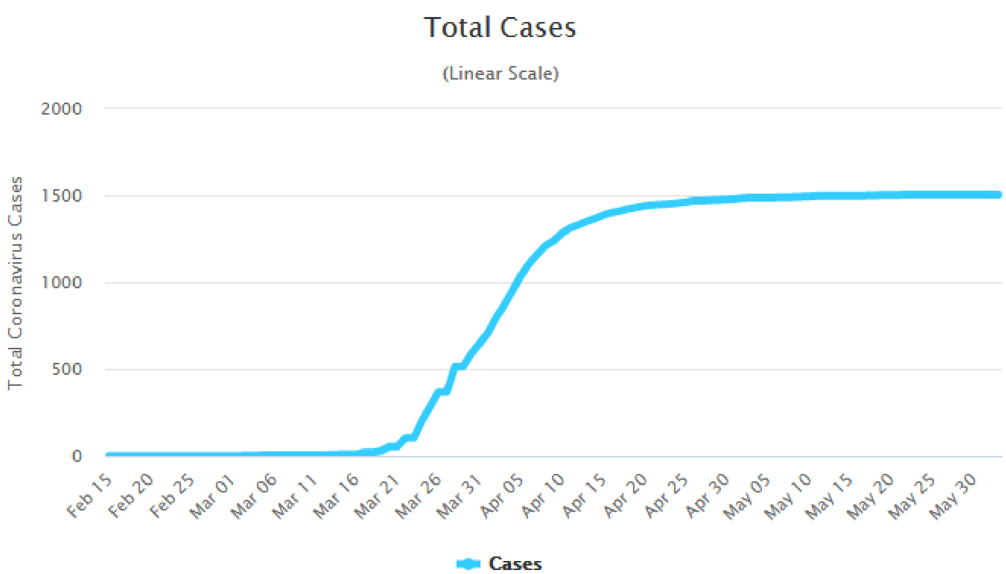


Figure 10. New Zealand total observed cases to June 3rd (this figure is inflated in comparison the that of the Ministry of Health 'confirmed' cases, which records 1151 to June 3rd, 2020).

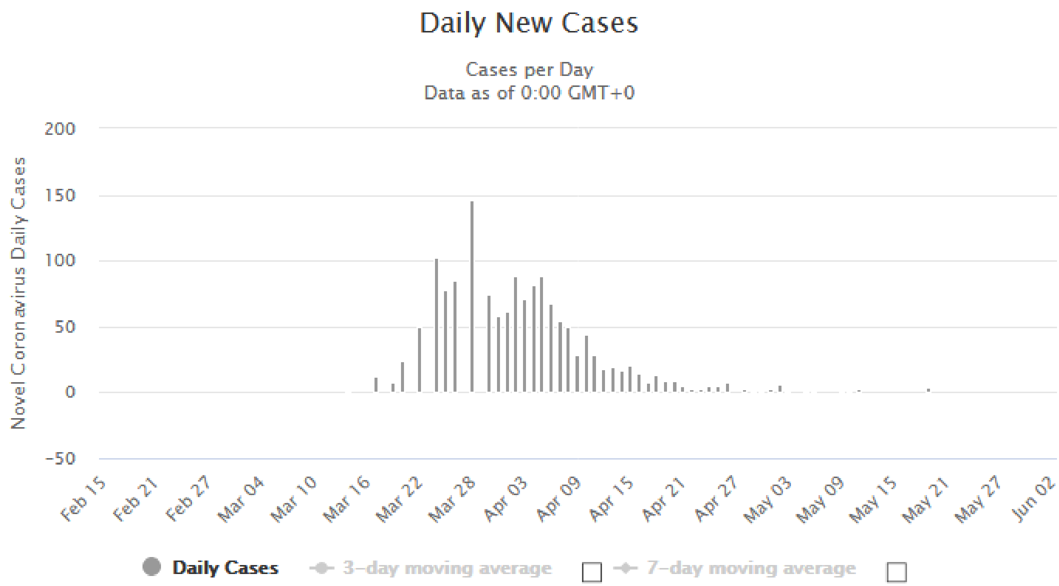


Figure 11. Observed daily new cases in New Zealand to June 3rd 2020

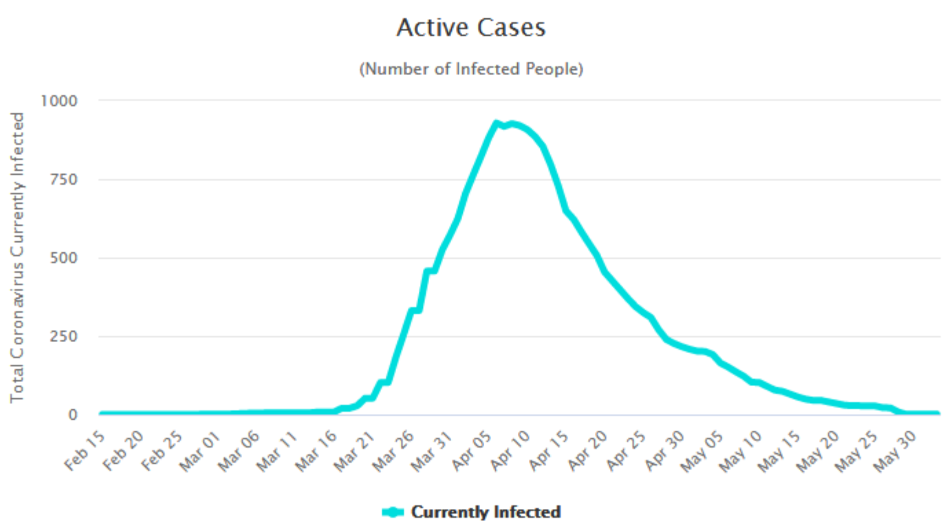


Figure 12. Observed active cases in New Zealand to June 3rd 2020

4.4.2. Disease progression and prediction of minimum decay to achieve 80% likelihood of elimination in Australia.

The following panel shows the estimated pattern of disease progression in Australia under a decay in adherence scenario, where the residual level of decay is set between 30% and 80% for both the proportion of people who avoid contact with others and the proportion of time contact is reduced for.

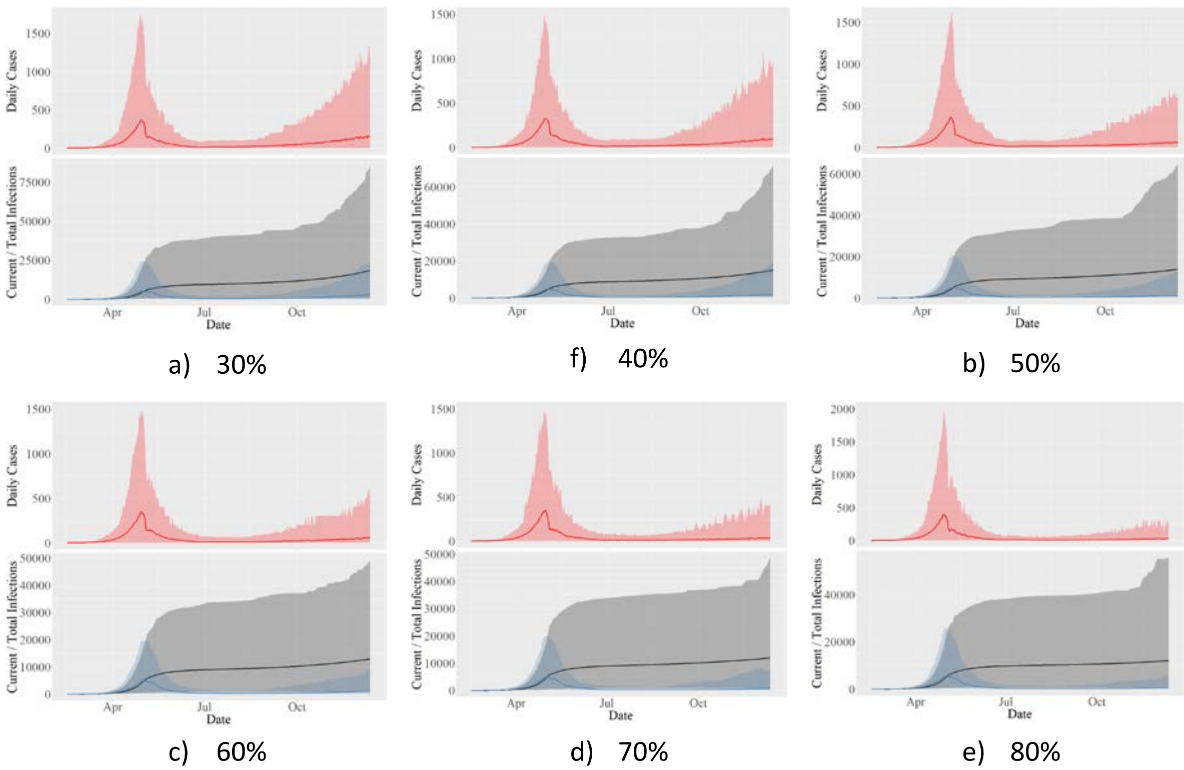


Figure 13. Estimated disease progression under various residual adherence scenarios for Australia of between 30% and 80%.

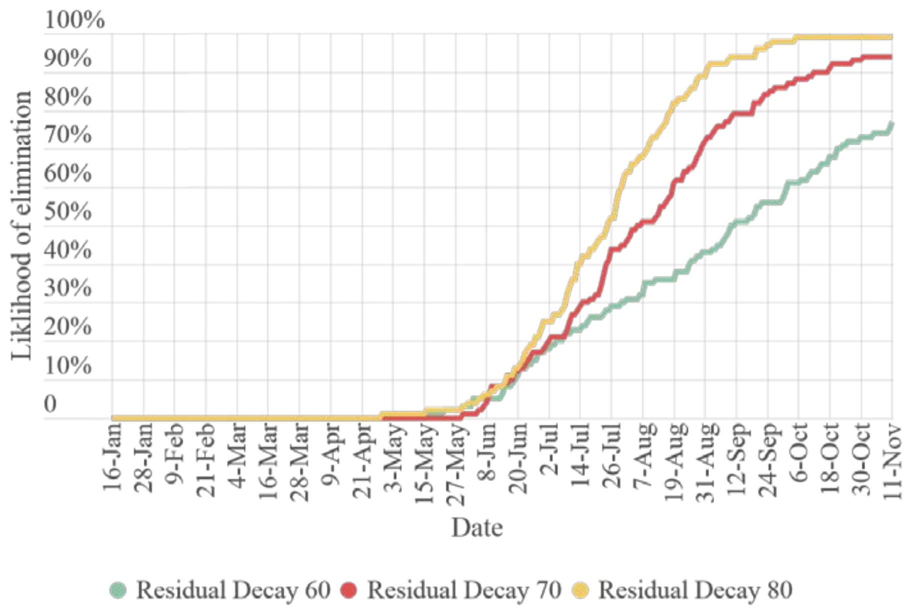


Figure 14. Estimated likelihood of elimination in Australia under residual adherence decay settings of 60%, 70% and 80%.

4.4.3. Prediction of minimum decay to achieve 80% likelihood of elimination in NZ.

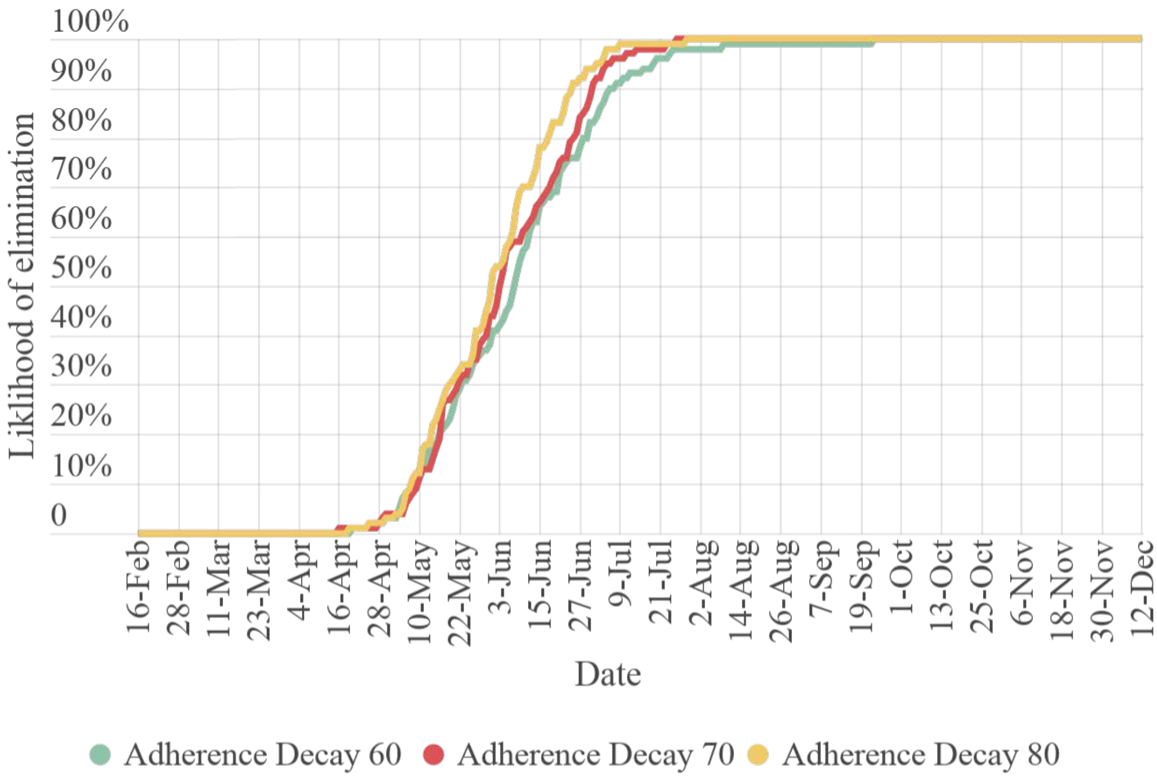


Figure 15. Estimated likelihood of elimination in NZ under residual adherence decay settings of 60%, 70% and 80%.

4.4.4. Variation with changes to asymptomatic cases – Australian adherence scenario

The following panel compares outcomes based on 100 runs across 4 scenarios based on variations to Australia, Scenario 1 but with changes to the proportion of asymptomatic cases in each trial across 30%, 40%, 50% and 60%.

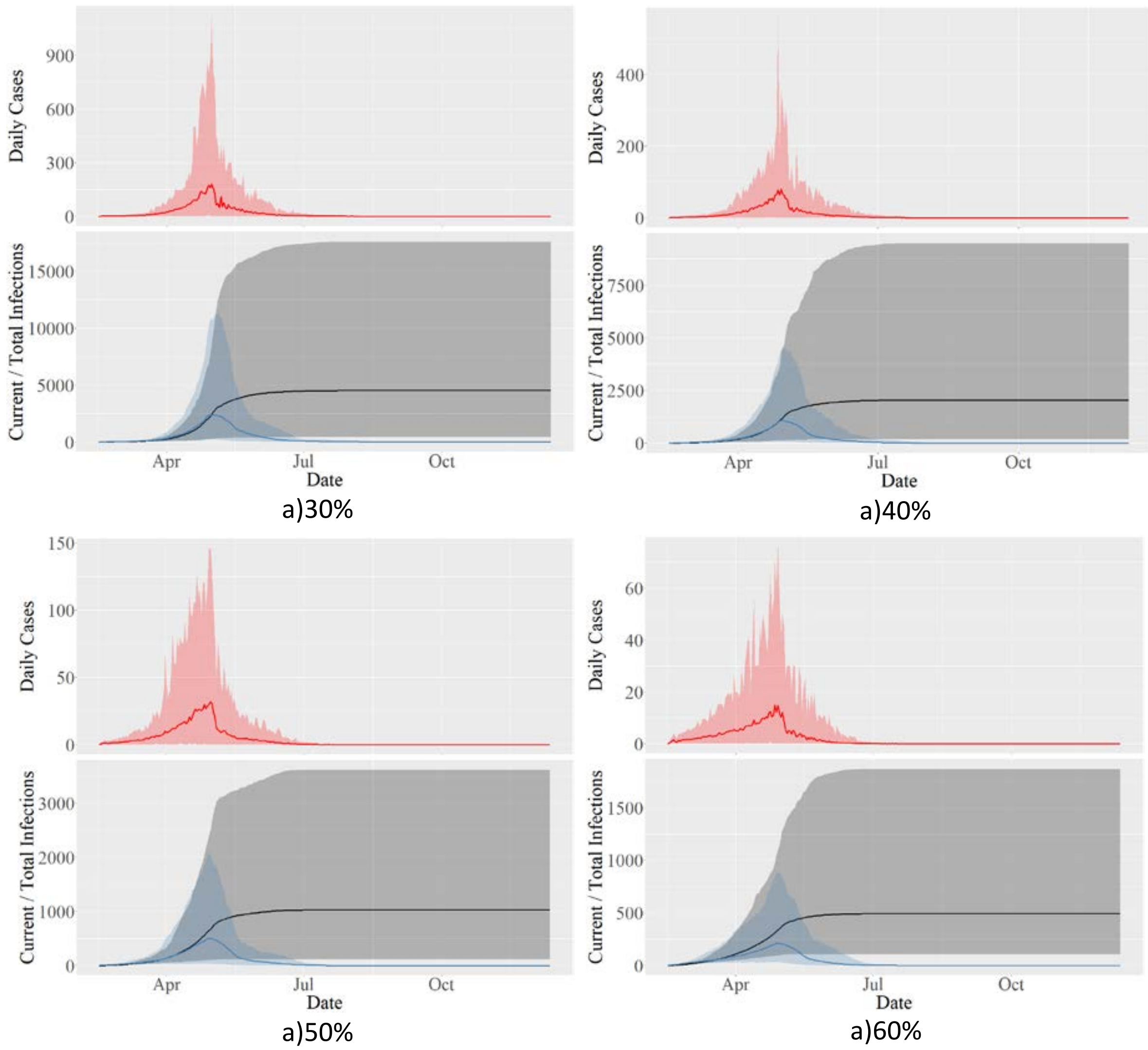


Figure 16. Comparison of daily cases, current cases and total cases under each of 4 scenarios of 30% asymptomatic cases, 40%, 50% and 60%.

4.5. Sensing

Simulated people within the model have three levels of sensing. Firstly, they can determine whether they are located at the same place as another person. Secondly, they can 'see' space around themselves, enabling them to move into unoccupied space if it is available. Lastly, they can sense the opinions or emotions of any other people in their surrounding space.

This third sense is not used in the COVID-19 policy example but can be utilised by the model user in other functions concerning anxiety and panic-buying.

4.6. Stochasticity

Numerous input variables are stochastic, driven by pseudo-random numbers that drive events at each time-step. In general, these are generated by random number draws from a flat distribution of between 0-100 (integer) or 0.00 to 1.00 (float) that must be either above or below a set threshold for actions to take place. They include

- Infection events
- Deaths as a result of infection by age-group
- Movement of people to new locations
- Avoidance of others
- Compliance with isolation
- Superspreading events (e.g., movement of people to new, random locations)
- Tracking and tracing of infected people

Stochasticity was used in these processes to make them variable without delving into the mechanics of each process, which was outside the scope of interest.

4.7. Collectives

Collectives were limited to types of people, who then acted on modified rules pertaining to movement, infection, etc. They included:

- Susceptible people – (coloured blue) not yet infected. These people could move freely around the environment in the pre-lockdown period but were susceptible to infection from infected people.
- Infected people – (coloured red) who had acquired a COVID-19 infection either through overseas or local transmission. These people could move freely until they were tracked by the health system or unless the lockdown period had already taken hold.
- Recovered people – (coloured yellow) who had been infected and had recovered and were not susceptible to new infection. Similar to susceptible people, they could move freely unless lockdown was enacted.
- Deceased people **-** (coloured black) who had died as a result of COVID-19 infection. Deceased people were 'hidden' in the hospital in the model and could not interact with others.
- Essential Workers – People between the age of 18 and 69 who continued to work through the lockdown period, making them more exposed to potential infectious others.
- Age Groups – People of various age-groups (deciles) from 0 to 100.
- Students – people who were under 18 years of age (student functions were not used in the current model).

4.8. Observations

The following outputs were monitored at each time-step:

- The number of people in the model
- The time-step of the model (equivalent to days)
- The total number of people who had been infected over the course of the simulation
- The number of people who had recovered from infection
- The number of people who had died
- The number of people who had died in each age-range
- The number of people who had died as a proportion of the number of people who had been infected (case fatality ratio)

- The number of ICU beds required under the assumption that 5% of infected people would require an ICU bed
- The number of new cases reported per day (reported on the 6th day of their illness)
- The number of people who were currently infected
- The date at which the simulation achieved no active cases (referred to as the elimination date)
- The Mean R_0 of all infected cases in the model on their last day of infection
- The growth rate of infections over time
- The number of close contacts made per person per day
- The difference between ICU bed demand and availability
- The mean number of days each infected person had been infected for
- The total population of the jurisdiction
- The proportion of the population physically distancing and the proportion of time they were distancing for
- The proportion of people who were compliant with isolation orders
- The mean speed of people moving through the environment
- The mean infectiousness or personal virulence of people
- The social and public health policy settings of the environment
- The proportion of infected cases that were acquired overseas
- The distribution of R for individuals
- The distribution of illness periods for individuals
- The distribution of incubation periods for individuals
- The age ranges of individuals
- Infections by age range
- The scale phase of the model

5. Initialisation

The model is initialised by placing a hospital agent on a black, 60 x 80 (4800 patch) area and then allocating a number of white pixels to the area under the hospital scaled to its capacity and which designate it as a separate area for the purposes of agent navigation. 2500 susceptible people are then randomly allocated to a black area in the environment and all variables described in Section 2.1 are allocated to people.

A random selection of initial people (minimum of 1) governed by the 'current_cases' variable are then selected to become the index case(s). Apart from a model depicting the area of Wuhan, China, where the COVID-19 virus originated, these people will represent 'imported' cases and will be given an advanced illness period equivalent to their own incubation period minus approximately 1 day designated by the 'timenow' variable. They will be colored red and assigned an 'infected' tag and an 'imported' tag (see model code for details).

The distribution of variables assigned to individual agents as well as global variables controlling the model environment is designed to be generic, but can be adjusted to fit the circumstances of individual jurisdictions (see Australian and NZ examples, above). The model can therefore be run under many combinations of settings representing many different scenarios.

6. Input data

Table 1. Parameter estimates and 'agent' characteristics for presented scenarios.

Key Parameters	**Parameter Estimates (Australia)**	**Parameter Estimates (NZ)**
Physical distancing (% of people limiting movement and maintaining a distance of 1.5m (Aus) or 2.0m (NZ) in public) (Hale et al., 2020)	85%	90%
Physical distancing - time (% of time that people successfully maintain a distance of 1.5m (Aus) or 2.0m (NZ) in public) (Hale et al., 2020)	85%	90%
Proportion of essential workers[¥]	30% of working age-people	20% of working age-people
Mean incubation period (days, log-normal)(Lauer et al., 2020)	m = 6, sd = 0.44	m = 6, sd = 0.44
Mean illness period (days, log-normal)(Bi et al., 2020)	m = 20.8, sd = 2	m = 20.8, sd = 2
Mean adherence with isolation of infected cases (%, beta distribution (28,2)) [¥]	m = 0.93, sd = 0.05	m = 0.93, sd = 0.05
Super-spreaders as a proportion of population[¥¥]	10%	10%
Number of days after infection that new cases are publicly reported ¥	8	8
Day of case 0 (Day 0)	January 16th, 2020	February 16th, 2020
Days from case 0 to policy enactment	72 (March 28th, 2020)	39 (March 26th, 2020)
Asymptomatic cases (% of cases) **(Bi et al., 2020; Kamalini Lokuge et al., 2020)**	20%	20%
Infectiousness of asymptomatic cases vs symptomatic cases (He et al., 2020)	33%	33%
Physical distancing anticipation time-window(Google Inc, 2020)	14 days	14 days
Decay in physical distancing adherence window(Daly, 2020)	60 days (May 26th)	60 days (May 28th)
Public compliance with isolation orders ¥	95%	95%
Target peak effective reproduction number (Rt) across model runs	2.2 – 2.7	2.2 – 2.7
Proportion of imported cases at lockdown(Australian Government Department of Health, 2020; New Zealand Ministry of Health, 2020)	60%	40%

Agent Characteristics	**Definition**
Infection status	Infected, susceptible, recovered, deceased
Time now	The number of days (integer) since an infected person first became infected with SARS-CoV-2
Age-range	The age-bracket (categorical) of the person, calibrated to census data deciles from 0 to 100.

Risk of death	The overall risk of death (float) for this person based on their age-profile
Location	The current location of the simulated person (agent) in the model interface
Pace	The speed at which the person moves around the environment – higher speeds resulted in more close contact with other people (agents) in the model
Heading	The direction of travel of the person at the current time-step. In conjunction with the scaling approach, the heading variable was used to create local communities and control interaction between and across communities
Contacts	A count (integer) of contacts the person (agent) had interacted with in the past day as they moved within the model's environment

¥ Assumed parameter based on expert opinion

¥¥ 10% of the population potentially transmit infections widely through occasional travel to random locations.

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