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Supporting Information

Technical appendix

This appendix was part of the submitted manuscript and has been peer reviewed.
It is posted as supplied by the authors.

Appendix to: Hanly MJ, Churches T, Fitzgerald O, et al. The impact of re-opening the international border on COVID-19 hospitalisations in Australia: a modelling study. *Med J Aust* 2022; doi: 10.5694/mja2.51291.

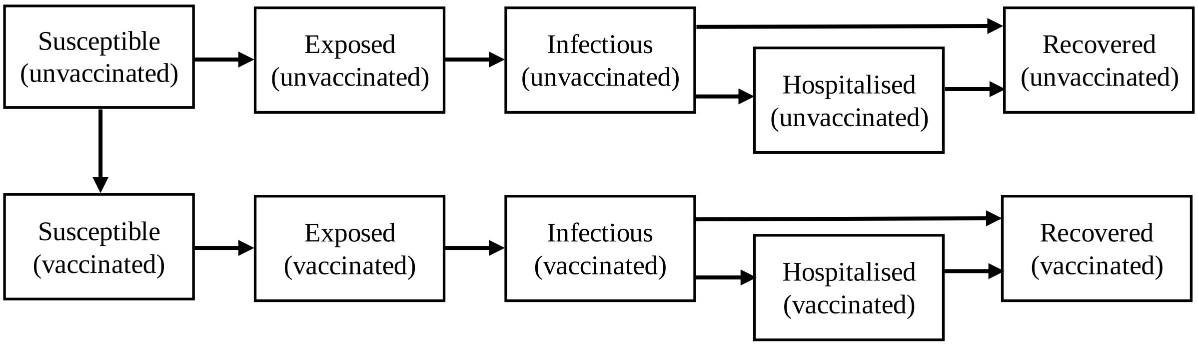
Technical appendix

The model

Overview

This analysis uses an age-structured deterministic compartmental model implemented in the R package COVOID (COVID-19 Opensource Infectious Dynamics). In this extension of the widely used SIR epidemic model, individual disease status is classified as one of five states: Susceptible, Exposed, Infectious, Hospitalised or Recovered (SEIHR). The model also distinguishes between vaccinated and unvaccinated individuals, resulting in a total of 10 compartments (Figure 1).

Figure 1. The deterministic age-structured compartmental model



This is one of several epidemic models included in the COVOID R package. Further details of the model implementation and estimation, and instructions on how to download and use the software, are available on the companion website https://cbdrh.github.io/covoidance/.

Model parameterisation

The parameters required to specify the SEIHR compartmental model, and their assumed values, are summarised in Table 1. The reproduction number in the absence of any interventions or measures to supress the virus was alternatively set to 3.5 and 7.0, emulating the Alpha and Delta variants respectively. The average latency period was set to 6 days, the average infectious period was set to 10 days and the average hospitalisation period was set to 7 days.

Vaccine efficacy was operationalised as the reduction in the probability of infection for a vaccinated person relative to an unvaccinated person and this was set to 80% based on estimates of the pooled average effectiveness against symptomatic disease for two doses of the Pfizer or Astra Zeneca vaccines against the Delta variant.[2] The probability of an infected unvaccinated person being hospitalised ranged from 2% for those aged 14 and below to 36% for those aged 60 and above, based on data from the National Notifiable Diseases Surveillance System published in Mackay, Stobart and Crowley (2021).[3] The probability of hospitalisation for infected vaccinated individuals was reduced by 71% for all four age groups based on the pooled estimate of effectiveness against hospitalisation for individuals infected with the Delta variant, following two doses of the Pfizer or AstraZeneca vaccine.

Table 1. Summary of model parameters

Parameter	Description	Value
R_0	Reproduction number in the absence of any interventions or measures to suppress the virus	Alternatively set to 2.5 and 7.0
sigma	Inverse of average latency period	1/6
gamma	Inverse of average infectious period	1/10
v_{eff}	Vaccine efficacy - reduction in the probability of infection for a vaccinated person relative to an unvaccinated person	80%
t_{hosp}	Average number of days a hospitalised individual spends in hospital	7
p_{hosp}	Probability of an infected person being hospitalised by age group for the unvaccinated	0-15y: 0.02 16-39y: 0.04 40-59y: 0.10 60y+: 0.36
p_{hospV}	Probability of an infected person being hospitalised by age group for the vaccinated	0-15y: 0.0058 16-39y: 0.0116 40-59y: 0.0290 60y+: 0.1044

Demographic and age structure

The analysis fixes the population of Australia at 25.7 million individuals, divided into four age groups: 0-15 years, 16-39 years, 40-59 years and 60 years and above (Table 2).

Table 2. Assumed population age distribution across four age groups.

Age group (years)	Size (millions)	Population percent
0-15	5.7	22.2
16-39	9.9	38.5
40-59	6.8	26.5
60+	3.3	12.8
Total	25.7	100

The model assumes heterogenous mixing between the population age groups. The mean number of daily contacts between these age groups was generated by aggregating the total social contact matrix for Australia provided by Prem, Cook and Jit (2017)[4] and is summarised in Table 3.

Table 3. Average number of daily contacts between age group

	0-15	16-39	40-59	60+
0-15	7.2	1.8	1.4	0.7
16-39	3.7	10.1	5.4	1.0
40-59	2.4	4.1	5.3	1.1
60+	0.7	0.8	0.9	1.8

Responsive restrictions

The SEIHR deterministic compartmental model includes two mechanisms that can be used to limit the spread of the disease through public health measures. The first is to reduce the average number of daily contacts between age groups. The second is to reduce the probability of transmission when a susceptible person comes in to contact with an infectious person. These mechanisms do not directly model specific interventions; rather they are simply mathematical operations in the calculation of flows of individuals between compartments in the deterministic model. They can be thought of as capturing the cumulative effect of multiple commonly used public health measures. For example, reducing the average number of daily contacts between age groups can emulate the cumulative net effect of school closures, working-from-home, stay-at-home orders and any other measures that limit the number of day-to-day interactions between people. On the other hand, reducing the probability of transmission emulates mask-wearing, hand sanitising, maintaining social distance and the net effect of any other measures that limit the chances of an infected person transmitting the virus to someone they come in to contact with. A worked example is provided in the companion website to the COVOID package.[1]

All of our models impose a 30% reduction in the probability of transmission when a susceptible person comes in to contact with an infectious person, reflecting that relatively unobtrusive measures such as mask-wearing in crowded places will likely remain in place. In our models that include responsive restrictions on social contacts, when that restriction is activated the number of daily contacts is reduced by 70% for all age groups, emulating public health measures that limit social contacts. These specifications were guided by a calibration exercise using data from the Sydney Delta outbreak.[5] The responsive restriction is triggered when the number of active infectious cases exceeds 10,000 individuals and remains in place until cases are reduced to below 2,000 for 14 successive days.

Vaccine rollout assumptions

To project the rate of vaccine rollout in Australia we used an updated version of our published algorithm which accounts for availability of vaccine doses, eligibility of different age groups and vaccine hesitancy in the population.[6] We varied assumptions regarding available doses and vaccine hesitancy to generate two vaccine rollout scenarios, one faster and one slower. We assumed that all adult age groups (≥16 years) were eligible at the start of the simulation period 1 September 2021, and that vaccination would be opened to younger age groups from 1 February 2022.

We assumed that 7 million people had received both doses by September 1 2021, corresponding to 35% of the population aged 16 years and above, with higher coverage in the older age groups.[7] The resulting projections reached 80% coverage of the population aged 16 and above in mid-October and late-December 2021 under the fast and slow rollout scenarios respectively (Figure 2A). 80% coverage of the total population is achieved in mid-February and late March 2022 under the fast and slow rollouts respectively (Figure 2B).

Here once a person is vaccinated it is assumed they have received both doses, i.e., we do not explicitly model the two-dose regimen. This assumption is conservative because it ignores the partial protection provided by the first dose, however we also assume that full protection is acquired immediately, offsetting this somewhat.

Table 4. Summary of parameter specifications underpinning the vaccine rollout projections.

<table>
<tr><th>Assumption</th><th>Fast vaccine rollout</th><th>Slow vaccine rollout</th></tr>
<tr><td>Available daily doses</td><td>200,000</td><td>80,000</td></tr>
<tr><td>Vaccine hesitancy (How likely are you to receive the vaccine)</td><td><table><tr><td>Definitely will</td><td>60%</td></tr><tr><td>Probably will</td><td>24%</td></tr><tr><td>Probably won’t</td><td>12%</td></tr><tr><td>Definitely won’t</td><td>4%</td></tr></table></td><td><table><tr><td>Definitely will</td><td>36%</td></tr><tr><td>Probably will</td><td>28%</td></tr><tr><td>Probably won’t</td><td>24%</td></tr><tr><td>Definitely won’t</td><td>12%</td></tr></table></td></tr>
<tr><td>Scheduled opening for age groups</td><td><table><tr><td>0-15y</td><td>1 Feb 2022</td></tr><tr><td>16-39y</td><td>Eligible from start of simulation period</td></tr><tr><td>40-59y</td><td>Eligible from start of simulation period</td></tr><tr><td>60y+</td><td>Eligible from start of simulation period</td></tr></table></td><td><table><tr><td>0-15y</td><td>1 Feb 2022</td></tr><tr><td>16-39y</td><td>Eligible from start of simulation period</td></tr><tr><td>40-59y</td><td>Eligible from start of simulation period</td></tr><tr><td>60y+</td><td>Eligible from start of simulation period</td></tr></table></td></tr>
<tr><td>Individuals fully vaccinated at start of simulation period</td><td><table><tr><td>Age group</td><td>N (millions)</td><td>%</td></tr><tr><td>0-15y</td><td>0</td><td>0</td></tr><tr><td>16-39y</td><td>2</td><td>20</td></tr><tr><td>40-59y</td><td>3</td><td>44</td></tr><tr><td>60y+</td><td>2</td><td>61</td></tr></table></td><td><table><tr><td>Age group</td><td>N (millions)</td><td>%</td></tr><tr><td>0-15y</td><td>0</td><td>0</td></tr><tr><td>16-39y</td><td>2</td><td>20</td></tr><tr><td>40-59y</td><td>3</td><td>44</td></tr><tr><td>60y+</td><td>2</td><td>61</td></tr></table></td></tr>
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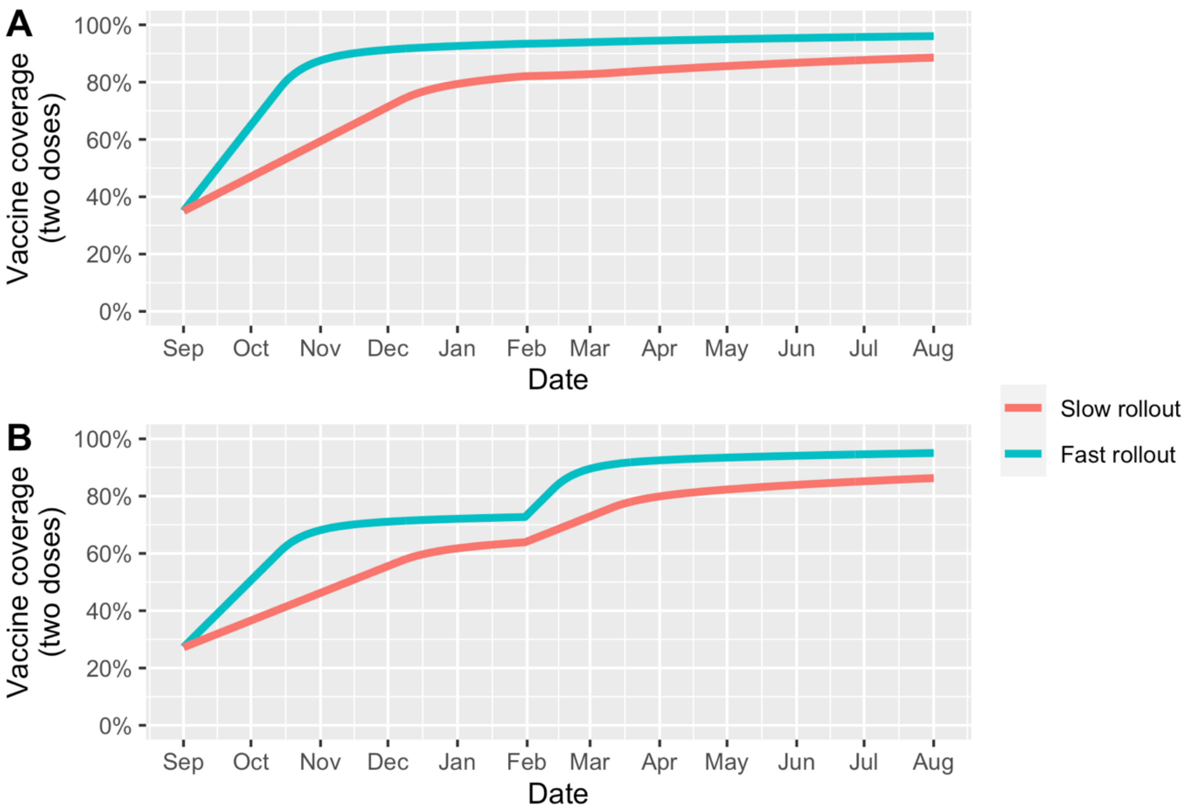
Figure 2. Vaccine rollout projections. Note: Panel A shows vaccine coverage of adult population aged 16 years and over. Panel B shows vaccine coverage of total population.



International border opening and seeding events by international arrivals

Our simulations assumed no locally circulating virus at the start of the simulation period but that borders would open from December 1 2022 introducing the risk of new cases arriving from overseas. The number of new daily arrivals was set alternatively at 2,500 or 13,000 corresponding to approximately 10% and 50% or the total daily arrivals in 2019.

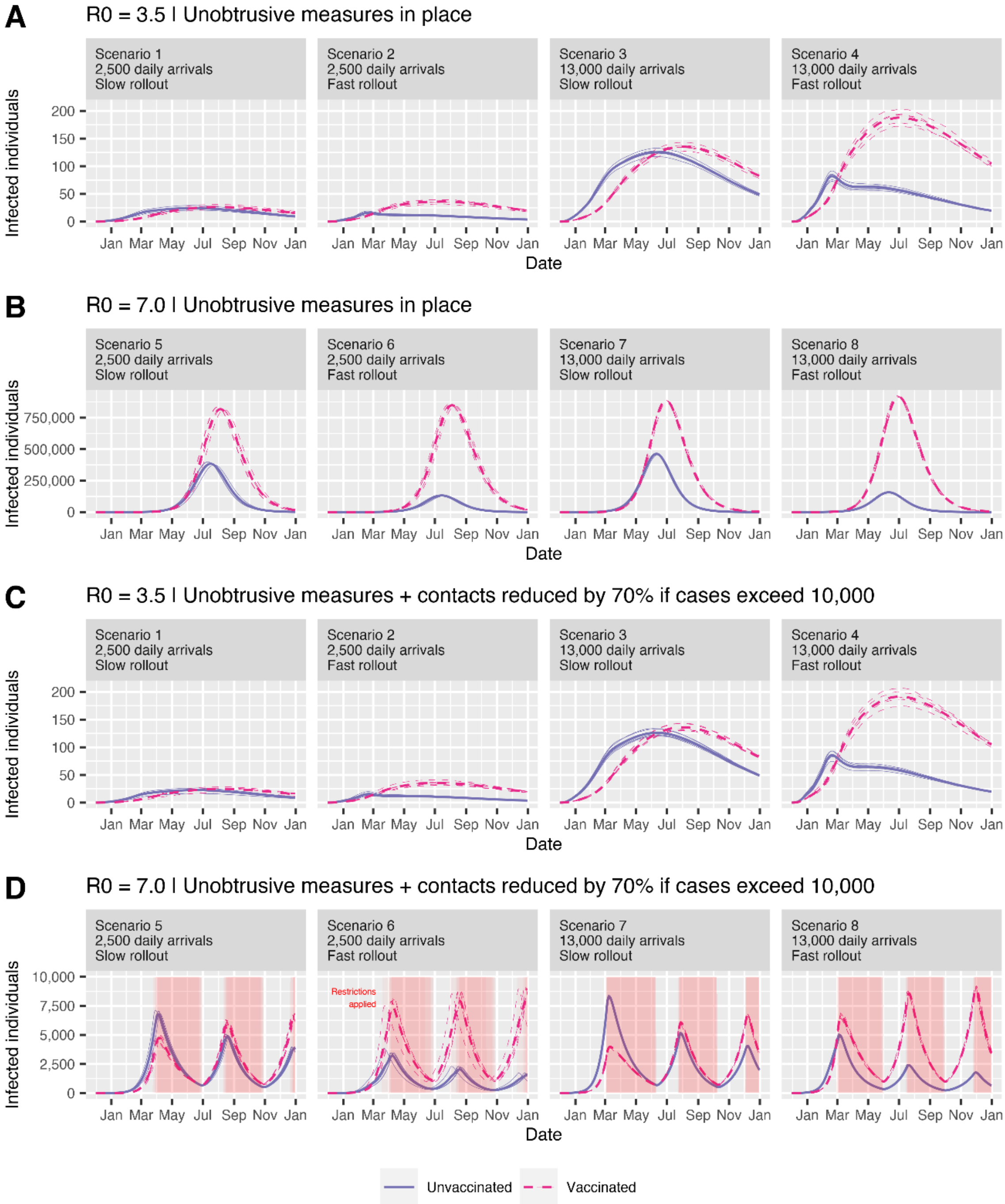
We assumed a rate of new infections from incoming passengers of 3.1 per 100,000 arrivals based on the estimated failure rate of the Australian hotel quarantine system between 1 April 2020 and 31 January 2021.[8] This rate was averaged across the 14 days following the date of arrival and daily stochastic seeding events were generated according to a binomial distribution with the number of trials equal to the total number of arrivals in the previous 14 days and probability of a 'success' of 3.1/10000/14. Based on this rate, 2,500 daily arrivals generates approximately 1 newly seeded case every 14 days and 13,000 daily arrivals results in 5-6 seeded cases every 14 days. These random seeding events are the only stochastic component of this otherwise deterministic model, although they introduce minimal noise i.e. the epidemic curves are very similar across replications. In the final analysis we present the average across five simulation runs.

Software and code

Our models are implemented in the R package COVOID.[1] Details on how to install this package together with a technical description of the implementation and worked examples of using the package in practice can be found at the companion website https://cbdrh.github.io/covoidance.

The analysis was performed using R version 4.0.3[9] and associated packages.[10] All of the code necessary to reproduce, adapt or extent are models is openly available at https://github.com/CBDRH/vaccineBorders.

Figure 3. Estimated numbers of people infected with SARS-CoV-2 (1 December 2021 – 31 December 2022) without responsive restrictions (A, B) and with responsive social restrictions (C, D*), by viral transmissibility, scale of international border opening, and vaccine rollout speed



COVID-19 = coronavirus disease 2019.

* The shaded red bars in panel D mark periods of restrictions on social contacts imposed in response to number of active infections exceeding 10,000. This threshold was not reached in the panel C scenarios.

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