

Electronic Supplementary Material

Modelling the impact of travel restrictions on COVID-19 cases in Newfoundland and Labrador

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1. Model description

1. Infected individuals either: (i) will show clinical symptoms at some point during their infection (with probability $1-\pi$), or (ii) will be asymptomatic (with probability π).
2. Individuals that are pre-clinical, clinical, or asymptomatic (see Figure 1) are all infectious with different levels of infectivity given contact with a susceptible person. The infectivity of infected individuals changes depending on the number of days since infection onset and follows a Weibull distribution that is parameterized such that peak infectivity occurs approximately 5 days after the initial infection, and 90% of infections occur between 2.0 and 8.4 days after the infection onset. It is also assumed that 21 days after infection onset an individual is no longer infective. See Ferretti et al. 2020 for a justification of this assumption.
3. Individuals with asymptomatic infections are less likely than pre-clinically infected individuals to infect a susceptible person given a contact, where η_s is a coefficient that scales the infectivity of asymptomatic individuals relative to pre-clinically infected individuals.
4. Clinically infected individuals are assumed to self-isolate, which reduces their infectivity by a factor c_{iso} relative to individuals with pre-clinical infections.
5. Infected individuals that will progress to have a clinical infection have an initial period when they are pre-clinical, T_1 . This distribution is the same as the distribution for the period from the date of infection to self-isolation, and is gamma-distributed, $s \sim \Gamma(6.1, 1.7)$. Note that we let $s \approx T_1 + T_2$, where T_1 and T_2 appear in Plank et al. 2020.
6. Each infected individual j , per unit time, generates a Poisson-distributed number of new infections with a mean equal to $\lambda_j(t) \Delta t$. This mean number of secondary infections depends on the fraction of susceptible people in the population, $1 - N(t)/N_{pop}$, the type of infection the infective person has, $F_j(t)$, the infectivity of the infected individual a given number of days since the date of infection, whether the infected person is in self-isolation, and the rate of contacts between individuals in the population.

The rate of infection for the j^{th} individual (infected at the time t_j) on the time interval $(t, t+\Delta t]$ is $\lambda_j(t)\Delta t$, where

$$\lambda_j(t) = R_0 \left(1 - \frac{N(t)}{N_{pop}}\right) C(t) F_j(t) \int_0^\infty d_j(t - \tau) f_W(\tau) d\tau \quad (1)$$

and,

$$d_j(t) = \begin{cases} 1 & \text{if the } j^{th} \text{ individual became infected in the interval } (t, t + \Delta t], \\ 0 & \text{otherwise;} \end{cases} \quad (2)$$

$f_w(\tau)$ is the density of the serial-interval time, W , and $F_j(t)$ and $C(t)$ are given by,

$$F_j(t) = \begin{cases} 1.00 & \text{if the } j^{th} \text{ individual is pre-symptomatic at the time } t \\ 0.50 & \text{if the } j^{th} \text{ individual is in isolation at time } t, \\ 0.75 & \text{if the } j^{th} \text{ individual is infective-asymptomatic at the time } t. \end{cases} \quad (3)$$

and, $C(t)$, the function that accounts for public health measures is defined as,

$$C(t) = \begin{cases} 1 & \text{if } t < t_1, \\ c_1 & \text{if } t_1 \leq t < t_2, \\ c_2 & \text{otherwise,} \end{cases} \quad (4)$$

where t_1 = March 18, 2020 is the date of the declaration of the health emergency in NL, and t_2 = May 4, 2020, the date when we consider scenarios representing different contact rates between NL residents.

We performed additional simulations where the number of new infections followed a negative binomial distribution. Our results were strongly consistent with the simulations when the Poisson distribution was assumed (Figure A.3).

7. The time between an individual becoming infected and infecting another individual, the generation time, follows a Weibull distribution with a shape parameter equal to 2.83 and a scale parameter equal to 5.67 (mean value is 5 days). The infection times of all N_j secondary infections from an individual j are independent identically distributed random variables from this distribution.
8. On an interval of length Δt , the rate that infected travellers arrive and fail to self-isolate is $\lambda_v(t)\Delta t$, which follows a Poisson distribution with the parameter $\lambda_v(t)$ given as,

$$\lambda_v(t) \sim \begin{cases} 0.1 & \text{if } t < t_2, \\ 0.008 & \text{if } t \geq t_2 \text{ and } r = \text{restrictions,} \\ 0.1 & \text{if } t \geq t_2 \text{ and } r = \text{no restrictions,} \end{cases} \quad (5)$$

where $r = \text{restrictions}$ corresponds to travel restrictions, $r = \text{no restrictions}$ corresponds to no travel restrictions, and t_2 corresponds to May 4, 2020.

The model is a stochastic birth-death process where births correspond to new infections and deaths correspond to the recovery of infected individuals. The counts arise from a non-homogeneous Poisson process, and the model describes a lagged process owing to the consideration of the serial interval distribution. The model is implemented in R using Euler's method (Gardner 2009).

Definitions of the mean rates appearing in Figure 1

Susceptible individuals become infected at a mean rate, $\lambda_s(t)\Delta t$, with $\lambda_s(t) = \sum_j \lambda_j(t)$ where $\lambda_j(t)$ is given by equation 1. Infected travellers that fail to self-isolate enter the population at a rate $\lambda_v(t)$ (equation

5). At a rate, $\lambda_p(t)\Delta t$, with $\lambda_p(t) = \sum_j \gamma_j^P(t)$ individuals with pre-clinical infections develop clinical infections. Finally, both individuals with asymptomatic and clinical infections recover at rates $\lambda_A(t)\Delta t$ with $\lambda_A(t) = \sum_j \gamma_j^A(t)$ and $\lambda_C(t)\Delta t$ with $\lambda_C(t) = \sum_j \gamma_j^C(t)$, respectively. The probability of removing the j^{th} individual from the K class in the time interval $(t, t+\Delta t]$, given that this individual has not been removed before is,

$$\gamma_j^K(t) = \int_0^\infty d_j(t-\tau) \frac{f_K(\tau)}{1 - F_K(\tau)} d\tau \quad \text{for } K \in \{P, C, A\} \quad (6)$$

where $f_K(\tau)$ and $F_K(\tau)$ are the density and distribution functions for the time to removal from the K class

2. Negative binomial distribution of secondary infections

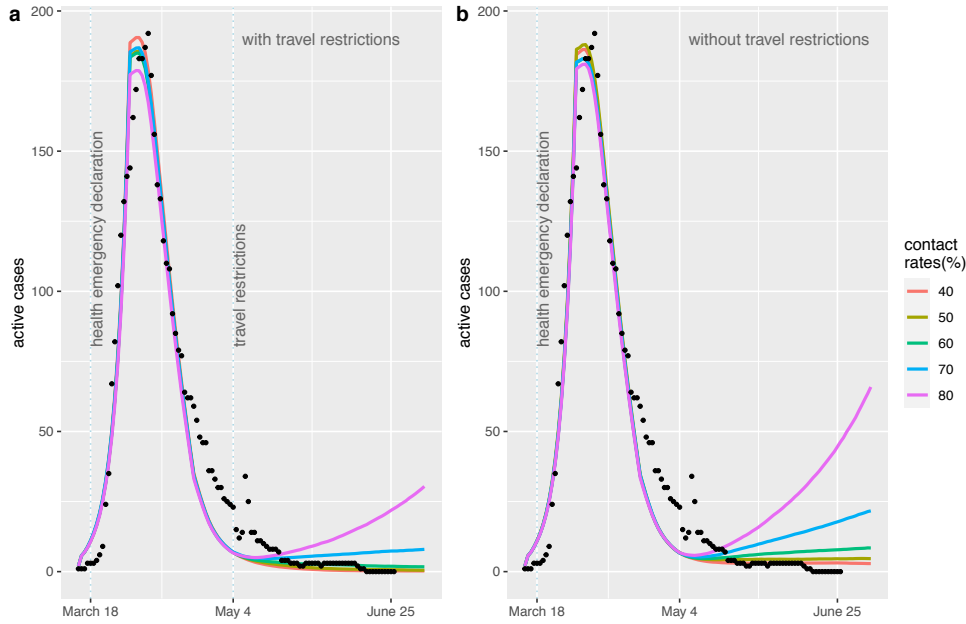


Figure A.1. We repeated our simulations assuming that the number of secondary infections followed a negative binomial distribution with $k = 0.1$ (Endo et al. 2020) rather than a Poisson distribution (see 6. of Model description in this Appendix). For the negative binomial distribution, we set $R_0 = 4.67$ so that the model predictions were consistent with the NL data from March 16th-June 26th, 2020, as shown in this figure.

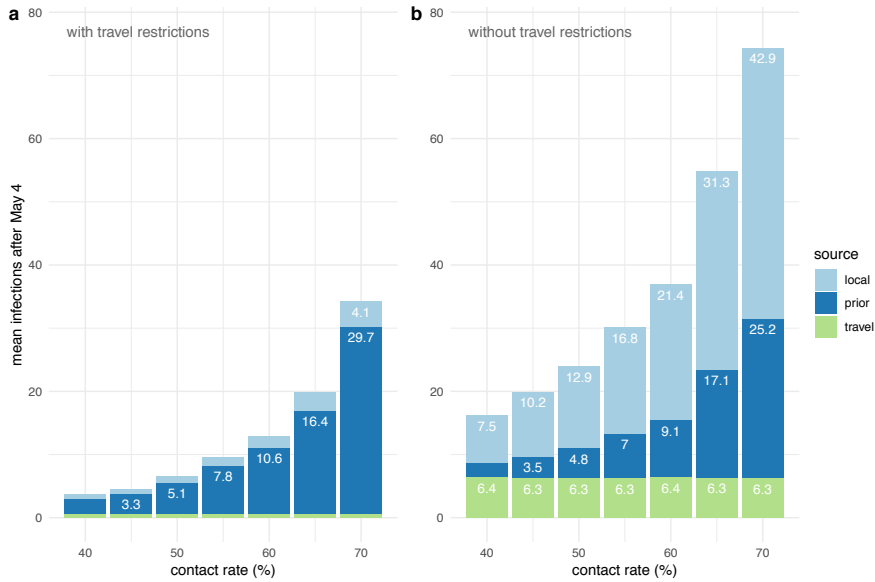


Figure A.2. We repeated our simulations assuming that the number of secondary infections followed a negative binomial distribution with $k = 0.1$ (Endo et al. 2020) rather than a Poisson distribution (see 6. of Model description in this Appendix). For the negative binomial distribution, we set $R_0 = 4.67$ so that the model predictions were consistent with the NL data from March 16th-June 26th, 2020 (Figure A.1). This figure is comparable to Figure 3, which assumed a Poisson distribution of secondary infections.

3. Model Calibration

We estimated the percentage of contacts between March 19 and May 4, 2020, relative to the pre-pandemic level as $c_1 = 30\%$. To estimate c_1 , we used model calibration, where different values of c_1 were considered and the resulting agreement with the data was observed. In Figure A.3, we show that when $c_1 = 20\%$ (red) the peak number of active cases occurs too early, and the number of active cases during the decline is under-predicted. When $c_1 = 40\%$ (Figure A.3, blue), the number of active cases before and after the peak is over-estimated. For our analysis, we used $c_1 = 30\%$ (Figure A.3, green), as this value was consistent with the epidemic data (black dots). We did not consider a formal fitting algorithm due to the long computational times associated with fitting stochastic models, because we cannot precisely estimate the other model parameters, and because Figure A.3 demonstrates that the estimated c_1 value is likely between 20 and 40%.

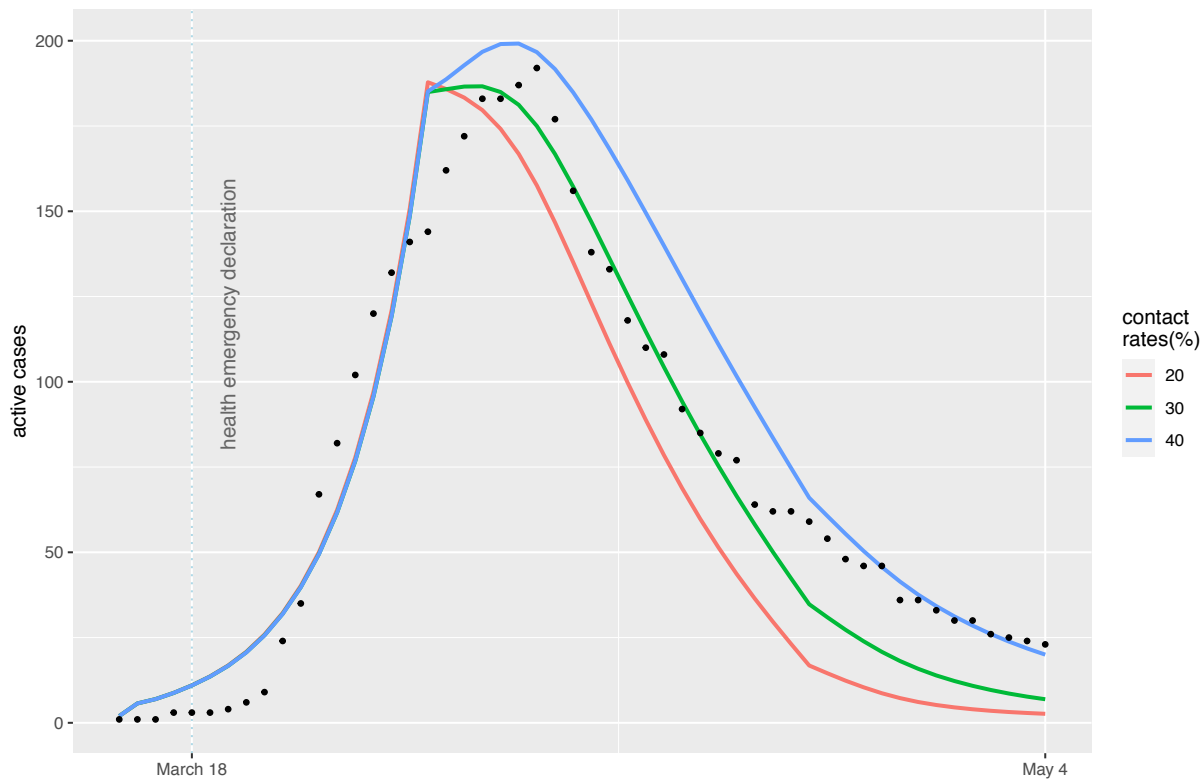


Figure A.3. Our analysis assumed the percentage of contacts between March 19 and May 4, 2020 relative to the pre-pandemic baseline was $c_1 = 30\%$ (green line). This value was estimated using model calibration and observing the agreement of the model with the epidemic data (black dots). If $c_1 = 20\%$ (red), the peak number of active cases occurs too early, and the number of active cases during the decline is under-predicted. If $c_1 = 40\%$ (blue), the number of active cases before and after the peak is over-estimated.

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