

APPENDIX

Section A: Modeling method

A1. Description

This study considered the entire population of Toronto with the “stay at home” policy (SAHP) that was enacted on Mar 12 and gradually relaxed after May 6,¹ as well as the document “A Framework for Reopening our Province” Ontario released on Apr 27.² The province gradually reopened all workplaces and public spaces. Stage 1, which began on May 19, allowed the opening of select workplaces and some small gatherings. On Jun 24, the city of Toronto entered Stage 2 of reopening, opening more workplaces and outdoor spaces, allowing gatherings of up to 10 people.¹

We divided the population into two groups: one consisting of individuals who follow SAHP (marked by a subscript q) and another consisting of individuals who do not opt for this intervention (marked by a subscript nq). Due to influences of self-protection consciousness and severity of the epidemic, people were assumed to move from one group to another with stay-at-home rate (denoted by $q(t)$) or going-out rate (denoted by $g(t)$). We noted that we omit demographic components, such as immigration, birth and natural death.

A detailed description of dynamical transmission of COVID-19 is described in the flowchart (Figure 1). Let $N_i(t)$ ($i = nq, q$) be the total number of individuals in each sub-group, nq, q , at time t . Each subpopulation was further divided into Susceptible ($S_i(t)$), Exposed ($E_i(t)$), Asymptomatic (subclinical) Infected ($A_i(t)$), Prodromal Infected (pre-symptomatic) ($I_{i1}(t)$) and Symptomatic Infected ($I_{i2}(t)$). Then the fully Isolated ($W(t)$), or Hospitalized ($H(t)$), or Recovered ($R(t)$) or Deceased ($D(t)$) are also included.

Both $A_i(t)$ and $I_{i1}(t)$ are considered to be infectious virus carriers. We assumed that individuals in $A_i(t)$ will never show symptoms, while individuals in $I_{i1}(t)$ develop into symptomatic classes ($I_{i2}(t)$) after a specified period of time. Although symptomatic and asymptomatic cases might have a different viral load, their transmission ability might differ in terms of contacts. Asymptomatic cases will maintain their routine without taking any extra precaution, resulting in having more contacts than any other symptomatic will have. We then assume that on average, their transmission is equal.

Mild symptomatic infections in classes ($I_{i2}(t)$), may choose to either isolate themselves at home (or other places). If the quarantine is respected well enough, these infections will be fully isolated ($W(t)$) and, consequently, will not contribute to the spread of the virus. Otherwise, they are still a source of infection until recovery. As the disease progresses, some mild infections ($I_{i2}(t), H(t)$) may become severe and require hospitalization. We included two further compartments: the fully isolated ($W(t)$), and the hospitalized ($H(t)$) who are severely affected. It is assumed that neither of these compartments contribute to infection transmission.

After the implementation of SAHP, the compliant people will stay at home and the number of people outside the household will decrease. Hence, we assume that the

contact rate will change with the proportion of the total number of compliant people to the total number of people.

Based on the classical SEIR framework, a household-based transmission model considering that the average family size in Toronto that is 2.4³ is proposed to describe the impact of SAHP on the development of the epidemic. In the model, we assumed the average household size is 3. Although within-household transmission is relatively strong, it only involves limited family members. To reflect this, and capture disease transmission within household members, we separated people who follow the SAHP into households. We classified those households into different types based on the individual's disease states in the household.

We explicitly modeled the transmission process between the household members in those different types of households. The number of certain types of household (eg, two susceptible 1 exposed) will change over time due to the dynamic of the epidemic in the household. The change rate of individuals in the group ($S_q(t), E_q(t), A_q(t), I_{q1}(t)$ or $I_{q2}(t)$) that follows SAHP can be calculated by the sum of the change rate of that individuals from all types of households.

The susceptible individuals in the non-compliance group were homogeneously mixed, and all individuals in a household were homogeneously mixed. Considering that an infected person quarantined at home is interacting only with family members, the number of contacts is limited, so we used the standard incidence rate in modelling.

The household following SAHP can only infect their household members and will not transmit the virus to other households. Hence for family members following SAHP, susceptible individuals ($S_q(t)$) will only be infected by infectious individuals in the home $A_q(t), I_{q1}(t)$ or $I_{q2}(t)$. When no cases are reported in a household, the family is safe and no longer involved in the transmission of COVID-19.

Every family except for those with symptomatic members has an equal opportunity to be released from quarantine after the SAHP is relaxed. Households with infected symptomatic individuals will continue to be quarantined after the SAHP is relaxed.

A2. Rates definition

The key rates on which the model is based and the dynamical models for SAHP non-compliant, SAHP compliant and isolation population are presented in this section.

- **Stay-at-home rate**

Before the government implemented SAHP on Mar 12, 2020,¹ due to the impact of self-prevention awareness and the severity of the epidemic, a small number of people would consciously stay at home, so we assume that the stay-at-home rate is a very small constant, which we express as

$$q(t) = q, \quad t \leq T_1,$$

where T_1 is the time when the SAHP is implemented, and q is the average daily stay-at-home rate before the policy is put into action.

Appendix 1, as supplied by the authors. Appendix to: Yuan P, Li J, Aruffo E, et al. Efficacy of a "stay-at-home" policy on SARS-CoV-2 transmission in Toronto, Canada: a mathematical modelling study. *CMAJ Open* 2022. doi: 10.9778/cmajo.20200242.

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After the SAHP was implemented, some people chose to stay at home based on their own behavior and their knowledge of the epidemic. We denote the maximum compliance rate (Q_1) as the maximum proportion of the number of people in the group that will carry out SAHP, which is used to reflect the degree of the behavioral tendency of the population to change their original daily lifestyle and accept the SAHP under the requirements of prevention and control policies after the outbreak. The implementation of SAHP will directly affect the stay-at-home rate

$$q(t) = q_q(Q_1, t), \quad t > T_1.$$

Then,

$$q(t) = \begin{cases} q, & t \leq T_1, \\ q_q(Q_1, t), & t > T_1. \end{cases}$$

where $q_q(t)$ is the daily stay-at-home rate after SAHP implementation. In order to better reflect the impact of the SAHP on the epidemic in the early stage of implementation, we assume the transition rate of SAHP compliance in each group is a random variable X_i ($i=1 \dots 5$), denotes the different groups $S_{nq}, E_{nq}, A_{nq}, I_{nq1}, I_{nq2}$ which assumed to follow the exponential distribution⁴ and X_i is independent and identically distributed. We denote τ is the time from SAHP enacted to the uptake of individuals and then the transition rate of SAHP compliance in five groups ($X = X_1 + X_2 + X_3 + X_4 + X_5 = 1/\tau$) is also a random variable. Hence, X follows a Gamma distribution,

$$\begin{aligned} & X \sim \text{Gamma}(k, \theta) \\ \text{with } f(X) &= \begin{cases} \frac{1}{\Gamma(k)\theta^k} X^{k-1} \exp\left(-\frac{X}{\theta}\right), & X \geq 0, \\ 0, & X < 0. \end{cases} \end{aligned}$$

where $k = 5, \Gamma(k) = \int_0^{+\infty} X^{k-1} e^{-X} dX, k > 0$.

The expectation of $X = \bar{X} = k * \theta = 1/\Delta T_Q$ ($1/\Delta T_Q$ is the average transition rate of SAHP compliance), and $f(\tau)$ is the probability that the average time from SAHP enacted to the uptake of five groups is τ days. Then we derived the expression of $q_q(t)$ by the following process.

The total population that may follow SAHP of Toronto at T_1 is $P_1 = S_{nq}(T_1) + A_{nq}(T_1) + E_{nq}(T_1) + I_{nq1}(T_1) + I_{nq2}(T_1)$. The number of people who uptakes SAHP on $T_1 + \tau$ days was $\Delta P_1(T_1 + \tau) = Q_1 * P_1 * f(\tau) = (Q_1 * f(\tau)) * P_1$. Let $q_1(T_1 + \tau)$ be the daily stay-at-home rate on day $T_1 + \tau$, then $q_1(T_1 + \tau) = Q_1 * f(\tau)$. And it satisfies $\int_0^{\infty} q_1(T_1 + \tau) d\tau = Q_1$.

We also assume that each group has the same daily stay-at-home rate, $q_q(T_1 + \tau)$, which is the daily stay-at-home rate of the people who began to stay at home on day $T_1 + \tau$. Then the number of people newly stay-at-home on that day is

$$q_q(T_1 + \tau) \left(S_{nq}(T_1 + \tau) + A_{nq}(T_1 + \tau) + E_{nq}(T_1 + \tau) + I_{nq1}(T_1 + \tau) + I_{nq2}(T_1 + \tau) \right).$$

The newly stay-at-home number on day $T_1 + \tau$ ($\tau > 0$) is equal to the number of people conducting SAHP on that day, i.e.,

$$q_q(T_1 + \tau) \left(S_{nq}(T_1 + \tau) + A_{nq}(T_1 + \tau) + E_{nq}(T_1 + \tau) + I_{nq1}(T_1 + \tau) + I_{nq2}(T_1 + \tau) \right).$$

$$+I_{nq2}(T_1 + \tau) = \Delta P(T_1 + \tau).$$

Hence, we have

$$q_q(T_1 + \tau) = \frac{Q_1 * P_1 * f(\tau)}{S_{nq}(T_1 + \tau) + A_{nq}(T_1 + \tau) + E_{nq}(T_1 + \tau) + I_{nq1}(T_1 + \tau) + I_{nq2}(T_1 + \tau)}, \tau > 0.$$

Let $t = T_1 + \tau$, then we obtained the expression of $q_q(t)$, where

$$q_q(t) = \frac{Q_1 * P_1 * f(t - T_1)}{S_{nq}(t) + A_{nq}(t) + E_{nq}(t) + I_{nq1}(t) + I_{nq2}(t)}, t > T_1.$$

• Quarantined rate

According to the relative policies of Toronto, people who are detected to be COVID-19 positive need to stay at home and self-isolate for 14 days.⁵ Combined with the flowchart shown in Figure 2, there are three different ways to allocate infectious patients: to be hospitalized, to isolate at home, or to isolate in a place other than home. Due to the strengthening effect of testing, the stay-at-home rate of the infected cases with symptoms is much higher than others. Here, we modify the quarantined rate of I_{nq2} (separately rewritten as $q_{nq2}(t)$) to be $q_{nq2}(t) = q(t) + \varepsilon d_c(t)$, where $d_c(t)$ is the completion rate of diagnosis of all symptomatic infections. $d_c(t)$ obtained from the episode data and the reported data shown in Section 2, and ε is an adjustment parameter to describe the impact of testing on the quarantined rate of I_{nq2} . Here, it is assumed that $q_{nq2}(t) = q(t)$ if there is no testing.

• Going out rate

Let T_2 ($T_2 > T_1$) be the day on which the SAHP is announced to be relaxed. That is, the individuals in group of S_q, E_q, A_q, I_{q1} may go outside home after that day. But households with infected symptomatic individuals will continue to be quarantined after the SAHP is relaxed. Similar to the formula derive process of $q(t)$, we now define $g(t)$, the proportion of households that are not stay-at-home versus all households, which is given by

$$g(t) = \begin{cases} 0, & t \leq T_1, \\ g, & T_1 \leq t \leq T_2, \\ \frac{G * h(t - T_2) * (S_q(T_2) + A_q(T_2) + E_q(T_2) + I_{q1}(T_2))}{S_q(t) + A_q(t) + E_q(t) + I_{q1}(t)}, & t > T_2, \end{cases}$$

where g is a small positive constant, G is the maximum proportion of the population who will not continue to stay at home compared to the total size of the stay-at-home population at time T_2 ,

$$h(\epsilon) = \begin{cases} \frac{1}{\Gamma(k)\theta^k} \epsilon^{k-1} \exp\left(-\frac{\epsilon}{\theta}\right), & \epsilon \geq 0, \\ 0, & \epsilon < 0. \end{cases}$$

$k = 4$ (individuals in 4 different groups S_q, E_q, A_q, I_{q1} , can go out after SAHP relaxed) and the expectation of $\epsilon = \Delta T_G$, where ΔT_G is the average time from SAHP relaxation to going outside for all people who stay at home (except those with symptoms).

A3. Models

SAHP compliant population

According to the infection and development process of the disease in the human body, at time t , an individual in a household can belong to one of the following categories: $S_q(t)$, $E_q(t)$, $A_q(t)$, $I_{q1}(t)$, $I_{q2}(t)$, $H(t)$, $W(t)$, $R(t)$ and $D(t)$. We assumed that all death comes from hospitalized cases so that $D(t)$ is already considered in $H(t)$. To avoid the duplicate calculation, we have 8 different disease states in the household. Corresponding to each disease class, we assign the number of individuals in each household to be i, j, k, l, m, x, y, z , respectively, and limit households to a size of n such that $n = i + j + k + l + m + x + y + z$. Therefore, each household at most consists of n different categories of individuals. Based on the classification and combination of individuals in households, all possible types of households in Toronto are C_{8+n-1}^n .

For each household type, the dynamics are determined by nine processes: within-household transmission; disease progression from Exposed to Asymptomatic subclinical infection or Prodromal Infection; disease progression from Prodromal Infection to Symptomatic Infected; recovery from Asymptomatic subclinical infection; recovery from Symptomatic Infected; hospitalization of Symptomatic Infected; isolation of Symptomatic Infected; and newly entered stay-at-home; the newly going out. Then the variation of the number of households $P_{i,j,k,l,m,x,y,z}$ with respect to time t can be given by

$$\begin{aligned} \frac{dP_{i,j,k,l,m,x,y,z}(t)}{dt} = & \beta_q [-i(k+l+m)P_{i,j,k,l,m,x,y,z}(t) + (i+1)(k+l+m)P_{i+1,j-1,k,l,m,x,y,z}(t)] \\ & + \frac{1}{\tau_1} [-jP_{i,j,k,l,m,x,y,z}(t) + (1-a)(j+1)P_{i,j+1,k-1,l,m,x,y,z}(t) + a(j \\ & + 1)P_{i,j+1,k,l-1,m,x,y,z}(t)] + \frac{1}{\tau_2} [-lP_{i,j,k,l,m,x,y,z}(t) + (l \\ & + 1)P_{i,j,k,l+1,m-1,x,y,z}(t)] \\ & + \gamma_a [-kP_{i,j,k,l,m,x,y,z}(t) + (k+1)P_{i,j,k+1,l,m,x,y,z-1}(t)] + \gamma_m [-mP_{i,j,k,l,m,x,y,z}(t) \\ & + (m+1)P_{i,j,k,l,m+1,x,y,z-1}(t)] \\ & + \theta_h [-mP_{i,j,k,l,m,x,y,z}(t) + (m+1)P_{i,j,k,l,m+1,x-1,y,z}(t)] \\ & + \theta_i [-mP_{i,j,k,l,m,x,y,z}(t) + (m+1)P_{i,j,k,l,m+1,x,y-1,z}(t)] + \Delta P_{i,j,k,l,m,x,y,z}(t) \\ & - g(t)P_{i,j,k,l,m,x,y,z}(t), \end{aligned}$$

where $P_{i,j,k,l,m,x,y,z}(t) \geq 0$ should be satisfied, $g(t)P_{i,j,k,l,m,x,y,z}(t)$ should be ignored for $m \neq 0$, and $\Delta P_{i,j,k,l,m,x,y,z}(t)$ is the number of new stay-at-home households with i susceptible, j exposed, k asymptomatic (subclinical) infected, l prodromal infected, m symptomatic infected, x hospitalized, y isolated and z removed members,

$$\Delta P_{i,j,k,l,m,x,y,z}(t) = \left[\frac{1}{n} (q(t) (S_{nq}(t) + E_{nq}(t) + A_{nq}(t) + I_{nq1}(t)) + q_{nq2}(t) I_{nq2}) \right] F,$$

where $[\cdot]$ is an integral function to return the value of a number rounded downwards to the nearest integer and F is the probability of each type of household newly entered stay-at-home state.

When $n = 2$,

$$F = \begin{cases} \frac{n_{ii}(n_{ii} - 1)}{A_{n_q}^n}, ii = 1,2,3,4,5, & \text{if one of } i, j, k, l, m \text{ is not } 0, \\ \frac{n_{jj}n_{ii}}{A_{n_q}^n}, ii, jj = 1,2,3,4,5, ii \neq jj, & \text{if two of } i, j, k, l, m \text{ is not } 0, \\ 0, & \text{others.} \end{cases}$$

When $n = 3$,

$$F = \begin{cases} \frac{n_{ii}(n_{ii} - 1)(n_{ii} - 2)}{A_{n_q}^n}, ii = 1,2,3,4,5, & \text{if one of } i, j, k, l, m \text{ is not } 0, \\ \frac{C_n^2 n_{jj} n_{ii} (n_{ii} - 1)}{A_{n_q}^n}, ii, jj = 1,2,3,4,5, ii \neq jj, & \text{if two of } i, j, k, l, m \text{ is not } 0, \\ \frac{A_n^3 n_{ii} n_{jj} n_{kk}}{A_{n_q}^n}, ii, jj, kk = 1,2,3,4,5, & \text{if three of } i, j, k, l, m \text{ is not } 0, \\ 0, & \text{others,} \end{cases}$$

with $n_q = \sum_{ii=1}^5 n_{ii}$, $n_q \geq n$, $n_1 = [q(t)S_{n_q}(t)]$, $n_2 = [q(t)E_{n_q}(t)]$, $n_3 = [q(t)A_{n_q}(t)]$, $n_4 = [q(t)I_{n_q1}(t)]$, $n_5 = [q_{n_q2}(t)I_{n_q2}]$.

With the above, we have the model describing the dynamics of the groups with stay-at-home and isolation as

$$\begin{cases} \frac{dS_q(t)}{dt} = \sum_{i,j,k,l,m,x,y,z} i \frac{dP_{i,j,k,l,m,x,y,z}(t)}{dt}, \\ \frac{dE_q(t)}{dt} = \sum_{i,j,k,l,m,x,y,z} j \frac{dP_{i,j,k,l,m,x,y,z}(t)}{dt}, \\ \frac{dA_q(t)}{dt} = \sum_{i,j,k,l,m,x,y,z} k \frac{dP_{i,j,k,l,m,x,y,z}(t)}{dt}, \\ \frac{dI_{q1}(t)}{dt} = \sum_{i,j,k,l,m,x,y,z} l \frac{dP_{i,j,k,l,m,x,y,z}(t)}{dt}, \\ \frac{dI_{q2}(t)}{dt} = \sum_{i,j,k,l,m,x,y,z} m \frac{dP_{i,j,k,l,m,x,y,z}(t)}{dt}, \end{cases}$$

where all parameters are positive, the interpretation of the variables and parameters are summarized in Table 2.

SAHP non-compliant population

$$\begin{cases} \frac{dS_{n_q}(t)}{dt} = -\beta_{n_q} c_0 e^{-\mu(1-N_{n_q}/P)} (A_{n_q} + I_{n_q1} + I_{n_q2}) \frac{S_{n_q}}{N_{n_q}} - q(t)S_{n_q} + g(t) \sum_{i,j,k,l,m=0,x,y,z} iP_{i,j,k,l,m,x,y,z}(t), \\ \frac{dE_{n_q}(t)}{dt} = \beta_{n_q} c_0 e^{-\mu(1-N_g/P)} (A_{n_q} + I_{n_q1} + I_{n_q2}) \frac{S_{n_q}}{N_{n_q}} - \frac{1}{\tau_1} E_{n_q} - q(t)E_{n_q} + g(t) \sum_{i,j,k,l,m=0,x,y,z} jP_{i,j,k,l,m,x,y,z}(t), \\ \frac{dA_{n_q}(t)}{dt} = (1-a) \frac{1}{\tau_1} E_{n_q} - \gamma_a A_{n_q} - q(t)A_{n_q} + g(t) \sum_{i,j,k,l,m=0,x,y,z} kP_{i,j,k,l,m,x,y,z}(t), \\ \frac{dI_{n_q1}(t)}{dt} = a \frac{1}{\tau_1} E_{n_q} - \frac{1}{\tau_2} I_{n_q1} - q(t)I_{n_q1} + g(t) \sum_{i,j,k,l,m=0,x,y,z} lP_{i,j,k,l,m,x,y,z}(t), \\ \frac{dI_{n_q2}(t)}{dt} = \frac{1}{\tau_2} I_{n_q1} - q_{n_q2}(t)I_{n_q2} - \theta_h I_{n_q2} - \theta_i I_{n_q2} - \gamma_m I_{n_q2}, \end{cases}$$

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where $N_{nq}(t) = S_{nq}(t) + A_{nq}(t) + E_{nq}(t) + I_{nq1}(t) + I_{nq2}(t)$, $P_{i,j,k,l,m,x,y,z}$ is the number of households with i susceptible, j exposed, k asymptomatic (subclinical) infection, l infectious without no symptoms, m infected with symptoms, x hospitalized, y isolated and z recovered members. The contact rate is $C = c_0 e^{-\mu(1-N_{nq}/P)}$, which will change with the proportion of the total number of non-compliant population to the total population. All parameters are positive, and the interpretation of other variables and parameters are given in Table 2.

Other compartment

The whole SAHP model consists the SAHP compliant and non-compliant population model, as well as the following equations

$$\begin{cases} \frac{dH(t)}{dt} = \theta_h(I_{nq2} + I_{q2}) + \sigma W - (\gamma + d)H, \\ \frac{dW(t)}{dt} = \theta_i(I_{nq2} + I_{q2}) - \gamma_m W - \sigma W, \\ \frac{dR(t)}{dt} = \gamma H + \gamma_m(I_{nq2} + I_{q2} + W) + \gamma_a(A_{nq} + A_q), \\ \frac{dD(t)}{dt} = dH. \end{cases}$$

All parameters are positive, and the interpretation of other variables and parameters are given in Table 2.

Model without SAHP

When there is no SAHP, the stay-at-home rate and going out rate is equal to 0. There is no group of the compliant population. Hence our model is simplified as follows

$$\begin{cases} \frac{dS_{nq}(t)}{dt} = -\beta_{nq} c_0 (A_{nq} + I_{nq1} + I_{nq2}) \frac{S_{nq}}{N_{nq}}, \\ \frac{dE_{nq}(t)}{dt} = \beta_{nq} c_0 (A_{nq} + I_{nq1} + I_{nq2}) \frac{S_{nq}}{N_{nq}} - \frac{1}{\tau_1} E_{nq}, \\ \frac{dA_{nq}(t)}{dt} = (1 - a) \frac{1}{\tau_1} E_{nq} - \gamma_a A_{nq}, \\ \frac{dI_{nq1}(t)}{dt} = a \frac{1}{\tau_1} E_{nq} - \frac{1}{\tau_2} I_{nq1}, \\ \frac{dI_{nq2}(t)}{dt} = \frac{1}{\tau_2} I_{nq1} - q_{nq2}(t) I_{nq2} - \theta_h I_{nq2} - \theta_i I_{nq2} - \gamma_m I_{nq2}, \\ \frac{dH(t)}{dt} = \theta_h I_{nq2} + \sigma W - (\gamma + d)H, \\ \frac{dW(t)}{dt} = \theta_i I_{nq2} - \gamma_m W - \sigma W, \\ \frac{dR(t)}{dt} = \gamma H + \gamma_m (I_{nq2} + W) + \gamma_a A_{nq}, \\ \frac{dD(t)}{dt} = dH, \end{cases}$$

As there is no SAHP, the population with subscript nq represents the total populations.

Interpretation of all parameters and variables are given in Table 2.

Section B: Reproductive number and risk index calculations

B1. Basic reproduction number

The basic reproduction number R_0 is estimated using exponential growth method⁶ (EG) based on case data by episode date.

$$R_0 = \frac{1}{M(-r)},$$

where M is the moment generating function ($M = (1 + r\theta)^{-k}$, $\text{Gamma}(k, \theta)$) of the generation time distribution and the discretized distribution of serial interval (Gamma distribution, with mean of 7.5, stand deviation 3.4⁷) were used in the estimation. r is the exponential growth rate, defined by the per capita change in number of new cases per unit of time. The exponential growth time period was chosen based on R-square (goodness of fit) statistic. The computation is conducted in R software with R0⁸ package.

B2. Effective reproduction number

The effective reproduction number R_t is also estimated by^{9,10}

$$R_t = \frac{I_t}{\sum_{j=1}^t p_j I_{t-j}},$$

where I_t is the new cases on day t and p_j is the discretized distribution of serial interval, assuming a Gamma distributed serial interval of 7.5 days (standard deviation 3.4 days⁷). The computation is conducted in R software with EpiEstim¹⁰ package.

B3. Risk index after reopening

We define a novel risk index R_{reopen} as,

$$R_{reopen} = c_0 \beta_{nq} \left(\frac{1-a}{\gamma_a} + a \left(\tau_2 + \frac{1}{\gamma_m + \theta_h + \theta_i + q_{nq2}} \right) \right)$$

to evaluate the risk of reopening by calculating the reproduction number applying next generation matrix¹¹ under the model without SAHP. The parameters descriptions are given in Table 3.

We can firstly calculate the disease-free equilibrium point $E_0(S_{nq}, 0, 0, 0, 0, 0, 0, 0, 0)$ and then define the vector F and V by applying the next generation matrix method¹¹ where

$$F = (\beta_{nq} c_0 (A_{nq} + I_{nq1} + I_{nq2}), 0, 0, 0, 0, 0, 0, 0, 0),$$

$$V = \left(\frac{1}{\tau_1} E_{nq}, \gamma_a A_{nq} - (1-a) \frac{1}{\tau_1} E_{nq}, \frac{1}{\tau_2} I_{nq1} - a \frac{1}{\tau_1} E_{nq}, (\theta_h + \theta_i + \gamma_m) I_{nq2} - \frac{1}{\tau_2} I_{nq1}, (d + \gamma) H - \theta_h I_{nq2} - \sigma W, (\sigma + \gamma_m) W - \theta_i I_{nq2} \right).$$

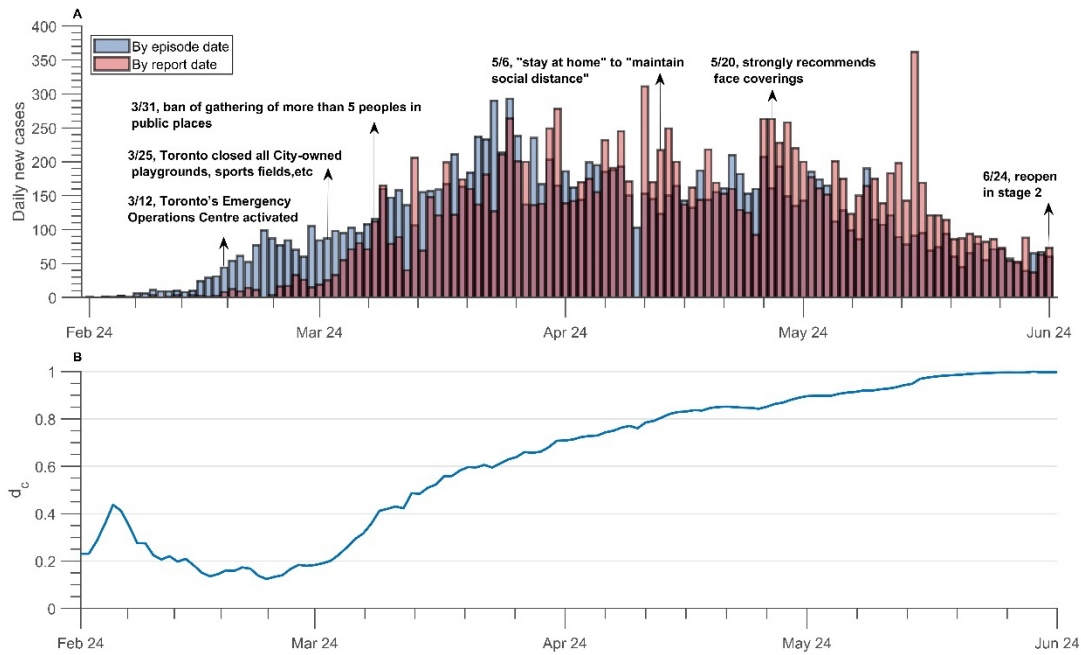
And calculate the Jacobian matrix of these two vectors at the disease-free equilibrium point respectively, and denoted by \mathcal{F} , and \mathcal{V} .

$$\mathcal{F} = \begin{pmatrix} 0 & c_0 \beta_{nq} & c_0 \beta_{nq} & c_0 \beta_{nq} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

$$\mathcal{V} = \begin{pmatrix} \frac{1}{\tau_1} & 0 & 0 & 0 & 0 & 0 \\ -\frac{1-a}{\tau_1} & \gamma_a & 0 & 0 & 0 & 0 \\ -\frac{a}{\tau_1} & 0 & \frac{1}{\tau_2} & 0 & 0 & 0 \\ 0 & 0 & -\frac{1}{\tau_2} & q_{nq2} + \gamma_m + \theta_h + \theta_i & 0 & 0 \\ 0 & 0 & 0 & -\theta_h & d + \gamma & -\sigma \\ 0 & 0 & 0 & -\theta_i & 0 & \sigma + \gamma_m \end{pmatrix}.$$

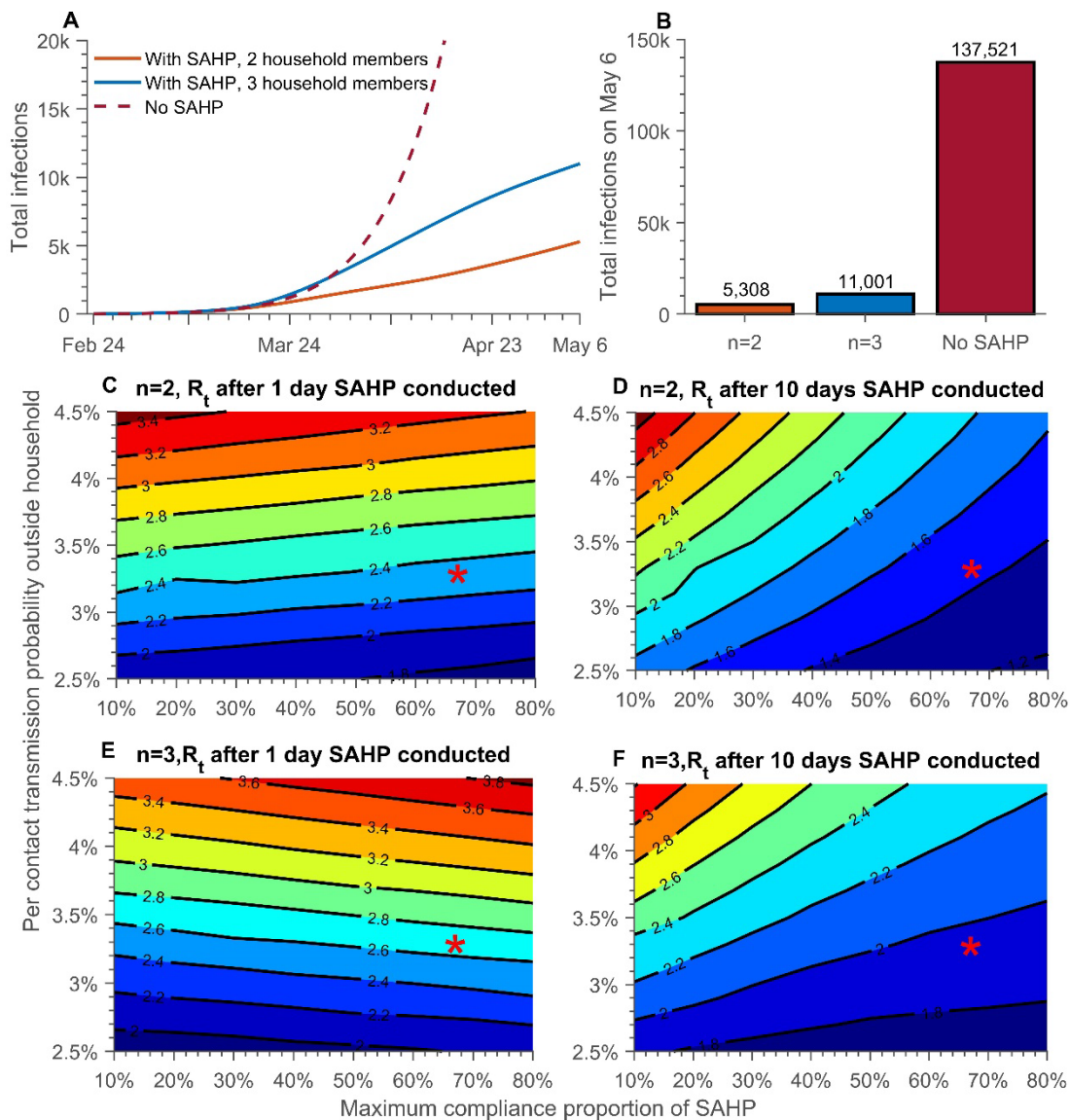
Then R_{reopen} is defined as the spectral radius of the matrix $\mathcal{F}\mathcal{V}^{-1}$.

Section C Figure 1: COVID-19 cases in Toronto by report date and episode date.



Caption (A) The major policies¹ enacted to control the epidemic and the daily new case of infection by episode date¹² and first report date¹³; (B) The change of symptomatic diagnosis' completion ratio (d_c) over time for the city of Toronto from Feb 24 to Jun 24, 2020.

Section C Figure 2: Effect of SAHP and different average household size.



Caption (A) The cumulative infection over time from Feb 24 to May 6 and (B) cumulative infection on May 6, without SAHP (dark red) and with SAHP when average household size is 2 ($n = 2$, orange) and 3 ($n = 3$, blue).

Contour plot of effective reproduction number (R_t) with different probability of transmission per contact outside household and maximum compliance proportion of SAHP (C) one day after SAHP conducted, $n = 2$; (D) ten days after SAHP conducted, $n = 2$; (E) one day after SAHP conducted, $n = 3$; (F) after ten days after SAHP conducted, $n = 3$.

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