COVID-19 Modelling

Instructions for Using the COVID-19 PHAC SEIR compartmental Model Description

The Public Health Agency of Canada (PHAC) COVID-19 mathematical model developed using Analytica software is a SEIR compartment model. **Analytica**¹ was selected to develop this particular model because of its ability to rapidly construct models, its reliance on influence diagrams which provide some degree of clarity and transparency when viewing models (making it easier to understand how variables influence each other), and its use of **smart arrays**. This makes it easy for a user to explore different simple scenarios quickly and to conduct rapid parametric analyses to help inform the development of additional, more complex models.

The following is a step-wise guide for users to explore and adapt the PHAC model for new research. The parameter values and ranges for the model have been set as depicted in Figure 1.

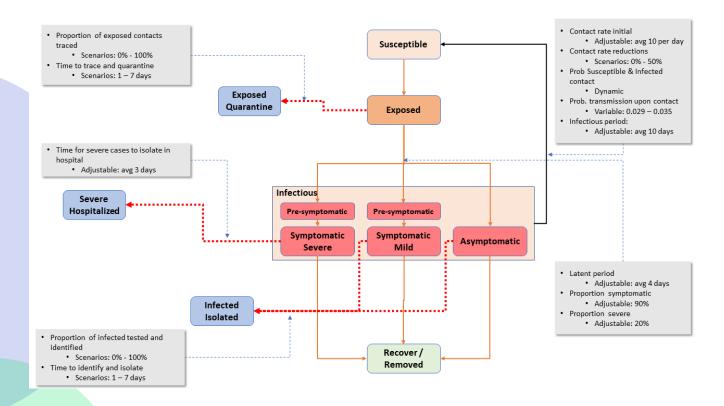


Figure 1: PHAC SEIR model overview as depicted in Analytica

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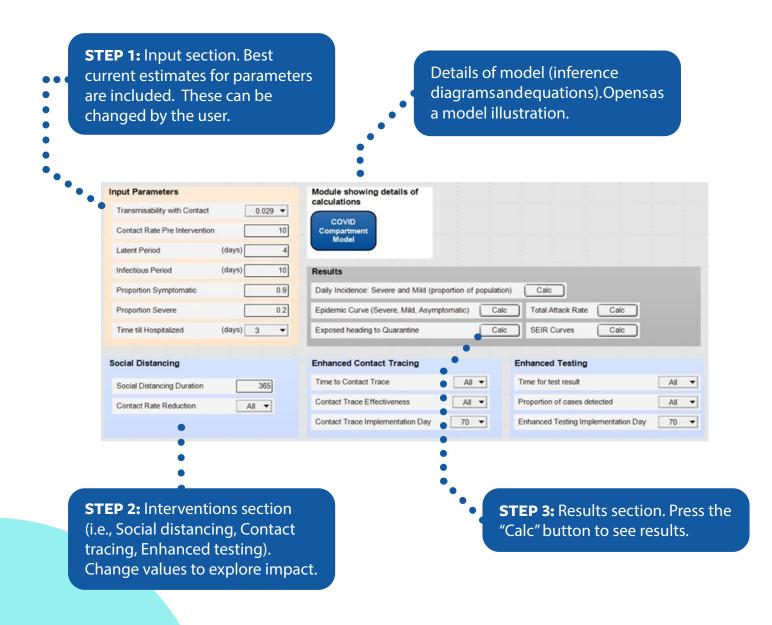
How to Download and Run the Model

1. To view and run this file you will need the free version of **Analytica**.

2. After downloading Analytica, download the **Model Code** from NCCID.

The file should automatically open with Analytica (Figure 2). But, if you run into any issues, the following tutorial explains how to open files using the software: **How to open or exit an Analytica Model**.

Figure 2: : PHAC SEIR Model dashboard, upon loading in Analytica



Step 1: Input section

• The default setting has values for input parameters that are within reasonable ranges for COVID-19, but these can be changed to explore alternatives.

• The "All" option can be selected for various parameters and this creates the ability to conduct interactive parametric analysis when viewing the results.

• Uncertainty can also be explored in the model by substituting point estimate parameter values with probability distributions. The use of probability distributions can have a significant impact on the model memory requirements and the time required to generate results.

Step 2: Interventions section

• The interventions section includes options for Social Distancing, Enhanced Contact Tracing and Enhanced Testing.

• This section includes the option to either select a predefined value, or to select the "All" option.

• If you select the "All" option, the model will run a simulation for every combination associated with that parameter and generate an array of results which makes it possible to quickly view various combinations in the results.

• The calculations necessary to present "All" options may run slowly. If your computer has limited memory, consider limiting the number of parameters tested. The combinations shown in the screen capture above will allow you to view various intervention combinations and should run on an average computer although there may be a slight delay between clicking the result button and being able to view the results.

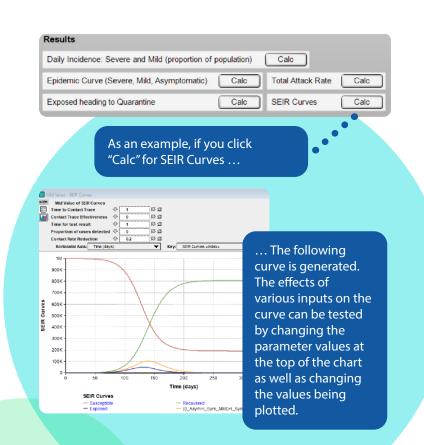
Step 3: Results section

• In the results section, simply click on the "Calc" button for the output of interest.

• If "All" or a range of values has been chosen for an input parameter, the results will include the ability to cycle through the parameter values and explore their impact on the output.

• If results charts do not appear different after making changes to input parameters, check the scale of the X and Y axes, as that may be where any difference is illustrated.

• Some chart features can be customized. You can select which variable is plotted on the x-axis, the key, and every parameter that the result depends upon.



Model Details Section

To see the logic and the calculations, you can double-click on the "COVID Compartment Model" module which will show you the model diagram (Figure 3).

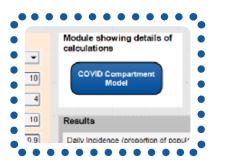
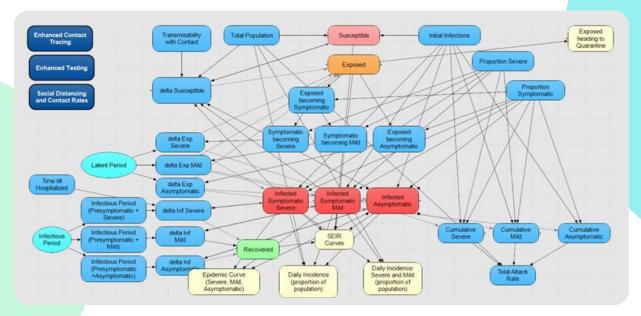


Figure 3. Model Diagram



If you double-click on a parameter you can see the value used, or the equations that generate values for that parameter, descriptions of the parameters, the parameter identifier and other details.

Additional Notes

1. The "transmissibility with contact" value gives you three choices that translate to R_0 values of 2.9, 3.2 and 3.5 at the start of the epidemic prior to social distancing, assuming the average contact rate of 10/day and average infectious period of 10 days. The effective R (Reff) value will change as interventions come into play.

2. Total population is set at 1,000,000, however this can be changed to any value and the outputs from the model are based on this new population value of initially susceptible number of people.

3. You can also run Monte Carlo simulations on uncertain parameters combined with parametric analysis.

4. If you start running into memory issues (depending upon your computer), reduce the number of parameters you have set to "All".

5. The starting values (initial infections and R_0) have been set to approximate the observations in the early period of the epidemic in Canada.

6. It should be noted that the model is designed to generate general insights into the epidemic trajectory, not exact predictions. The results from this model have not been used in isolation as the only advice for public health but rather, the results are compared and corroborated with other models from either in Canada or globally. For example, the model includes severe and mild infections, while the cases reported in a certain locale may be a mixture of those two (and perhaps with more severe cases).



Mathematical modelling was conducted by the Public Health Agency of Canada. This document is a joint production of the Public Health Agency of Canada and the <u>National Collaborating Centre for Infectious Diseases</u>.

