

A comprehensive introduction to mathematical modelling of COVID-19

August 2022

Researchers and supervisor

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Novelty

- 1 Introduction of Commutation matrix into the mathematical modelling of infectious disease.
- 2 A more deliberate usage of CoMix contact matrix.
- 3 Using MLP to predicate the population mobility, thus the season-specific feature is more pronounced.

A compartmental model

The population is divided into four (mutually exclusive) states (compartments).

Susceptibles (S)

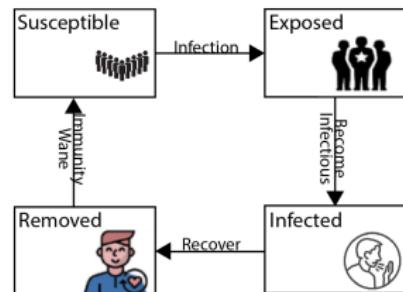
Exposed (E)

Infected (I)

Removed (R)

In real world, these quantities are natural numbers (there can't be 3.5 people!).

However, in our model, we use non-negative real number $\mathbb{R}_{\geq 0}$ for the ease of computation.



Terminologies - general

Susceptibles (S):

The "healthy" individuals.

People that are susceptible to the disease (who might be infected).

Exposed (E):

The "carrier" of the virus.

People who was infected by the virus, but are not yet transmissible (can't infect others).

Infected (I):

People who are infected by the virus, and are transmissible (can infect others).

Removed (R):

People who recovered from the disease or deceased due to the disease.

These quantities are constantly changing, but their sum is constant.

Terminologies - cont.

Population (P):

Total number of population within an area.

$$P = S + E + I + R$$

Assumed to be constant throughout a pandemic (i.e, no new born, no natural death)

Terminologies - cont.

There are some additional information to describe the transmission of a disease mathematically, including:

Infection rate (infectiousness): β

This quantity describes how likely an susceptible individual become infected per contact with infected individuals.

Rate of progression from exposed to infectious: σ

How fast an exposed individual turns into infected state.

Recovery rate: γ

How fast an infected individual recover/decease.

Note that σ and γ are not quantities! They are probability functions (tells the probability where an individual turns from exposed to infected on a day, but note all exposed individuals will become infected so it's a probability function!).

Basic ideas

In our model, we treat these quantities as C^1 (derivative exists and continuous) functions regarding time, as

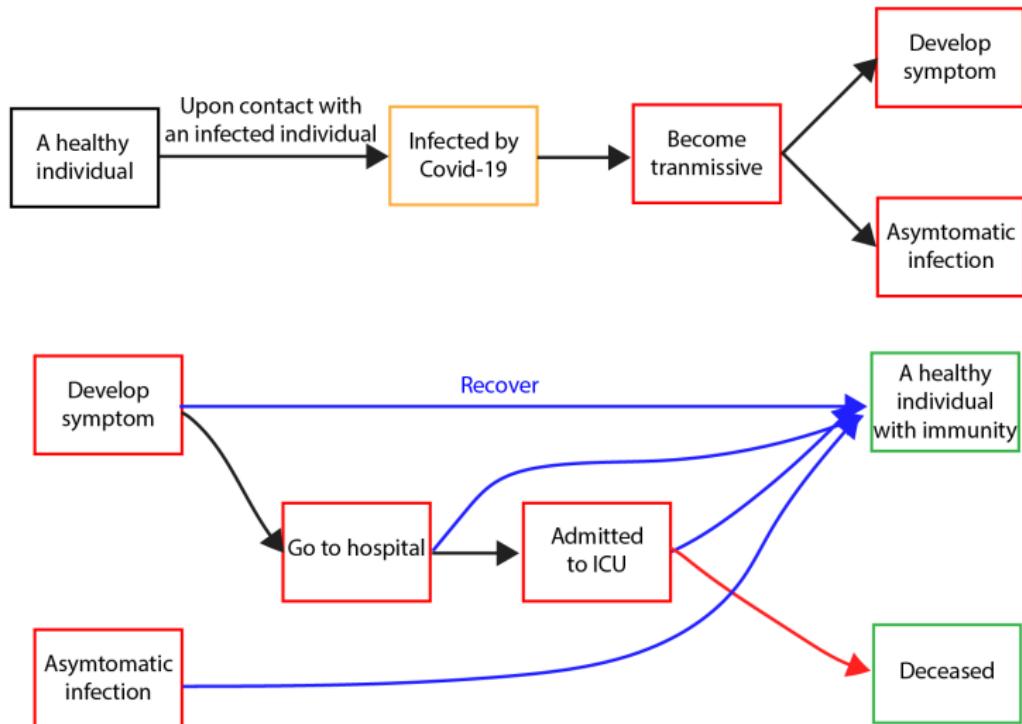
$$\begin{cases} P : \text{datetime} \rightarrow \mathbb{R}_{\geq 0}, P(t) = c \text{ where } c \text{ is a constant} \\ S : \text{datetime} \rightarrow \mathbb{R}_{\geq 0}, S(t) \in C^1 \\ E : \text{datetime} \rightarrow \mathbb{R}_{\geq 0}, E(t) \in C^1 \\ I : \text{datetime} \rightarrow \mathbb{R}_{\geq 0}, I(t) \in C^1 \\ R : \text{datetime} \rightarrow \mathbb{R}_{\geq 0}, R(t) \in C^1 \end{cases}$$

Where, at **any time**, we have:

$$c = P(t) = S(t) + E(t) + I(t) + R(t) \quad (1)$$

$$0 = dP(t) = dS(t) + dE(t) + dI(t) + dR(t) \quad (2)$$

Our model - COVID-19



Terminologies - COVID-19

COVID-19 is a bit tougher to deal with, after infection, there are **asymptomatic patients**.

In this model, we call them "**subclinical cases**" (I_s).

For those who develops clinical symptoms, we call then "**clinical cases**" (I_c).

Furthermore, we have the intuitive equality:

$$I = I_s + I_c \tag{3}$$

Subclinical cases does not have obvious symptoms (i.e. coughing, fever), and are less infectious (approx. 50 % less infectious).

Terminologies - COVID-19

Severe COVID-19 cases may lead to death, thus we may also want to track specific people who **deceased (D)** from COVID-19 and who survived and **recovered (r)**. Also, intuitively, we have:

$$R = D + r \quad (4)$$

$$\forall t, \quad R(t) = D(t) + r(t) \quad dR(t) = dD(t) + dr(t) \quad (5)$$

The naïve model - $S \rightarrow E$

Let $\Delta_{1day}E$ denote to the number of new exposed cases in a day (newly infected), then it is intuitive to derive the following equality:

$$\Delta_{1day}E := E(t+1) - E(t) = \bar{c}\beta I \quad (6)$$

Where \bar{c} denotes to the average number of contacts made between the **infected** and **susceptibles** in a day, and β denotes to the **infection rate**.

Then, for example we have an average infected individual makes 20 contacts with susceptible population a day, and 10% of which are effective. Then, we have $\bar{c} = 20$, $\beta = 0.1$, $I = 10$, thus

$$\Delta_{1day}E = 20 \times 0.1 \times 10 = 20$$

The naïve model - $S \rightarrow E$ - cont.

Nevertheless, recall that there are **subclinical cases of COVID-19**, thus we have the following equality

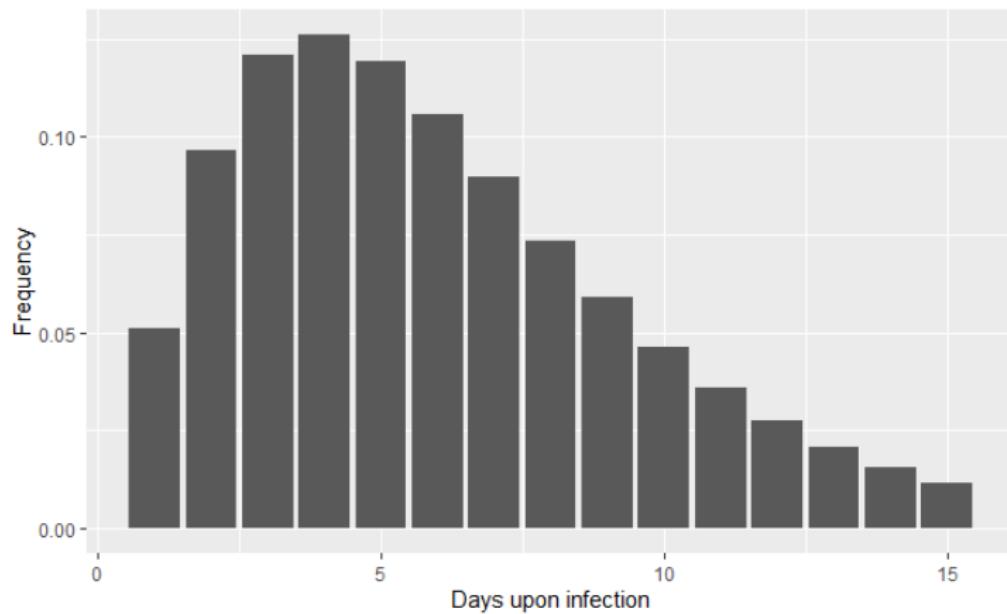
$$\Delta_{1day}E = \bar{c}\beta I_c + 0.5\bar{c}\beta I_s \quad (7)$$

Then, again we assume the same average infectiousness and average contacts as above, but now 5 of the infected individuals are subclinical, thus

$$\Delta_{1day}E = 20 \times 0.1 \times 5 + 0.5 \times 20 \times 0.1 \times 5 = 15$$

The naïve model - $E \rightarrow I$

Unlike the transition from $S \rightarrow E$, $E \rightarrow I$ is spontaneous. In other words, we describe the process of an exposed individual turning into an infected one by a probability function $\sigma : \text{datetime} \rightarrow [0, 1]$, where $\sigma(t)$ looks like this:



The naïve model - $E \rightarrow I$

Then, we can now compute the number of cases that are officially infected by the virus, using **convolutional function**, where t is the date of today.

$$\Delta_{1day}I = \sum_{d \leq t} E_d \sigma(t - d)$$

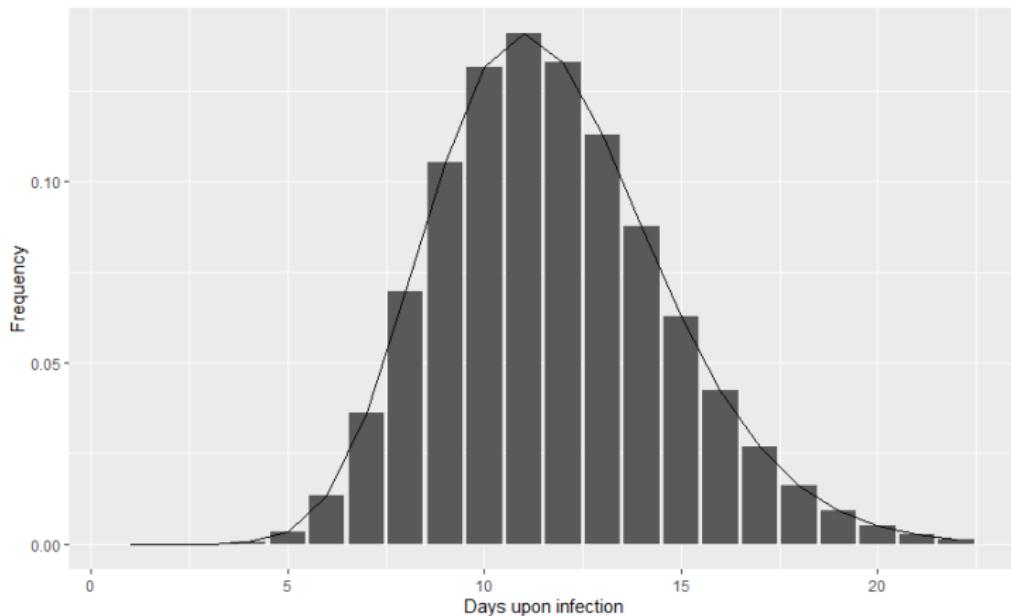
Essentially, let's assume that 50% of the exposed individuals turns into infected state 2 days since exposure, and 50% turns on the 3rd day, then we have:

$$\begin{aligned}\Delta_{1day}I &= 0 \times E_{today} + 0 \times E_{1daysago} + 0.5 \times E_{2daysago} \\ &\quad + 0.5 \times E_{3daysago} + 0 \times E_{4daysago} + \underbrace{\dots}_{=0}\end{aligned}$$

Note that people who turned into the infected state should be automatically **removed from the exposed state**. That's why we used **increment, ΔE , not dE** . ye

The naïve model - $I \rightarrow R$

Similarly, this is a probability function $\gamma : \text{datetime} \rightarrow [0, 1]$ as well, like:



The naïve model - $I \rightarrow R$

Similarly, we have:

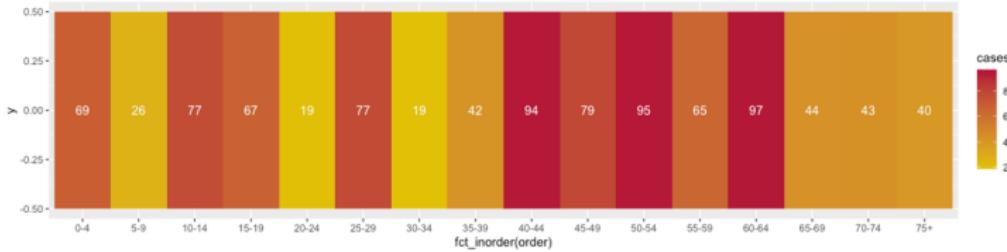
$$\Delta_{1day}R = \sum_{d \leq t} I_d \gamma(t - d)$$

Our model

Our model gives a more detailed description of the transmission of COVID-19. For each given area (**county**), we have the following epidemiological parameters, each in the form of a 16-dimensional $\mathbb{R}_{\geq 0}^{16}$ **vectors**, where each entry correspond to an age-band, like

$$S = \overbrace{(S_0 \text{ to } 4, S_5 \text{ to } 9, \dots, S_{70} \text{ to } 74, S_{75+})}^{\text{16 age bands}}$$

each of these parameters were stored as an **np.array** in our model, looking like this



Convention and Hadamard product

We firstly let **age bands** denotes to the set of all age-bands, where:

$$\text{age bands} = \{0 \text{ to } 4, 5 \text{ to } 9, \dots, 70 \text{ to } 74, 75+\} \quad (8)$$

Here, we introduce a new type of binary operation \circ which is used commonly in our model, **Hadamard product (entry-wise product)**.

$$\begin{aligned} (\cdot) \circ (\cdot) : \mathbb{R}^n \times \mathbb{R}^n &\rightarrow \mathbb{R}^n, (v_1, \dots, v_n) \circ (u_1, \dots, u_n) \\ &= (v_1 u_1, \dots, v_n u_n) \end{aligned}$$

This product is associative, transitive, and bilinear in fdips over \mathbb{R} .

Our model - cont.

Since our model use vector as input/output, it is bit more complicated, recall the standard relationships above.

Consider equation (6), it is tempting to give the following equivalence:

$$\Delta E = \bar{c} \circ \beta \circ I \quad (9)$$

Here we focus on \bar{c} and β .

Contact matrix

In our model, we use the contact matrix from the 2019 contact survey.
Contact matrix is a

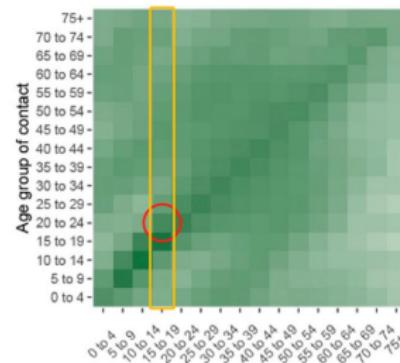
16×16 matrix, categorized into **4 contact types** (home, work, school, other) and **2 geographical groups** (urban, rural)

Each column represents a **five-year age-band i** of individuals

The i slice \mathcal{M}_i of each column represents the average number of individuals within age-band j contacted by an individual in age band i .

Here, if we want to know the contact pattern of a 15-19 yo individual, we will look at the yellow slice.

If we want to know how many 20-24 yo individuals does an average 15-19 yo individual contact in a day, we look at the red circle.



Contact matrix - cont.

Now, we can let the i slice of the matrix $M_i = \bar{c}_{0,i}$, and making equation (8) output an age-specific vector, where we formally define M_i as:

$$M_i := (M_{i,1}, \dots, M_{i,16}) \quad (10)$$

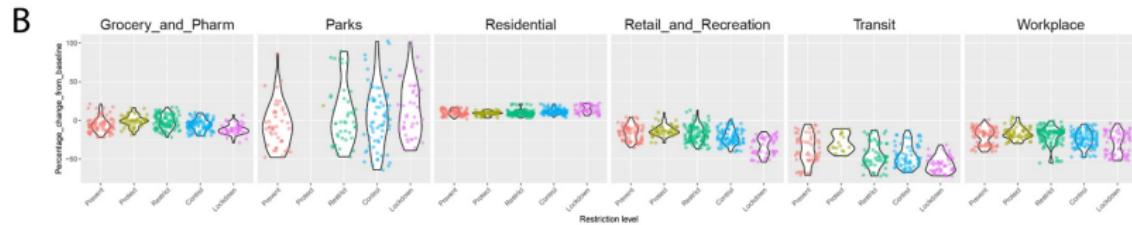
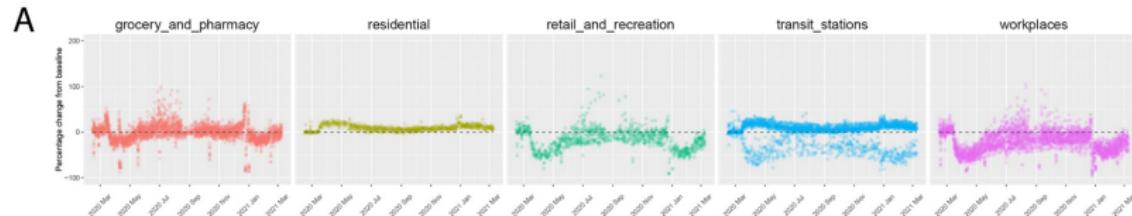
However, note we used $\bar{c}_{0,i}$, **not** \bar{c}_i , this is because this contact matrix was **surveyed in 2019**, before the pandemic!

During the pandemic, social distancing, mask wearing, and more intervention has altered the contact pattern, thus we will have to do some calibration.

Calibrating the matrix

To describe the change in contact pattern, we used **Google mobility index**, through this we have been provided an insight into the **change of population mobility** in Ontario, **compared to baseline in 2019**.

The following figure is the population mobility pattern in Ontario in 2020 and 2021.



Calibrating the Google Mobility

We will use an MLP (multi-layer perception) network to forecast the population mobility in Ontario in the **next 3 years**.

Why?

Population mobility pattern varies based on time (i.e, Christmas, Summer break)

More precise

Calibrating the matrix - cont.

We see the mobility data was categorized into 6 groups: Grocery and Pharmacy, Parks, Residential, Transit, and Workplace.

While, our matrix is in 4 groups: school, work, residential, and other.

Where we made the following assumption.

$$\begin{cases} m_s = m_{work} \\ m_w = \text{avg}(m_{transit}, m_{work}) \\ m_r = m_{resident} \\ m_o = \text{avg}(m_{grocery}, m_{retail}, m_{transit}) \end{cases}$$

Where, intuitively, $m_s, m_w, m_r, m_o \in [-1, \infty)$ denotes to the change in population mobility in school, workplace, residence, and other (this is a scalar!).

Contact matrix - cont.

Then, let $C = \{\text{work, school, residential, other}\}$ denotes to the set of contact types, and $M^{x \in C}$ denotes to the corresponding contact matrix, we have

$$\Delta E = \sum_{x \in C} \left(\sum_{i \in \text{age bands}} \overbrace{m_x M_i^x}^{=\bar{c}_x} \circ \beta I_i \right) \quad (11)$$

$$= \sum_{x \in C} m_x \beta \circ (M^x)^T I \quad (12)$$

And this is the first part of the puzzle!

Susceptibility

However, β is also a bit more complicated in our model. In fact it is not (never) even a constant.

We introduce a new concept, **basic infection rate (susceptibility)**, β_0 , as the unadjusted susceptibility of **a specific age-band i** the disease without intervention and immunity. This value only depend on the disease and age-band.

And age-specific **COVID-19 immunity level** μ_i , which is derived from the incidence rate of COVID-19 in the past 2 years and the vaccination level of this age band i . We will address this in detail later. (page 34-36)

Susceptibility - cont.

Then, we can write out β , in the form of:

$$\beta = (1_{16} - \mu) \circ \beta_0 \quad (13)$$

And the complete equation, after considering the presence of subclinical cases, on a **day t** , we have

$$\Delta E_t = \sum_{x \in C} \left(\overbrace{m_x M_i^x}^{=\bar{c}} I_t \circ \overbrace{(1 - \mu) \circ \beta_0}^{=\beta} \right) \quad (14)$$

$$= \sum_{x \in C} \left(m_x \beta_0 \circ (1_{16} - \mu) (M^x)^T (I_{t,c} + 0.5 I_{t,s}) \right) \quad (15)$$

Where $1_{16} = (1, \dots, 1) \in \mathbb{R}^{16}$

Infection - cont.

Recall that, upon exposure, the patient will either become **subclinical** or **clinical**.

The patient will not be infectious throughout their whole "infected state", but rather be infected in the first 5 days ($\text{gamma}(\mu = 5.0, k = 4)$).

The subclinical case ratio is also age-specific, this is very intuitive, as younger individuals tend to be more likely to be asymptomatic cases. We let a vector v denote to the age-specific subclinical case ratio, then it is intuitive that on **day t** :

$$\Delta I_t = \sum_{d \leq t} E_d \sigma(t-d) \quad \begin{cases} \Delta I_{t,s} = \sum_{d \leq t} v \circ E_d \sigma(t-d) \\ \Delta I_{t,c} = \sum_{d \leq t} (1_{16} - v) \circ E_d \sigma(t-d) \end{cases}$$

Where $1_{16} := (1, \dots, 1) \in \mathbb{R}^{16}$

Hospitalization

Recall the flow chart on Page 6, where a clinical case might become a severe case and become hospitalized, thus

$$I_c = I_{\text{non-hosp}} + I_{\text{hosp}} + I_{\text{ICU}} \quad (16)$$

We define the probability function of hospitalization regarding age to be $h : \text{age bands} \rightarrow [0, 1]$ based on Salje et al (older individuals tend to be hospitalized). Essentially,

$$h(i) = \mathbb{P}(\text{hosp}|I)_i = \text{logistic}(-7.37 + 0.068i) \quad (\text{this is for delta, revision!})$$

is the probability of hospitalization given age band and infection

Similarly, we define the ICU admission probability function $g : \text{age bands} \rightarrow [0, 1]$, as

$g(i)$ Pending data, due to new variant

Hospitalization - cont.

Also, we consider the mean delay from infection to hospital admission as a probability function (integral = 1), as:

$$T_{hosp} \sim \text{normal}(7.5, 1) \quad T_{ICU} \sim \text{normal}(11.1, 1)$$

Then, we can compute the increment of cases that were hospitalized and admitted into ICU **on a day t for an age-band i** , as

$$\Delta I_{t,i,hosp} = \sum_{d \leq t} I_{d,i} h(i) (1 - g(i)) T_{hosp}(t - d) \quad (17)$$

$$\Delta I_{t,i,ICU} = \sum_{d \leq t} I_{d,i,hosp} h(i) T_{ICU}(t - d) \quad (18)$$

Where all entries are scalar-valued.

Hospitalization - cont.

Finally, we have:

$$\Delta I_{hosp,t} = \left(\sum_{d \leq t} I_{i,d} h(i) (1 - g(i)) T_{hosp}(t-d) \right)_i^{i \in \text{age bands}} \quad (19)$$

$$\Delta I_{ICU,t} = \left(\sum_{d \leq t} I_{hosp,d} g(i) T_{ICU}(t-d) \right)_i^{i \in \text{age bands}} \quad (20)$$

$$= \left(\sum_{d \leq t} I_{i,d} h(i) g(i) T_{hosp}(t-d) T_{ICU}(t-d) \right)_i^{i \in \text{age bands}} \quad (21)$$

$$\Delta I_{t,i,\text{non-hosp}} = \Delta I_{c,t} - \Delta I_{hosp,t} - \Delta I_{ICU,t} \quad (22)$$

Removed

Finally! We will discuss the removal of infected cases. It is much simpler here!

Subclinical and non-hospitalized cases: For subclinical and non-hospitalized, it is very simple, they are removed by the date they lost their infectiousness, or we say, for them,

$$\gamma_s \equiv \gamma_{non-hosp} \sim \text{gamma}(\mu = 5, k = 4)$$

However, it is more complicated for the hospitalized and ICU-admitted cases.

Removed - cont.

Again, we use probability function and convolution here, from CO-CIN data.

$$\Delta\gamma_{hosp} \sim lognormal(\mu_{log} = 11.08, \sigma_{log} = 1.20)$$

$$\Delta\gamma_{ICU} \sim lognormal(\mu_{log} = 13.33, \sigma_{log} = 1.25)$$

Removed - cont.

Here, we apply convolution to all of the above data, and recall the relationships in 12 and 14

$$\begin{cases} \Delta R_s = \sum_{d \leq t} I_s \gamma_s(t-d) \\ \Delta R_{non-hosp} = \sum_{d \leq t} I_{non-hosp} \gamma_{non-hosp}(t-d) \\ \Delta R_{hosp} = \sum_{d \leq t} I_{hosp} \gamma_{hosp}(t-d) \\ \Delta R_{ICU} = \sum_{d \leq t} I_{ICU} \gamma_{ICU}(t-d) \end{cases} \quad (23)$$

$$\Delta R = \Delta R_s + \Delta R_{non-hosp} + \Delta R_{hosp} + \Delta R_{ICU} \quad (24)$$

Deceased

Recall the case-fatality rate of COVID-19 is non-zero, thus we consider the age-specific $cfr \in [0, 1]^{16}$, and let

$$\Delta D = cfr \circ \Delta R \quad \Delta r = (1_{16} - cfr) \circ \Delta R \quad (25)$$

Here, after being removed, the patients actually gets moved into the S pool again, but we tunes the immunity level of the original susceptible population.

Vaccination and immunity

The vaccination rate of Ontario has reached over 0.9, providing shielding immunity to the population. However, this ratio varies based on age band and the **immunity wanes**. We combined the result from two papers to estimated the actual immunity within the population.

Let $\mu_{0,v,i}$ denotes to the starting immunity gained from vaccination against **general infection**, $\mu_{0,n,i}$ denotes to the starting immunity gained from natural infection against **general infection**.

Let $\mu_{0,v,s}$ denotes to the starting immunity gained from vaccination against **severe infection**, $\mu_{0,n,s}$ denotes to the starting immunity gained from natural infection against **severe infection**.

Immunity against infection - cont.

Let $\varphi : \text{datetime} \rightarrow [0, 1]$ denotes to the immunity waning function, and V denotes to the age-specific increment in vaccination level (number of individuals **newly vaccinated**), it is intuitive to derive that, on a **day t** ,

$$\mu_{t,v,i} = \frac{\sum_{d \leq t} V_d \varphi(t-d) \mu_{0,v,i}}{P} \quad (26)$$

$$\mu_{t,n,i} = \frac{\sum_{d \leq t} I_d \varphi(t-d) \mu_{0,v,i}}{P} \quad (27)$$

$$\mu = \mu_t := \frac{\mu_{t,i} = \sum_{d \leq t} I_d \varphi(t-d) \mu_{0,v,i} + \sum_{d \leq t} V_d \varphi(t-d) \mu_{0,v,i}}{P} \quad (28)$$

Here, recall page **24** for immunity level.

Immunity against severe infection

The immunity against severe infection **affects cfr only**, in the following way:

$$\begin{aligned}\mu_{t,v,s} &= \frac{\sum_{d \leq t} V_d \varphi(t-d) \mu_{0,v,s}}{P} \\ \mu_{t,n,s} &= \frac{\sum_{d \leq t} I_d \varphi(t-d) \mu_{0,v,s}}{P} \\ \mu_{t,s} &= \frac{\sum_{d \leq t} I_d \varphi(t-d) \mu_{0,v,s} + \sum_{d \leq t} V_d \varphi(t-d) \mu_{0,v,s}}{P} \\ cfr &= cfr_0 \circ \mu_{t,s}\end{aligned}$$

where cfr_0 denotes to the un-intervened baseline case-fatality rate.

Demographics of Ontario

The province of Ontario was stratified into:

26 PHUs (Public health units)

50 administrative districts

528 counties (147 cities + 381 rurals)

We have the population and commutation data of each county.

Time step

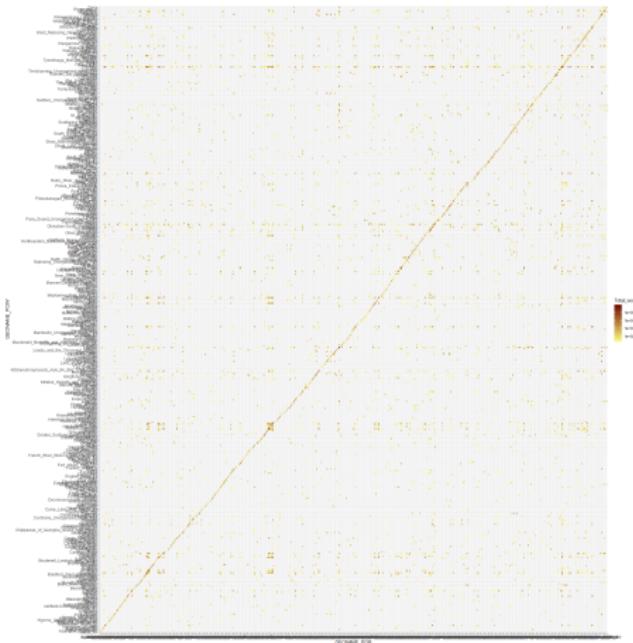
Our model adopted 2-compartmental transmission (work and non-work), and splitted the day into 8 discrete time steps (Δt), 4 for each.

For work-place transmission, we introduced the **commutation matrix** to describe the mobility of population **across** the counties.

Commutation

We modelled the commutation of each Ontario county in a 528×528 **matrix C** .

Let w denotes to the age-specific ratio of labour force. Here, both i, j slice will be used to model the commutation.



Commutation

The i -slice (column slice) of the matrix is a 528-dimensional vector, or

$$C_{i,k} := (C_{i,1}, \dots, C_{i,528})$$

Where, in our model, Toronto has index 1, Hamilton has index 5, thus $C_{1,5}$ is the number of commuters who **live** in Toronto and **work** in Hamilton, and $C_{5,1}$ is the converse.

Thus, the i column slice tells us how many commuters live in the county i .

Commutation - cont.

Similarly, the j -slice (row slice) of the matrix is a 528-dimensional vector,
or

$$C_{k,j} := (C_{1,j}, \dots, C_{528,j})$$

The j column slice tells us how many commuters works in the county j .

Commutation - cont.

Then, let $I_{c,t}$ denotes to the number of infected individuals on a day t and $S_{c,t}$ denotes to the number of susceptible individuals in a county c , then we can calculate the age-specific vector of out-going infected individuals $out_{c,t,I}$ and he age-specific vector of out-going infected individuals $out_{c,t,S}$, as

$$out_{c,t,I} = I_{c,t} \circ w, \quad out_{c,t,S} = S_{c,t} \circ w \in \mathbb{R}^{16}$$

Then, we have the out-going number of commuters who are infected or are susceptible as

$$\begin{aligned} OUT_{c,t,I} &\in \mathbb{R}^{528 \times 16}, \quad OUT_{c,t,I,j} := \frac{C_{i,j}}{\text{sum}(C_i)} out_{c,t,I} \\ OUT_{c,t,I} &:= \left(\frac{C_{i,j}}{\text{sum}(C_i)} out_{c,t,I} \right)_{j \in \{1, \dots, 528\}}_j \end{aligned}$$

Where the definition for $OUT_{c,t,S}$ is similar.

Commutation - cont.

The definition is bit abstract and hard to comprehend since it is based on iterated conditional probability.

Note that here I, S are not numbers but dummy index (just string). Here, we recall that, the commuters who are infected and live in Hamilton while work in Toronto on a given day t with number of infected individuals $I_{5,t}$ is:

$$OUT_{5,t,I,1} = \frac{\text{number of commuters from Ham to Trt}}{\frac{\overbrace{(C_{5,1})}^{\text{number of total commuters in Ham}}}{\underbrace{C_5}_{\text{age-specific work force ratio}}}}$$
$$I_{5,t} \circ \underbrace{w}_{\text{age-specific work force ratio}}$$

Commutation - cont.

During work-session, the number of susceptible and infected individuals in a county **both changes**, where on a day t and in a county c ,

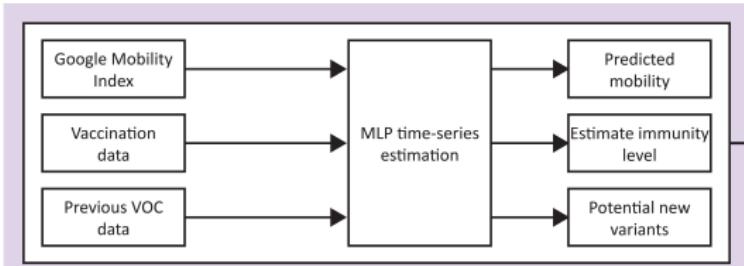
$$I_{t,c} = I_{t,c}^0 - \underbrace{\sum_{\substack{i=1 \\ i \neq c}}^{528} OUT_{c,t,I,i}}_{\text{infected individuals that lives in } c \text{ but works in another}} \quad (29)$$

$$+ \underbrace{\sum_{\substack{j=1 \\ j \neq c}}^{528} OUT_{j,t,I,c}}_{\text{infected individuals that work in } c \text{ but lives in another}} \quad (30)$$

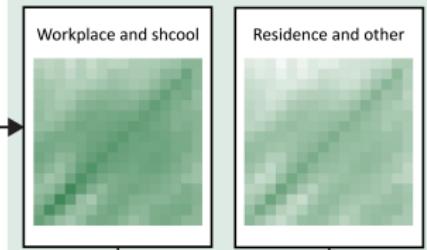
Where $I_{t,c}^0$ is the infected individuals in the county **without commutation (at the beginning of the day)**. The definition for susceptible individuals is similar.

Model - methodology

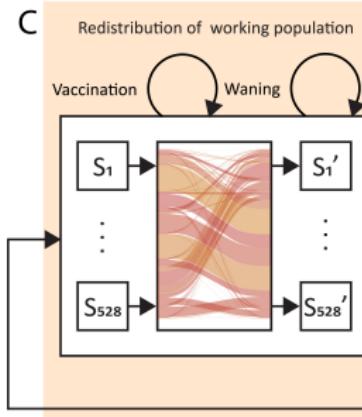
A



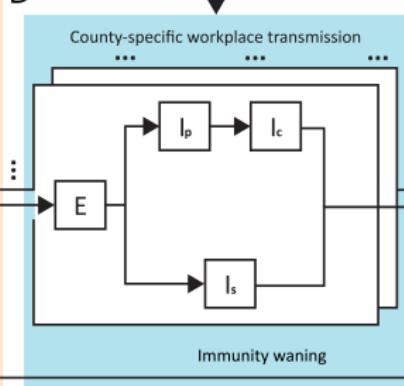
B



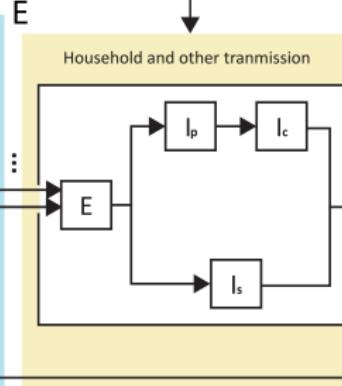
C



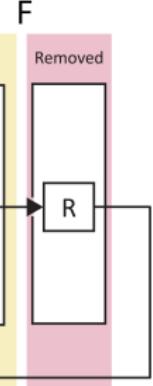
D



E



F



Model - legends

Figure 1: The epidemiological compartmental model. The transmission (infection) was divided into two stages: workplace and school, and household and others. **A).** Data calibration using time-series forecast. The Ontario-specific google mobility index, vaccination status, and epidemiological data of previous VOCs, were sent into a MLP network to forecast the trend in the following three years. **B).** The age-specific effective contact matrix synthesized from the relevant data output from the MLP network by categories. **C).** The susceptible compartment of the SEIR(S) model, stratified into 528 subgroups according to demographical data. The susceptible individuals in 528 counties will be redistributed by the starting of time-step 1 at the beginning of each transmission cycle due to commutation and will be restored by time-step 5. We assumed all of the removed individuals will be moved into the susceptible group 15 days after recovery with immunity (waning).

Model - legends - cont.

D). The exposed and infected compartment of the model during the workplace and school transmission cycle. This stage uses synthesized workplace and school contact matrix, after redistribution due to commutation. **E).** The exposed and infected compartment of the model during the household and others transmission cycle. This stage uses synthesized residence and others contact matrix, after restoration of commutation. **F).** The removed stage of the compartmental model. We assumed all of the recovered individuals will move to susceptible state 15 days after recovery due to immunity waning. The recovered individual still has shielding immunity against infection.

Model

Eventually, after making the time step Δt infinitesimal, or dt , we have the following **differential equations**:

$$dS(t) = - \sum_{x \in C} \left(m_x \beta_0 \circ (1_{16} - \mu) (M^x)^T (I_{t,c} + 0.5I_{t,s}) \right)$$

$$dE(t) = \sum_{x \in C} \left(m_x \beta_0 \circ (1_{16} - \mu) (M^x)^T (I_{t,c} + 0.5I_{t,s}) \right) - (dI_s(t) + dI_{non-hosp}(t) + dI_{hosp}(t) + dI_{ICU}(t))$$

$$dI_s(t) = \sum_{d \leq t} (v \circ E_d \sigma(t-d) - \gamma_s I_s) - dR_s(t)$$

$$dI_c(t) = \sum_{d \leq t} ((1_{16} - v) \circ E_d \sigma(t-d) - \gamma_s I_s) - dR_c(t)$$

$$dI_{hosp}(t) = \left(\sum_{d \leq t} I_{i,d} h(i) (1 - g(i)) T_{hosp}(t-d) \right)_i^{i \in \text{age bands}}$$

Model - cont.

$$dI_{ICU}(t) = \left(\sum_{d \leq t} I_{hosp,d} g(i) T_{ICU}(t-d) \right)_i^{i \in \text{age bands}}$$

$$dI_{t,non-hosp}(t) = dI_{c,t} - dI_{hosp,t} - dI_{ICU,t} - dR_{ICU}$$

$$dI(t) = dI_s(t) + dI_{non-hosp}(t) + dI_{hosp}(t) + dI_{ICU}(t)$$

$$dR_s(t) = \sum_{d \leq t} I_s \gamma_s(t-d)$$

$$dR_{non-hosp}(t) = \sum_{d \leq t} I_{non-hosp} \gamma_{non-hosp}(t-d)$$

$$dR_{hosp}(t) = \sum_{d \leq t} I_{hosp} \gamma_{hosp}(t-d)$$

$$dR_{ICU}(t) = \sum_{d \leq t} I_{ICU} \gamma_{ICU}(t-d)$$

Model - cont.

$$dR(t) = dR_s(t) + dR_{non-hosp}(t) + dR_{hosp}(t) + dR_{ICU}(t)$$

$$dD(t) = cfr \circ dR(t)$$

$$dr(t) = (1_{16} - cfr) \circ dR(t)$$

$$\mu_{t,v,s} = \frac{\sum_{d \leq t} V_d \varphi(t-d) \mu_{0,v,s}}{P}$$

$$\mu_{t,n,s} = \frac{\sum_{d \leq t} I_d \varphi(t-d) \mu_{0,v,s}}{P}$$

$$\mu_{t,s} = \frac{\sum_{d \leq t} I_d \varphi(t-d) \mu_{0,v,s} + \sum_{d \leq t} V_d \varphi(t-d) \mu_{0,v,s}}{P}$$

$$cfr = cfr_0 \circ \mu_{t,s}$$

Model - commutation

$$out_{c,t,I} = I_{c,t} \circ w$$

$$out_{c,t,S} = S_{c,t} \circ w$$

$$OUT_{c,t,I} = \left(\frac{C_{i,j}}{\sum(C_i)} out_{c,t,I} \right)_j^{j \in \{1, \dots, 528\}}$$

$$OUT_{c,t,S} = \left(\frac{C_{i,j}}{\sum(C_i)} out_{c,t,S} \right)_j^{j \in \{1, \dots, 528\}}$$