

Note: This paper has not yet undergone formal peer review

The effect of border controls on the risk of COVID-19 reincursion from international arrivals - Appendix

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Model Overview

The model is a direct simulation of individuals arriving, interacting, being tested, and leaving managed isolation and quarantine (MIQ) facilities. It consists of discrete time steps of one-day, where each day the following occurs (in algorithmic order):

1. Individuals that tested positive or met the clinical definition on the preceding day are moved to a stricter facility. This facility is assumed to have perfect containment and is not explicitly modelled. Those that have otherwise reached the end of their stay (default length of stay (*LOS*) of 14 days) leave.
2. New individuals arrive. The number can either be set by data or some fixed value. These new individuals are assigned infection status, exposure dates and onset dates.
3. Individuals on specified days of stay (default 3 and 12) are tested and all individuals are checked for symptoms. Tests have a sensitivity, which is a function of time since exposure. Those that are symptomatic (i.e. are clinical and have reached their symptom onset date) have a set chance of meeting the clinical definition.
4. Individuals mix, having a Poisson distributed number of mean contacts randomly selected from the other guests. Individuals have secondary attack rates, which is a function of time since symptom onset, describing the probability that an interaction results in transmission.

The model does not explicitly consider individual quarantine facilities, assuming that internal transmission and incoming prevalence is sufficiently low that the size of the facility is irrelevant.

Model Specification

The model tracks nine vectors: *statusInfected*, *statusSubclin*, *flagDetected*, *flagExemp*, *tArr*, *tExp*, *tOns*, *tDisch*, & *tExemp*. The i^{th} element of each vector corresponds to the state of individual i . The first four vectors are indicators, where a 1 indicates the individual is a member of that group (i.e. is infected, or has been granted an exemption). The latter five give the integer day of arrival, exposure, symptom onset, discharge, and exemption. These vectors vary in length throughout the simulation, corresponding to the total number of individuals in the quarantine facilities at time t . When individual i leaves their element is deleted from each vector. New individuals are introduced by appending values to the end of each vector.

On arrival, individuals are assigned values according to the following rules. $U(0,1)$ represents the realisation of a continuous uniform random variable on $(0, 1)$ and $U\{a, b\}$ represents the realisation of a discrete uniform random variable on $\{a, \dots, b\}$.

- $statusInfected_i = \begin{cases} 1, & U(0,1) < pInf \\ 0, & otherwise \end{cases}$
- $statusSubclin_i = \begin{cases} 1, & U(0,1) < pSub \text{ and } statusInfected_i = 1 \\ 0, & otherwise \end{cases}$
- $flagDetected_i = 0$
- $flagExemp_i = \begin{cases} 1, & U(0,1) < pExemp \\ 0, & otherwise \end{cases}$
- $tArr_i = t$
- $tExp_i = \begin{cases} t - U\{0,9\}, & statusInfected_i = 1 \\ NaN, & otherwise \end{cases}$
- $tOns_i = tExp_i + \text{round}(\text{Gamma}(5.8, 0.95))$
- $tDisch_i = t + LOS$
- $tExemp_i = \begin{cases} t + U\{1,13\}, & flagExemp_i = 1 \\ NaN, & otherwise \end{cases}$

Individuals are tested when $(t - tArr_i) \in testDays \cup \{tExemp_i - 1\}$. If $statusInfected_i = 1$ and $U(0,1) < S(t - tExp_i)$ then $flagDetected_i$ is set to 1. $S(x)$ is the function describing test sensitivity as a function of time since exposure. The shape is taken from (Kucirka et al, 2020), but scaled so the false negative rate is lower (Wikramaratna et al, 2020). Subclinical cases have a lower probability of testing positive (Woloshin et al, 2020). Reflecting the possibility that a clinical individual meets the case definition (and is detected by their symptoms), each day individuals for whom $t \geq tOns$ have $flagDetected_i$ set to 1 with probability $pDetectSymptoms$. Individuals that test positive or meet the clinical definition are moved facility *the following day*. This incorporates the implicit assumption that the delay from testing until results is one day.

Any individual displaying symptoms before departure ($tOns_i < tArr_i$) has a chance of $pDetectSymptoms$ of not travelling. For simplicity, this occurs with the same probability that an individual meets the case definition on any day during their stay. They are removed immediately. This does result in a daily arrival numbers being slightly lower than the chosen parameter, although with low overseas prevalence this can be ignored.

Each infected individual is assigned a $C_i \sim \text{Poisson}(\text{meanContacts})$ number of contacts. These result in a $I_i \sim \text{Binomial}(C_i, SAR(t - tOns_i))$ number of secondary infections. $SAR(x)$ gives the secondary attack rate as a function of days since symptom onset. This is estimated from the generation time distribution described in (Feretti et al, 2020), with the value on day x proportional to the integral of the generation time distribution between time x and $x + 1$, and scaled so the peak secondary attack rate (which occurs on the day of symptom onset) is 0.7% (Cheng et al, 2020). This is given in figure 2. Subclinical cases are assumed to

be less infectious, by a scaling factor of $reInf$ (default = 50%; Davies et al, 2020) which multiplies their value of $SAR(x)$.

These secondary infections are randomly assigned to other individuals, chosen with replacement from all individuals in quarantine. Sampling with replacement allows an individual to have contact with the same person multiple times. If an individual is infected during their stay, $statusInfected_i$ is set to 1 and $tExp_i$ is set to t , with the other infection-related variables set according to the rules described for arrivals.

Note: strictly speaking there are slightly more than 5 contacts on average, with this increasing as the number of infected individuals increases. For computational reasons, a full contact network is not generated, with this approximation a valid alternative for the small number of infections simulated.

The simulation is initialised with a fixed number of individuals, chosen to be approximately equal to the long-term average at equilibrium, none of which are assumed to be infected. A wind-in period of 50 days is used, allowing for more than 3 complete cycles of 14 days for the model to reach equilibrium (although 14 days is sufficient).

Individuals are moved to a stricter MIQ facility the day after testing positive or being detected by symptoms. They are assumed to have no contacts within this facility and are held until they are no longer infectious. Individuals that are not infected, or not detected, are released on their final day of stay $tDisch_i$ or on the day of their exemption $tExemp_i$.

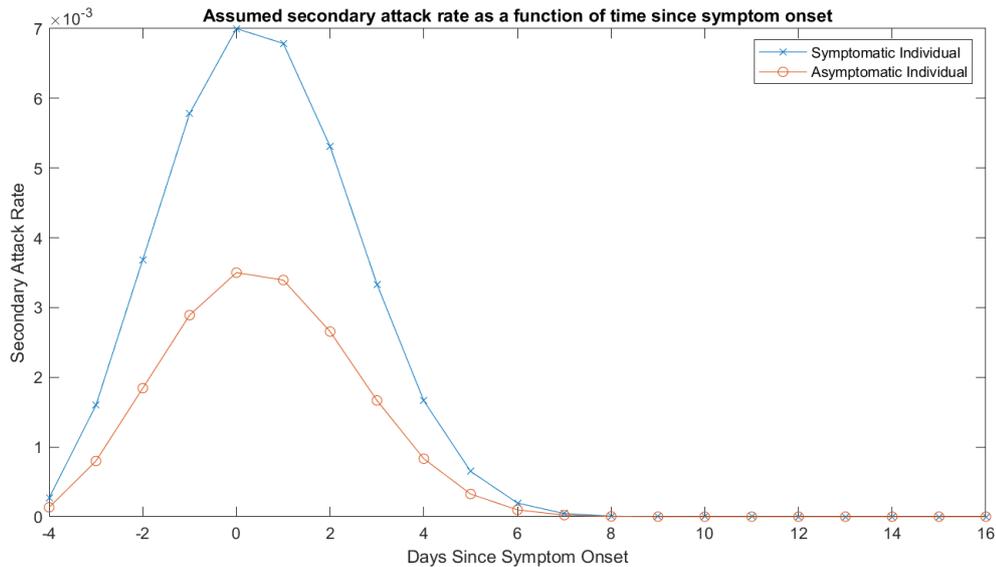


Figure 1. Assumed secondary attack rate as a function of time since symptom onset. The value at time t is proportional to the integral from t to $t + 1$ in the generation time distribution from (Feretti et al, 2020). The values are scaled so the peak SAR for symptomatic individuals is equal to that found in (Cheng et al, 2020). The values for asymptomatic individuals are assumed to be proportional to those for symptomatic individuals, scaled by a factor of $reInf$ (default = 50%).

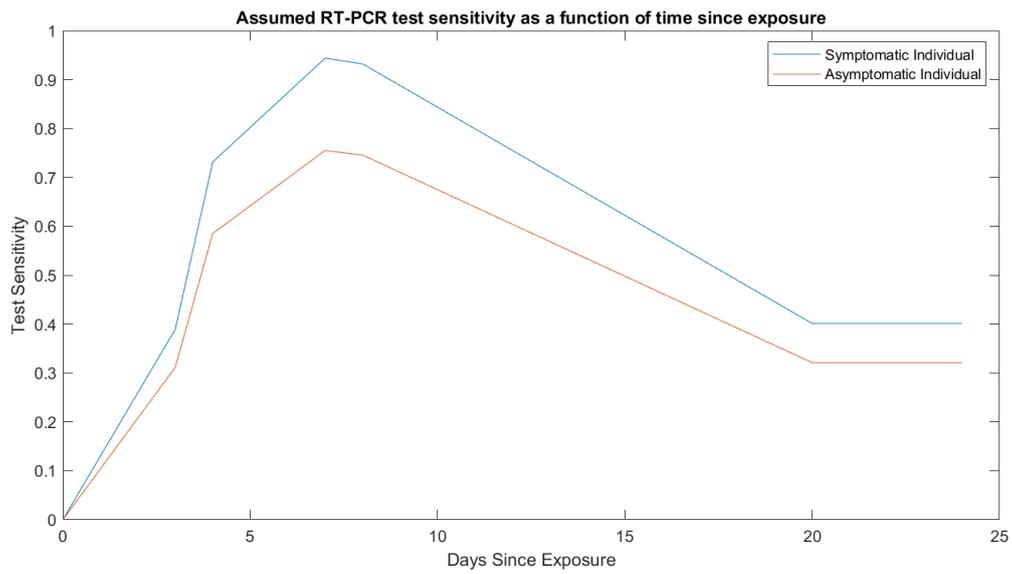


Figure 2. COVID-19 assumed test sensitivity as a function of time since exposure. Values for symptomatic individuals are linearly interpolated from those reported in (Kucirka et al, 2020). Values for asymptomatic individuals are assumed to be proportional to those for symptomatic individuals, scaled by a factor of *relSens* (default = 80%).