Covid19 Transmission Model – CTM -v2.0

Contents

BACKGROUND

Covid19 is an infectious disease transmitted from one human to another. Thus, when an infected person comes into a population that was not infected, the disease spreads. This is also called disease transmission. This software utility helps predict the Covid19 transmission. The underlying model is called the SEIR model.

Not everyone infected by Covid19 exhibits symptoms. Those who are infected but do not show symptoms are called *asymptomatic.* The rate at which the disease spread depends on several factors. For example, if there is strict social distancing and sufficient precautions (such as wearing a mask) are taken, then Covid19 does not spread much. A person who does not show symptoms (asymptomatic person) may mingle with others and may cause more transmission than a person exhibiting symptoms. A small fraction of the population that is infected by Covid19 will suffer death. The death rate may also depend on the age of the person infected.

What does this software do?

This is a MATLAB® based program or App that you can use in Windows® family operating systems. This can be used to predict the transmission of Covid19 using the SEIR model. This software uses 1st March 2020 as the first day.

Please see the description below for details*. Note that the results are only as good as the assumptions and the input.*

We are providing this app so that users, who may not be familiar with the models and coding, can still visualize the disease transmission and effect. Several 'what if' scenarios can be evaluated. e.g., What if the fraction of the symptomatic population is higher? What if the value of R_0 (Basic reproduction number) is lower for symptomatic? What if the fraction treated is higher? What if the treatment is better so that the fraction dead is smaller?

The value of R_0 can also depend on whether there is a lockdown in place, and if the population adheres strictly to the rules, and so on. The extent of lockdown and the corresponding rules also vary each month. In this Software, the values of R_0 can be altered based on the month. There is a provision to vary the fraction of symptomatic persons treated and the fraction of asymptomatic persons treated, although whether it will vary each month is doubtful.

The infected population is split into 'Symptomatic' and 'Asymptomatic.' In addition, the Basic Reproduction Number (an indicator of how effectively Covid19 spreads) can be different for those showing symptoms and those who do not show any symptom but are infected nevertheless. The mortality (i.e., death) rates are also dependent on whether someone is treated or not and whether someone shows symptoms or not. In addition, the mortality rate can be strongly dependent on age, with senior citizens being more vulnerable.

For example, when someone shows symptom, they are likely to be treated. In these conditions, we expect that the 'Fraction of Symptomatic persons treated' to be high, perhaps 0.9. We can choose these values based on what we think is an appropriate representation of a real-life scenario would be.

In addition, when someone shows symptoms, everyone else will be watchful and will take precautions. So, Covid19 will not spread easily from the patient to others. Basic reproduction number may be low (e.g., if it is 0.1, then out of 10 cases, in one case Covid19 may spread from patient to others).

When someone doesn't show symptom, then they are not likely to be treated (unless they are tested for Covid19 and found to be positive). A person without symptom will probably move

around freely and is likely to spread Covid19 more than a person without symptoms. When someone is infected but does not show symptom, then the basic reproduction number will remain high.

The effect of Covid19 also appears to depend on the person's age. We have provided three groups, viz., Children, Adults and Senior Citizens. In this model, the death rate can vary depending on the age group too. The user can select a death rate for each group and simulate.

The results are saved in an Excel file, and plots of various categories of individuals are shown.

We provide the code so that programmers can modify the code as they wish and add features if they desire so. The app and the code are given under MIT license.

INSTALLATION

This App can be installed on Windows 10 ® operating system. You will need administrator privilege to install this App.

This App is written in Matlab®. You will also need to have Matlab Compiler Runtime. The Matlab Compiler Runtime can be downloaded for free from Mathwork ® website. It is ~ 1 GB, so it may take quite some time to download, depending on your network connection speed.

If you want to use the source code, and modify it, you will need to have Matlab 2020a or a latter version.

SVEIR MODEL

The population is divided into the following groups. Each individual is either susceptible, exposed, infected (treated or untreated), recovered and dead. They move from one group to another based on certain factors, as described below.

Age distribution: - Population is divided into 3 groups, based on their age, viz. Children ("below 10"), Adults ("between 10 and 60"), and Senior Citizens ("above 60"). The parameters (such as death rate) *can be* different for the three age groups. In the default setting, we have used the same parameter set for "below 10" and "between 10 and 60" groups. A higher death rate is used for "above 60".

Definitions:

*Susceptible (**S**)* – those who are not infected, but can be infected.

*Vaccinated (**V**)* – those who are vaccinated (i.e., completed two doses of vaccine). They will have a long-term immunity (e.g., 750 days ~ 2 years). After the immunity period, they will become susceptible. The vaccinated population can still contract the disease, but the impact is expected to be low. As an approximation, in this model, the vaccinated population is assumed to be non-infectible.

*Exposed (**E**)*- those who are in the initial stage of infection. They don't show any symptoms and they cannot infect others at this stage. They will be at this stage for a few days (5 days?)

*Infected (**I**)* – now they are a few days into the infection and they are able to infect others. They may be treated or not. They will be in this stage for a few days (14 days?).

Some of the infected may show symptom and some may not show symptom. In this model, we treat them differently. The infected are divided into 4 sub-groups. It is assumed that as soon as someone is infected, they will be put into one of these groups.

1. *Symptomatic, Treated* (**ST**) – After infection, some of them may be treated. Now, it is likely that those showing symptoms are treated. In general, if we have a lockdown, everyone is in some sort of quarantine and it will reduce the base reproduction number. We put together all these factors, and say that a fraction of infected population showing symptoms, is treated.
2. *Symptomatic, Untreated (**SU**)*- A few infected persons showing symptoms may not be treated due to lack of facilities.
3. *Asymptomatic, Treated* (**AT**)- Those who are infected, but do not show symptom, may be treated. In places with extensive testing, asymptomatic are likely to be identified and treated. In places where testing facilities are limited, they may not be treated.
4. *Asymptomatic, Untreated (**AU**)*- Those who are infected, but do not show symptom, and are not treated.

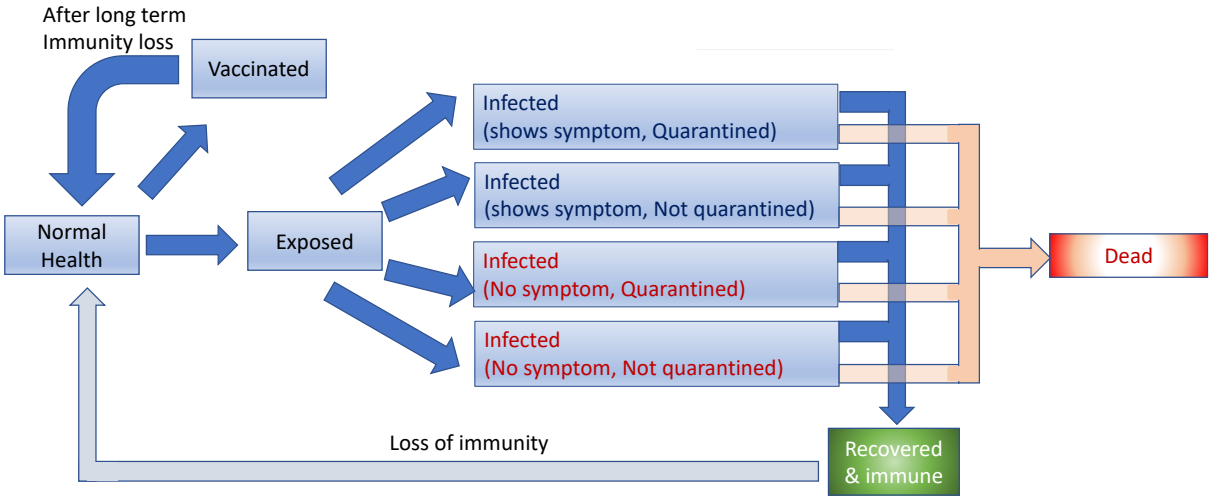
Recovered: Both, those who showed symptoms and recovered (**SR**) and those who didn't show symptom and recovered (**AR**) fall in this group. Most of the infected population will recover and the ones who are recovered will have short term immunity (90 days). Until that

time, they will not catch Covid19 again, and they will not spread it to others. After that time, they will lose immunity and will go back to 'susceptible' population.

Dead: A small fraction of infected population (whether they are symptomatic (**SD**) or asymptomatic (**AD**), whether they are treated or not) will die.

The rest of the infected population will recover. How much is the fraction that would die? It depends on various factors, and we choose a number to capture the average rate. We can choose different death rates for the four sub-groups mentioned above. We can think that someone treated will have lower death rate than the one who is not treated. Regardless, we have left the choice to the user.

Here is a pictorial of the various groups and the movement of individual from one group to another



Movement from one group to another:

A susceptible person will become exposed, if they interact with infected persons. So, the probability of this happening depends on a number called Basic reproduction number. It is estimated to be 2.28 for Covid19. We can choose a different number, if there is a reason to do so.

If we have a single person (A) infected with Covid19 introduced into a fresh population, then on the average, 2.28 persons will catch Covid19 from A. E.g. If a person remains in the 'infected' group for 14 days, then within those 14 days, they would have spread Covid19 to 2.28 person, on the average. These new patients will again spread Covid19 to others, but that is not counted in calculating the Basic reproduction number.

Once an individual has come to Exposed group, then after some (5) days, they will automatically go into 'Infected' group, regardless of whether they interact with others are not. They may show symptoms or may not show symptom. We can choose what fraction would really show symptom. Again, within these two groups, individuals may be 'treated' or 'untreated'. We can decide what fraction is treated and what is not. Once a person comes into 'Treated' group, they will be there for a certain number of days (14 days). After that, they will automatically move to 'Recovered' or 'Dead' group.

Once an individual comes into 'Recovered' group, after some days (90 days) they will automatically move to 'Susceptible' group. Of course, no one moves out of 'Dead' group!

In theory, anyone in susceptible or exposed or recovered group may get vaccinated. Since at any given time the susceptible fraction of the population is low, and recovered persons are advised to vaccinate after certain wait period, the model simplifies the situation and assumes that only the susceptible fraction of the population is vaccinated.

Model Equations

The model is converted to mathematical equations, and these are written in the form of differential equations.

Consider the SVEIR model, accounting for age distribution, and treatment

Notation: S stands for susceptible, V for vaccinated, E for exposed, I for infected, R for recovered, and D for dead. 'Chi' stands for child, 'Adu' for adult, and 'Sen' for senior citizen. 'Sym' stands for symptomatic and 'Asym' for asymptomatic. 'Tre' stands for treated and 'Untre' for untreated.

A population consists of N number of people, with 'FSen' as fraction of senior citizens, 'FAdu' as fraction of adults and 'FChi' as fraction of children. FChi = 1-FSen – FAdu.

The number of days that a person spends in Exposed conditions is τ_E and the number of days spent in Infected conditions is τ_I. The number of days in recovered mode (where there is immunity) is given by τ_R. The number of days in vaccinated mode is denoted by τ_V.

Fraction of vaccinated population is given by $S_{V\text{-}ADU}$ and $S_{V\text{-}SEN}$. This are respectively the fraction of the adult population under consideration or the fraction of the senior citizen under consideration.

Fraction of infected patients that are symptomatic is given by S_F. The fraction of infected patients that are asymptomatic are then given by 1- S_F. We expect that S_F will be the same for children, adults and senior citizens.

Fraction of symptomatic that are treated is given by q_{Sym}. This means 1-q_{Sym} are not treated. On the other hand, asymptomatic are not likely to be treated, unless they are tested and verified as Covid positive, or have been in close proximity to symptomatic patients. Fraction of asymptomatic treated is given by q_{Asym}, and the remaining fraction is 1- q_{Asym}. Again, these are not expected to be dependent on whether a person is Chi or Adu or Sen.

Base reproductive number is R_0. It can vary depending on whether someone is symptomatic or asymptomatic and treated or untreated. So, this can be split as $R_{0\text{-}SymTre}$, $R_{0\text{-}SymUntre}$, $R_{0\text{-}AsymTre}$ and $R_{0\text{-}AsymUntre}$. We can approximate that there is no difference between the R_0 of treated and untreated conditions, i.e., $R_{0\text{-}SymTre} = R_{0\text{-}SymUntre}$, and $R_{0\text{-}AsymTre} = R_{0\text{-}AsymUntre}$.

Death rate DR also depends on whether one is a Chi or Adu or Sen, and if they are symptomatic or asymptomatic and if they are treated or untreated. These are given by $DR\_{}_{ChiSymTre}$, $DR\_{}_{ChiSymUntre}$, $DR\_{}_{ChiAsymTre}$, $DR\_{}_{ChiAsymUntre}$, $DR\_{}_{AduSymTre}$, $DR\_{}_{AduSymUntre}$, $DR\_{}_{AduAsymTre}$, $DR\_{}_{AduAsymUntre}$, $DR\_{}_{AduSymTre}$, $DR\_{}_{SenSymUntre}$, $DR\_{}_{SenAsymTre}$, and $DR\_{}_{SenAsymUntre}$.

As of now, childred are not vaccinated, and hence the fraction of children vaccinated is zero.

For children, the equations describing the progression are given by

$$\frac{d\left[S\_\mathrm{Chi}\right]}{dt}=\left\{\begin{array}{l}\frac{1}{\tau_R}\left(R\_\mathrm{Chi}\_Sym+\mathrm{R}\_\mathrm{Chi}\_Asym\right)+\frac{1}{\tau_V}V\_\mathrm{Chi}\\ -S\_\mathrm{Chi}\times S_{V-\mathrm{Chi}}-\frac{1}{\tau_V}-\frac{1}{\tau_I}\times\left(R_{0-Sym}\times I_{Sym}+R_{0-Asym}\times I_{Asym}\right)\times S\_\mathrm{Chi}\end{array}\right\}$$

$$\frac{d\left[V\_\mathrm{Chi}\right]}{dt}=S\_\mathrm{Chi}\times S_{V-\mathrm{Chi}}-\frac{1}{\tau_V}V\_\mathrm{Chi}$$

$$\frac{d\left[E\_Chi\right]}{dt}=\frac{1}{\tau_I}\times\left(R_{0-Sym}\times I_{Sym}+R_{0-Asym}\times I_{Asym}\right)\times S\_Chi-\frac{1}{\tau_E}\times E\_Chi$$

$$\frac{d\left[I\_Chi\_Sym\_Tre\right]}{dt}=S_F\times q_{sym}\times\frac{1}{\tau_E}\times E\_Chi-\left(\frac{1}{\tau_I}+DR_{Chi-Sym-Tre}\right)\times I\_Chi\_Sym\_Tre$$

$$\frac{d\left[I\_Chi\_Sym\_Untre\right]}{dt}=S_F\times\left(1-q_{sym}\right)\times\frac{1}{\tau_E}\times E\_Chi-\left(\frac{1}{\tau_I}+DR_{Chi-Sym-Untre}\right)\times I\_Chi\_Sym\_Untre$$

$$\frac{d\left[I\_Chi\_Asym\_Tre\right]}{dt}=\left(1-S_F\right)\times q_{Asym}\times\frac{1}{\tau_E}\times E\_Chi-\left(\frac{1}{\tau_I}+DR_{Chi-Asym-Tre}\right)\times I\_Chi\_Asym\_Tre$$

$$\frac{d\left[I\_Chi\_Asym\_Untre\right]}{dt}=\left\{\begin{array}{l}\left(1-S_F\right)\times\left(1-q_{Asym}\right)\times\frac{1}{\tau_E}\times E\_Chi\\ -\left(\frac{1}{\tau_I}+DR_{Chi-Asym-Untre}\right)\times I\_Chi\_Asym\_Untre\end{array}\right\}$$

$$\frac{d\left[R\_Chi\_Sym\right]}{dt}=\left(\frac{1}{\tau_I}\right)\times\left(I\_Chi\_Sym\_Tre+I\_Chi\_Sym\_Untre\right)-\frac{1}{\tau_R}\times R\_Chi\_Sym$$

$$\frac{d\left[R\_Chi\_Asym\right]}{dt}=\left(\frac{1}{\tau_I}\right)\times\left(I\_Chi\_Asym\_Tre+I\_Chi\_Asym\_Untre\right)-\frac{1}{\tau_R}\times R\_Chi\_Asym$$

$$\frac{d\left[D\_Chi\_Sym\right]}{dt}=\left(DR_{Chi-Sym-Tre}\right)\times I\_Chi\_Sym\_Tre+\left(DR_{Chi-Sym-Untre}\right)\times I\_Chi\_Sym\_Untre$$

$$\frac{d\left[D\_Chi\_Asym\right]}{dt}=\left(DR_{Chi-Asym-Tre}\right)\times I\_Chi\_Asym\_Tre+\left(DR_{Chi-Asym-Untre}\right)\times I\_Chi\_Asym\_Untre$$

Note that

$$I_{Sym}=I\_Chi\_Sym\times F\_Chi+I\_Adu\_Sym\times F\_Adu+I\_Sen\_Sym\times F\_Sen$$

where

$$I\_Chi\_Sym = I\_Chi\_Sym\_Tre + I\_Chi\_Sym\_Untre$$
$$I\_Adu\_Sym = I\_Adu\_Sym\_Tre + I\_Adu\_Sym\_Untre$$
$$I\_Sen\_Sym = I\_Sen\_Sym\_Tre + I\_Sen\_Sym\_Untre$$

Likewise

$$I_{Asym} = I\_Chi\_Asym \times F\_Chi + I\_Adu\_Asym \times F\_Adu + I\_Sen\_Asym \times F\_Sen$$

where

$$I\_Chi\_Asym = I\_Chi\_Asym\_Tre + I\_Chi\_Asym\_Untre$$
$$I\_Adu\_Asym = I\_Adu\_Asym\_Tre + I\_Adu\_Asym\_Untre$$
$$I\_Sen\_Asym = I\_Sen\_Asym\_Tre + I\_Sen\_Asym\_Untre$$

Now, for adults, we can write

$$\frac{d\left[S\_Adu\right]}{dt} = \left\{ \begin{array}{l} \frac{1}{\tau_R}\left(R\_Adu\_Sym + \mathrm{R}\_Adu\_Asym\right) + \frac{1}{\tau_V} V\_Adu \\ -S\_Adu \times S_{V-ADU} - \frac{1}{\tau_V} - \frac{1}{\tau_I} \times \left(R_{0-Sym} \times I_{Sym} + R_{0-Asym} \times I_{Asym}\right) \times S\_Adu \end{array} \right\}$$

$$\frac{d\left[V\_Adu\right]}{dt} = S\_Adu \times S_{V-ADU} - \frac{1}{\tau_V} V\_Adu$$

$$\frac{d\left[E\_Adu\right]}{dt} = \frac{1}{\tau_I} \times \left(R_{0-Sym} \times I_{Sym} + R_{0-Asym} \times I_{Asym}\right) \times S\_Adu - \frac{1}{\tau_E} \times E\_Adu$$

$$\frac{d\left[I\_Adu\_Sym\_Tre\right]}{dt} = S_F \times q_{sym} \times \frac{1}{\tau_E} \times E\_Adu - \left(\frac{1}{\tau_I} + DR_{Adu-Sym-Tre}\right) \times I\_Adu\_Sym\_Tre$$

$$\frac{d\left[I\_Adu\_Sym\_Untre\right]}{dt} = S_F \times \left(1 - q_{sym}\right) \times \frac{1}{\tau_E} \times E\_Adu - \left(\frac{1}{\tau_I} + DR_{Adu-Sym-Untre}\right) \times I\_Adu\_Sym\_Untre$$

$$\frac{d\left[I\_Adu\_Asym\_Tre\right]}{dt} = \left(1 - S_F\right) \times q_{Asym} \times \frac{1}{\tau_E} \times E\_Adu - \left(\frac{1}{\tau_I} + DR_{Adu-Asym-Tre}\right) \times I\_Adu\_Asym\_Tre$$

$$\frac{d\left[I\_Adu\_Asym\_Untre\right]}{dt} = \left\{ \begin{array}{l} \left(1 - S_F\right) \times \left(1 - q_{Asym}\right) \times \frac{1}{\tau_E} \times E\_Adu \\ -\left(\frac{1}{\tau_I} + DR_{Adu-Asym-Untre}\right) \times I\_Adu\_Asym\_Untre \end{array} \right\}$$

$$\frac{d\left[R\_Adu\_Sym\right]}{dt} = \left(\frac{1}{\tau_I}\right) \times \left(I\_Adu\_Sym\_Tre + I\_Adu\_Sym\_Untre\right) - \frac{1}{\tau_R} \times R\_Adu\_Sym$$

$$\frac{d[R\_Adu\_Asym]}{dt} = \left(\frac{1}{\tau_I}\right) \times (I\_Adu\_Asym\_Tre + I\_Adu\_Asym\_Untre) - \frac{1}{\tau_R} \times R\_Adu\_Asym$$

$$\frac{d[D\_Adu\_Sym]}{dt} = \left(DR_{Adu-Sym-Tre}\right) \times I\_Adu\_Sym\_Tre + \left(DR_{Adu-Sym-Untre}\right) \times I\_Adu\_Sym\_Untre$$

$$\frac{d[D\_Adu\_Asym]}{dt} = \left(DR_{Adu-Asym-Tre}\right) \times I\_Adu\_Asym\_Tre + \left(DR_{Adu-Asym-Untre}\right) \times I\_Adu\_Asym\_Untre$$

and for senior citizen we can write

$$\frac{d[S\_Sen]}{dt} = \begin{Bmatrix} \frac{1}{\tau_R}(R\_Sen\_Sym + \mathrm{R}\_Sen\_Asym) + \frac{1}{\tau_V} V\_Sen \\ -S\_Sen \times S_{V-SEN} - \frac{1}{\tau_I} \times \left(R_{0-Sym} \times I_{Sym} + R_{0-Asym} \times I_{Asym}\right) \times S\_Sen \end{Bmatrix}$$

$$\frac{d[V\_Sen]}{dt} = S\_Sen \times S_{V-SEN} - \frac{1}{\tau_V} \times V\_Sen$$

$$\frac{d[E\_Sen]}{dt} = \frac{1}{\tau_I} \times \left(R_{0-Sym} \times I_{Sym} + R_{0-Asym} \times I_{Asym}\right) \times S\_Sen - \frac{1}{\tau_E} \times E\_Sen$$

$$\frac{d[I\_Sen\_Sym\_Tre]}{dt} = S_F \times q_{sym} \times \frac{1}{\tau_E} \times E\_Sen - \left(\frac{1}{\tau_I} + DR_{Sen-Sym-Tre}\right) \times I\_Sen\_Sym\_Tre$$

$$\frac{d[I\_Sen\_Sym\_Untre]}{dt} = S_F \times (1 - q_{sym}) \times \frac{1}{\tau_E} \times E\_Sen - \left(\frac{1}{\tau_I} + DR_{Sen-Sym-Untre}\right) \times I\_Sen\_Sym\_Untre$$

$$\frac{d[I\_Sen\_Asym\_Tre]}{dt} = (1 - S_F) \times q_{Asym} \times \frac{1}{\tau_E} \times E\_Sen - \left(\frac{1}{\tau_I} + DR_{Sen-Asym-Tre}\right) \times I\_Sen\_Asym\_Tre$$

$$\frac{d[I\_Sen\_Asym\_Untre]}{dt} = \begin{Bmatrix} (1 - S_F) \times (1 - q_{Asym}) \times \frac{1}{\tau_E} \times E\_Sen \\ -\left(\frac{1}{\tau_I} + DR_{Sen-Asym-Untre}\right) \times I\_Sen\_Asym\_Untre \end{Bmatrix}$$

$$\frac{d[R\_Sen\_Sym]}{dt} = \left(\frac{1}{\tau_I}\right) \times (I\_Sen\_Sym\_Tre + I\_Sen\_Sym\_Untre) - \frac{1}{\tau_R} \times R\_Sen\_Sym$$

$$\frac{d[R\_Sen\_Asym]}{dt} = \left(\frac{1}{\tau_I}\right) \times (I\_Sen\_Asym\_Tre + I\_Sen\_Asym\_Untre) - \frac{1}{\tau_R} \times R\_Sen\_Asym$$

$$\frac{d[D\_Sen\_Sym]}{dt} = \left(DR_{Sen-Sym-Tre}\right) \times I\_Sen\_Sym\_Tre + \left(DR_{Sen-Sym-Untre}\right) \times I\_Sen\_Sym\_Untre$$

$$\frac{d[D\_Sen\_Asym]}{dt} = \left(DR_{Sen-Asym-Tre}\right) \times I\_Sen\_Asym\_Tre + \left(DR_{Sen-Asym-Untre}\right) \times I\_Sen\_Asym\_Untre$$

There are 33 equations. The first 11 are for children, second 11 are for adults and third 11 are for senior citizens. They are coupled by the I_sym and I_asym terms, that are present in 1 and 2nd, 12th and 14th and 23rd and 25th equations.

We need 33 initial conditions. We remind the user that this software uses 1st March 2020 as the first day. Likewise, we need the following parameters.

1. F_{Adu} and F_{Sen}. Note that F_{Chi} = 1- F_{Adu} and $F_{Sen.}$ This is essentially information from the population data.
2. τ_E, τ_I,τ_V and τ_R. These are essentially disease characteristics and are well-defined. S_F is also fixed.
3. $R_{0\text{-}Sym}$ and $R_{0\text{-}Asym.}$ These can vary
4. q_{Sym} and q_{Asym}. These can vary based on patients (whether they exhibit symptoms) and facilities (if they are treated, or not)
5. $DR\_{}_{ChiSymTre}$, $DR\_{}_{ChiSymUntre}$, $DR\_{}_{ChiAsymTre}$, $DR\_{}_{ChiAsymUntre}$, $DR\_{}_{AduSymTre}$, $DR\_{}_{AduSymUntre}$, $DR\_{}_{AduAsymTre}$, $DR\_{}_{AduAsymUntre}$, $DR\_{}_{AduSymTre}$, $DR\_{}_{SenSymUntre}$, $DR\_{}_{SenAsymTre}$, and $DR\_{}_{SenAsymUntre}$. These depend on the type of patients, if they show symptoms, and if they are treated.
6. S_{V_Chi} is set to zero since children are not vaccinated yet (as of Sep 2021). Later, if children are vaccinated, we can easily modify the input to accommodate this. We need to specify S_{V_ADU} and S_{V_SEN}. These will vary from month to month.

Choose initial conditions, and parameter values and solve the above system of ODE to predict Covid19 propagation. Again, note that the results are only as good as the assumptions and the input.

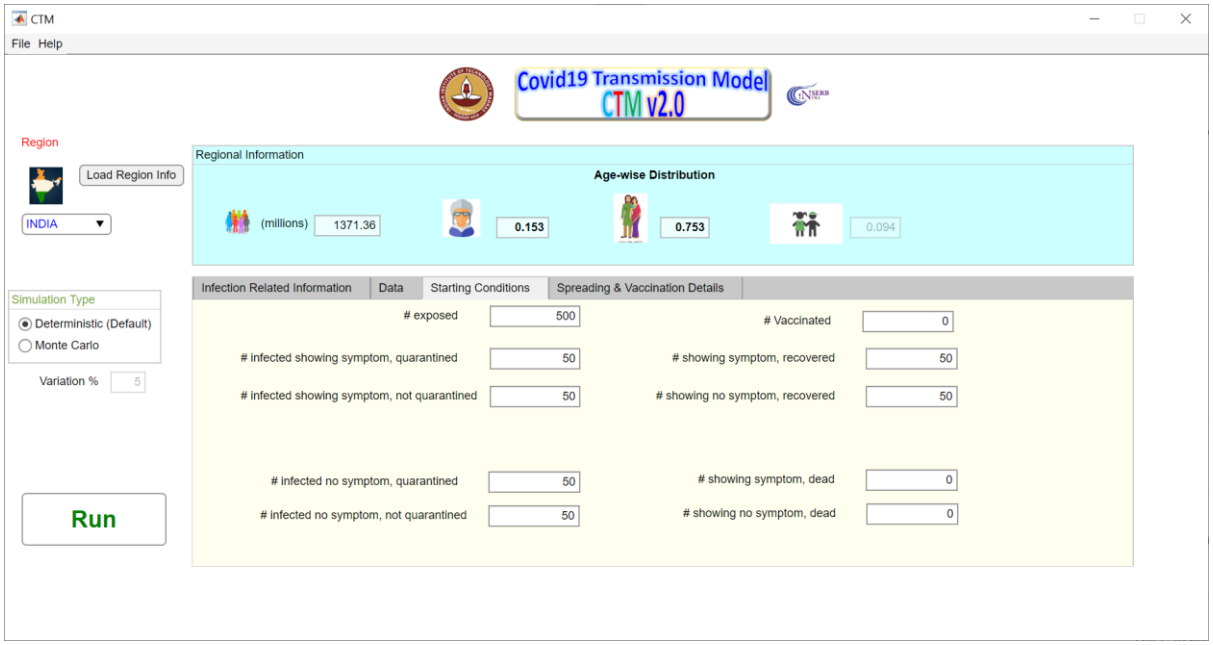
SOFTWARE

Appearance

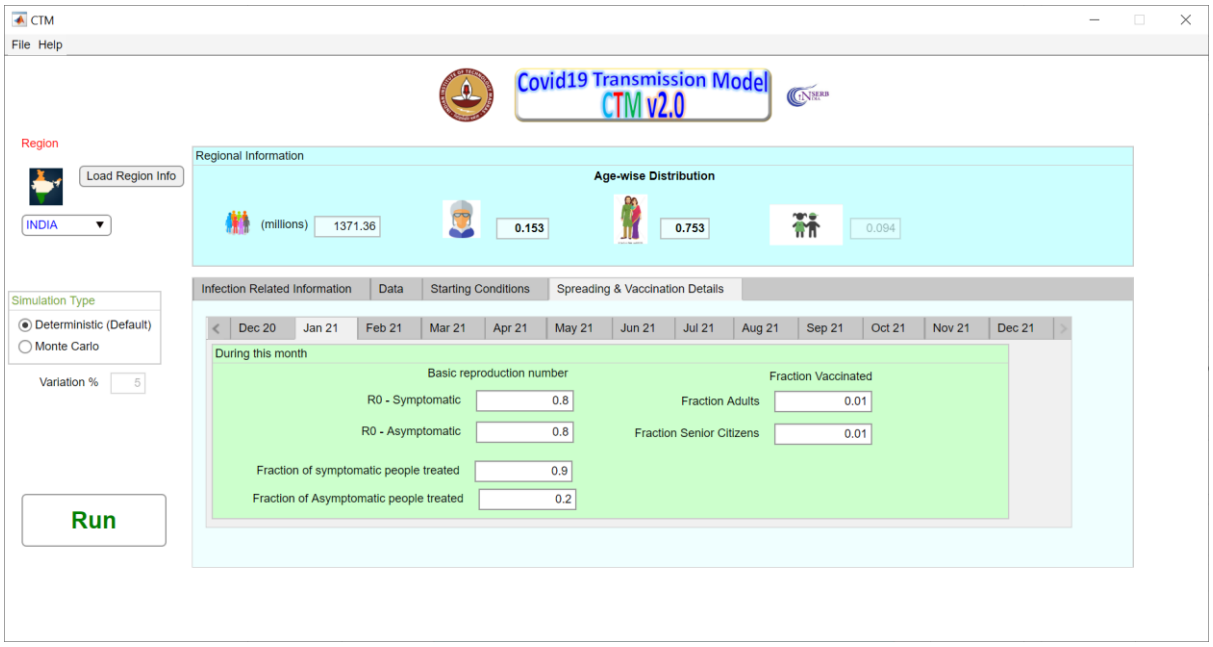
A few screenshots of the software interface are given here.

The infected related information should be submitted in the first tab in the bottom half of the software window. The fraction of infected population exhibiting symptoms, time it takes to exhibit symptoms (in symptomatic patients), time it takes to recover, and the duration of immunity are keyed in here. In addition, the death rates of patients, depending on whether they are (i) symptomatic or not, (ii) treated or not and (iii) Children or Adults or Senior Citizen, are all input here.

In the second tab, we will enable comparing model results with actual data.



The initial conditions are input in the third tab. The input fields are self-explanatory.



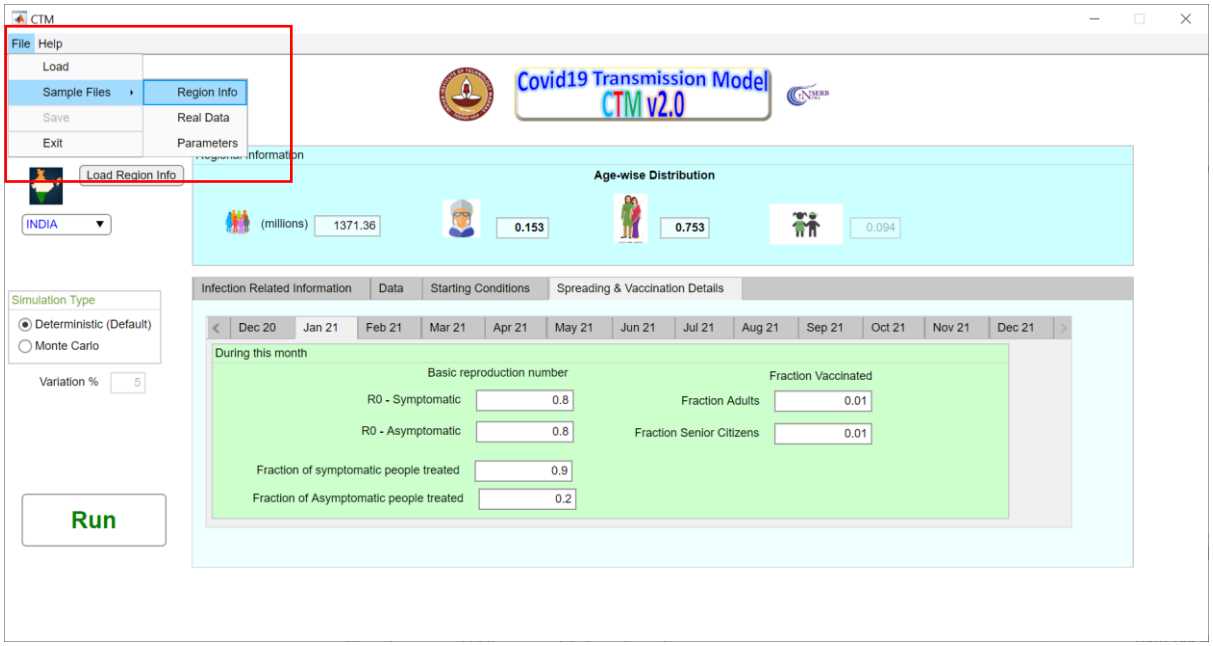
In the fourth tab, the values of Basic reproduction number and fraction of symptomatic persons treated and asymptomatic person treated can be given for each month. From Jan 2021 onward, the fraction of adult and senior citizen population vaccinated can also be given.

How to use the software?

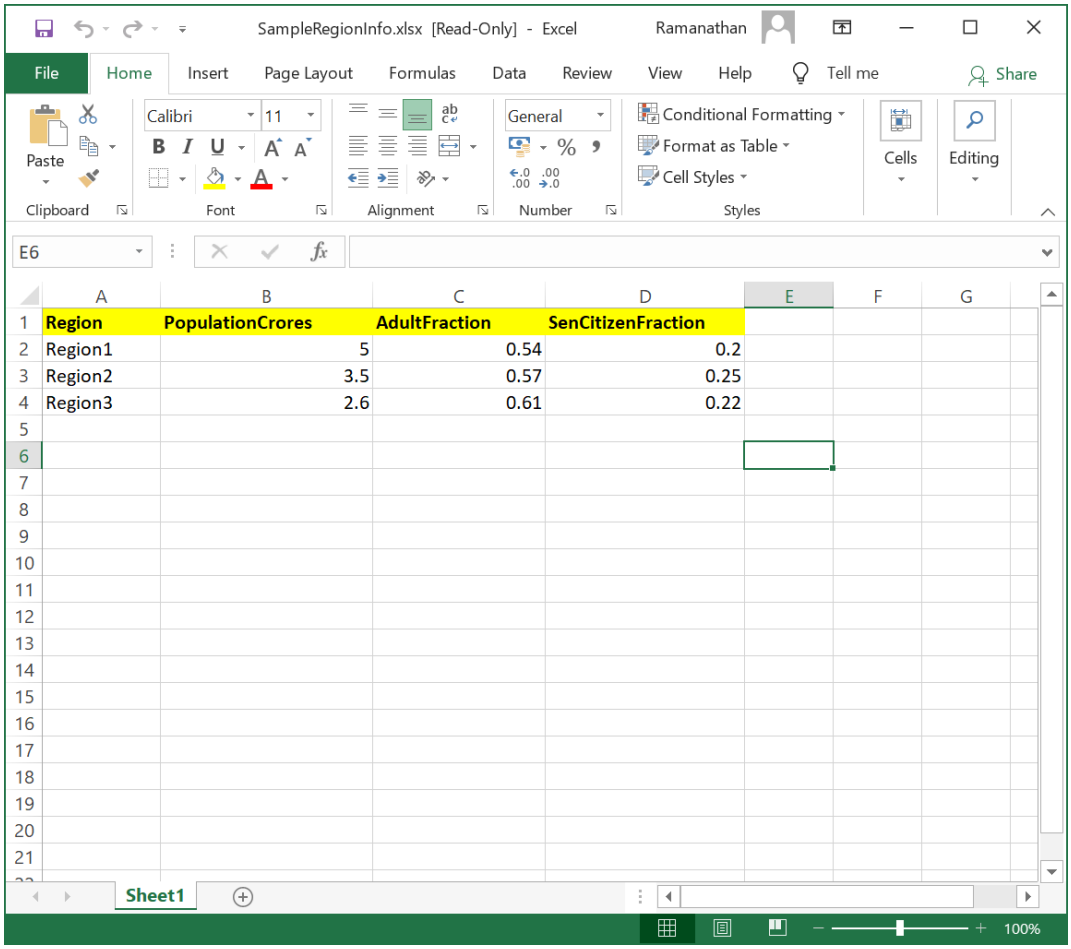
After installation, the user can open the software by double clicking on the Covid19 Transmission Model on the desktop. The main interface will appear. The desired values can be keyed-in in the appropriate fields.

Region: You can select the region of interest and the regional information will change accordingly. If you want to change the numbers, then please choose 'custom' and change the numbers.

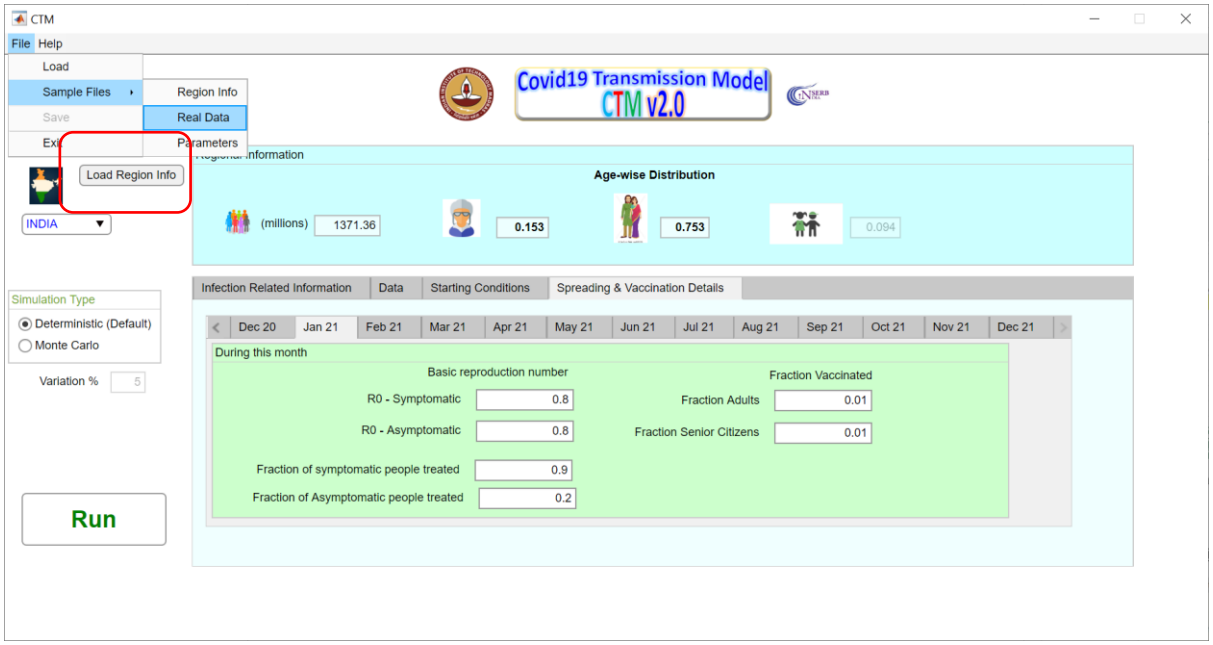
If you want to create a list of regions, along with the age-wise distribution information, for repeated use, then you can do so. Please click on 'File→ SampleFiles → Region Info'.



The software will open a sample region file, in read-only mode. You can save the file in a different name, and fill the region details as desired.

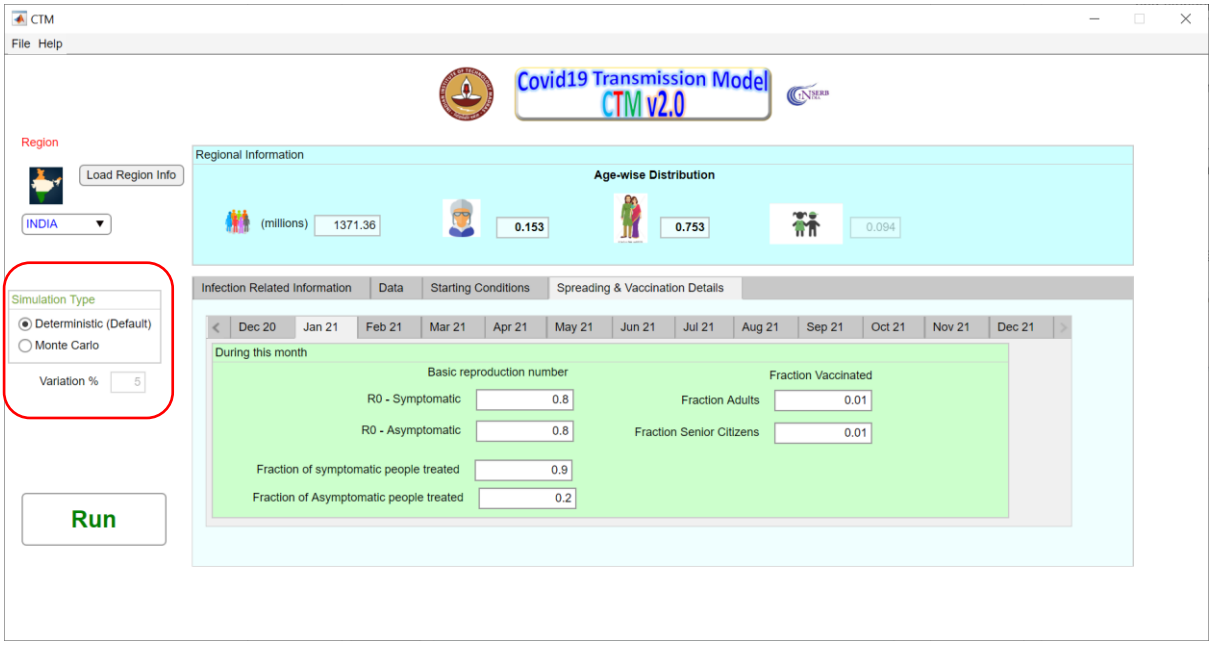


Now, you can click ‘Load Region Info’ button, and select the file you want to load.



The ‘Region dropdown menu’ will be populated with the list in the chosen Excel file. At the end of the list, the ‘custom’ option will be available. Note: Do not create a region called ‘custom’! The software will add that option after loading the Region Excel file.

Simulation Type: You can choose either ‘Deterministic’ or ‘Monte Carlo’, as shown below.



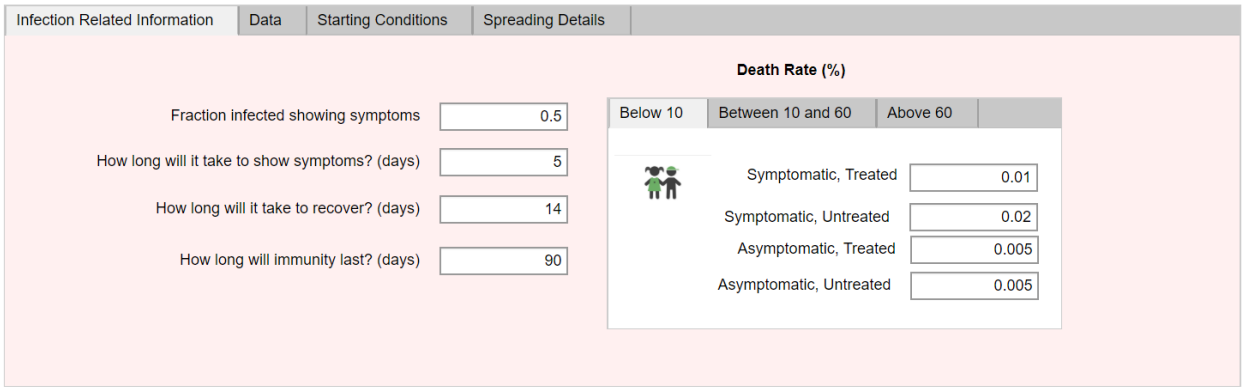
If you choose ‘Deterministic’ then the parameter values are assumed to be accurate and the results will be calculated. If you choose ‘Monte Carlo’, then you should also specify the expected variations in the parameter values.

The parameter values (except the population data and the initial conditions) will be varied randomly, but within the limit specified by the 'Variation %' parameters. The simulation will be performed 100 times, each time with a different combination of parameters. Then the average and standard deviation of the results will be calculated and plotted. This will give an idea of the 'spread' in the model results. The average, along with +1 sigma and -1 sigma values are plotted.

When the data is saved also (as described in the later part of this file), the mean value will be saved in one Excel® worksheet and the standard deviation values will be saved in another Excel® worksheet.

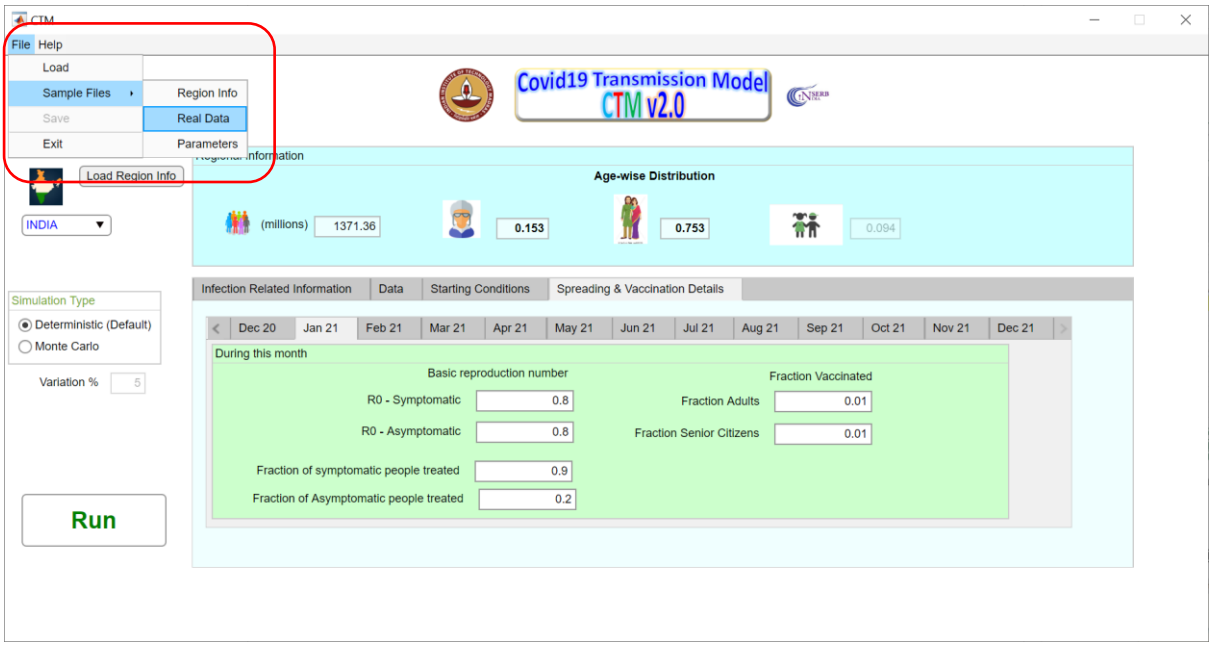
Note that the Monte Carlo type simulation requires 100 times more time than the deterministic type simulation, and hence it can take a few minutes to complete the run. The actual run time depends on the processor speed and the available memory.

Infection Related: The infection relation information can be modified in this tab.

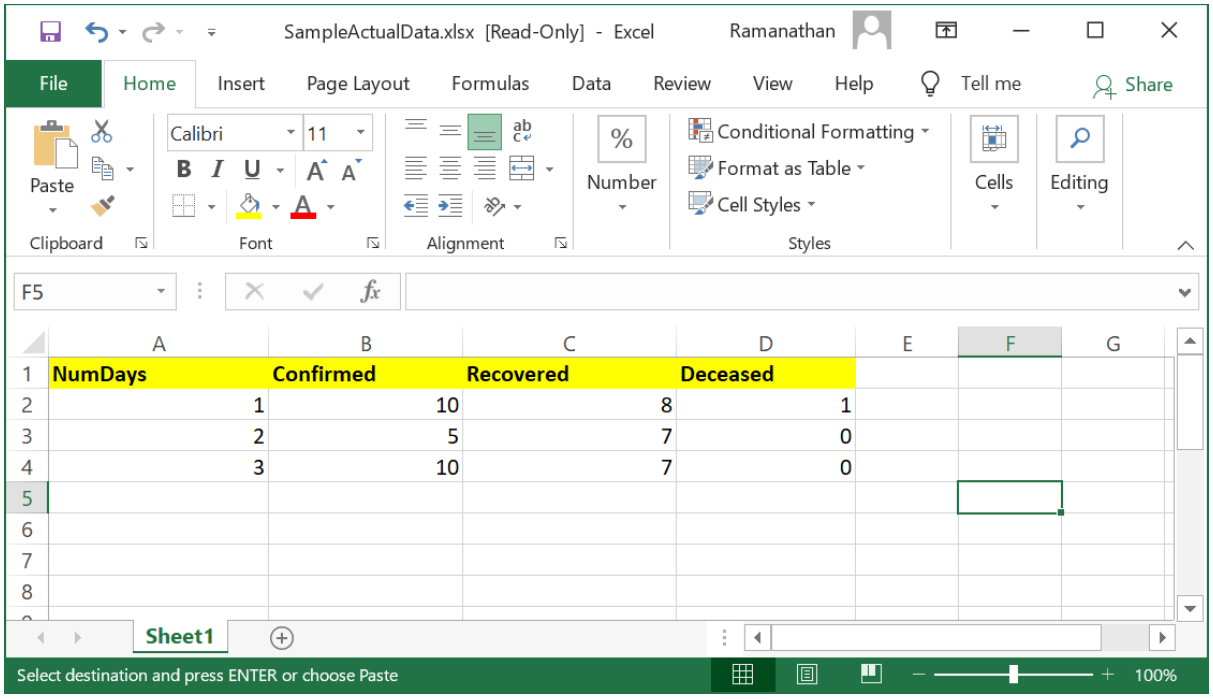


Data: If you want to load 'real data' and compare them with model results, then you can choose that option and the file name here. Note that you cannot type the file name in the text box, instead, you should click the browse button and select an existing file

The data has to be in a certain format. You can view or load sample data by selecting ‘File→ SampleFiles→ Real Data’, as shown below.

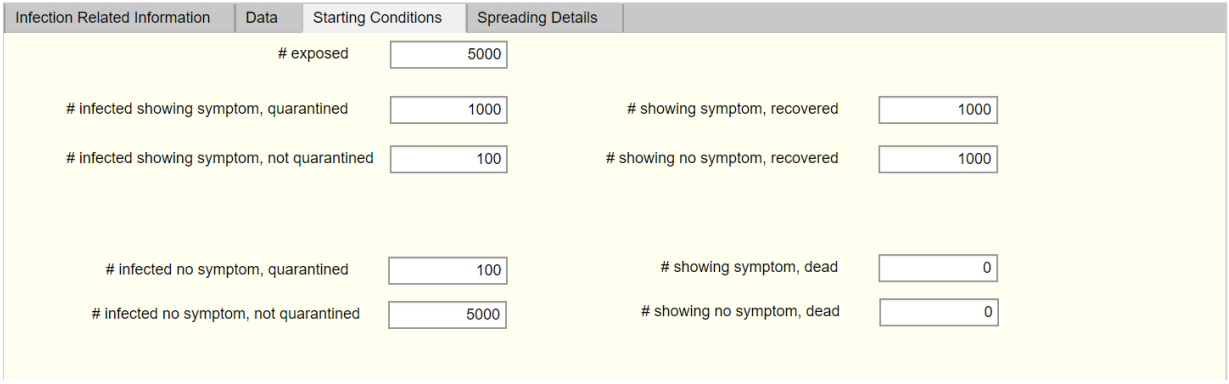


It will open a sample data file, which is read-only. A screenshot of that file is shown here.

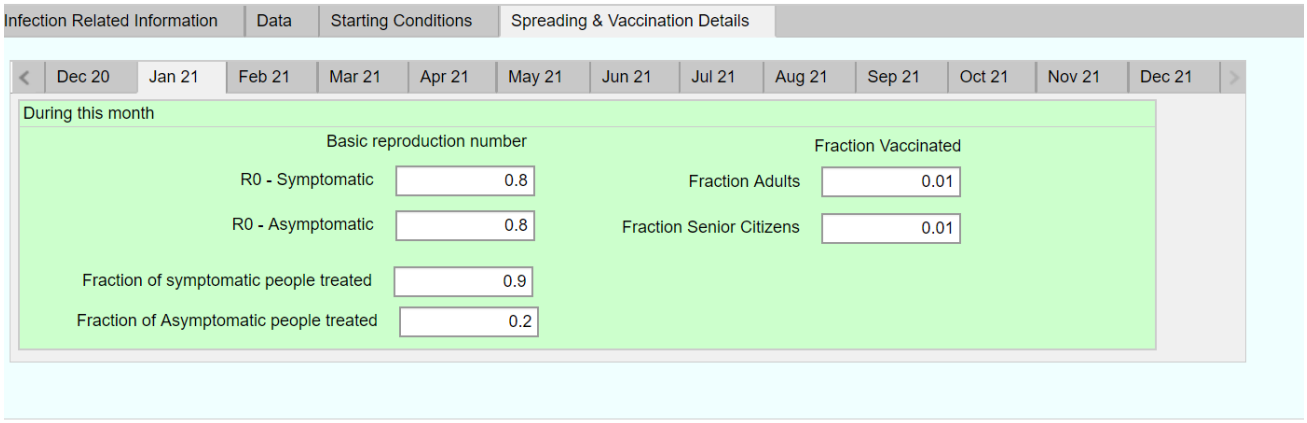


You can save it in a folder with a different name and fill the required data, to use with this software.

Initial Conditions: The starting conditions can be given here.

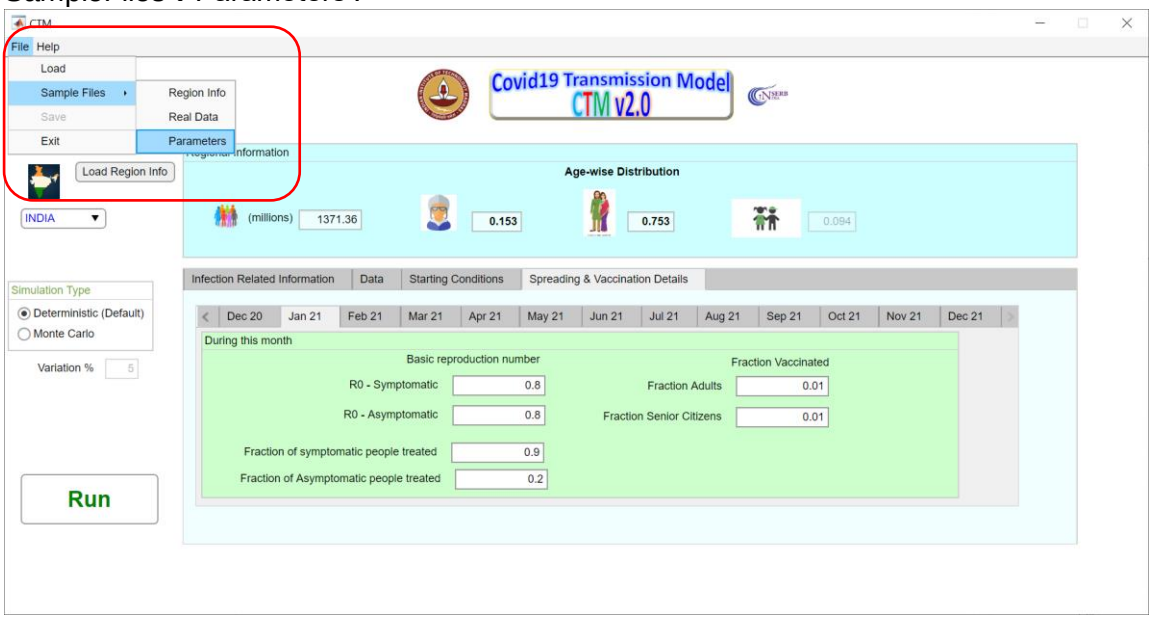


Spreading and vaccination details: The basic reproduction numbers, by month, for different categories of infected population, can be given here. In addition, the fraction of symptomatic and asymptomatic patients receiving treatment, can also be given here. From Jan 21 onward, the fraction of adults and senior citizens vaccinated can also be included in this tab.



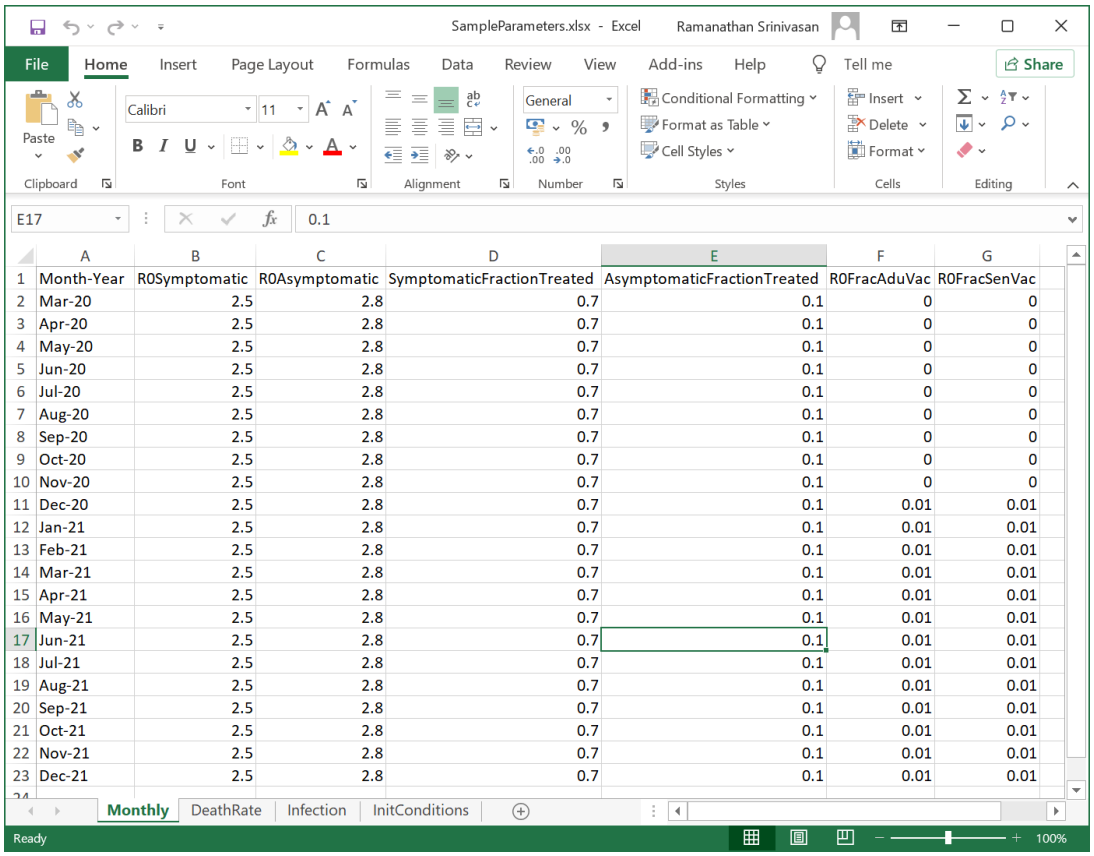
Loading parameters from an Excel file

You can click each tab and key-in the parameter values. If you want to type the values in an excel file and use it, that option is also available. The easiest way to do that is to click 'File→ SampleFiles→Parameters'.



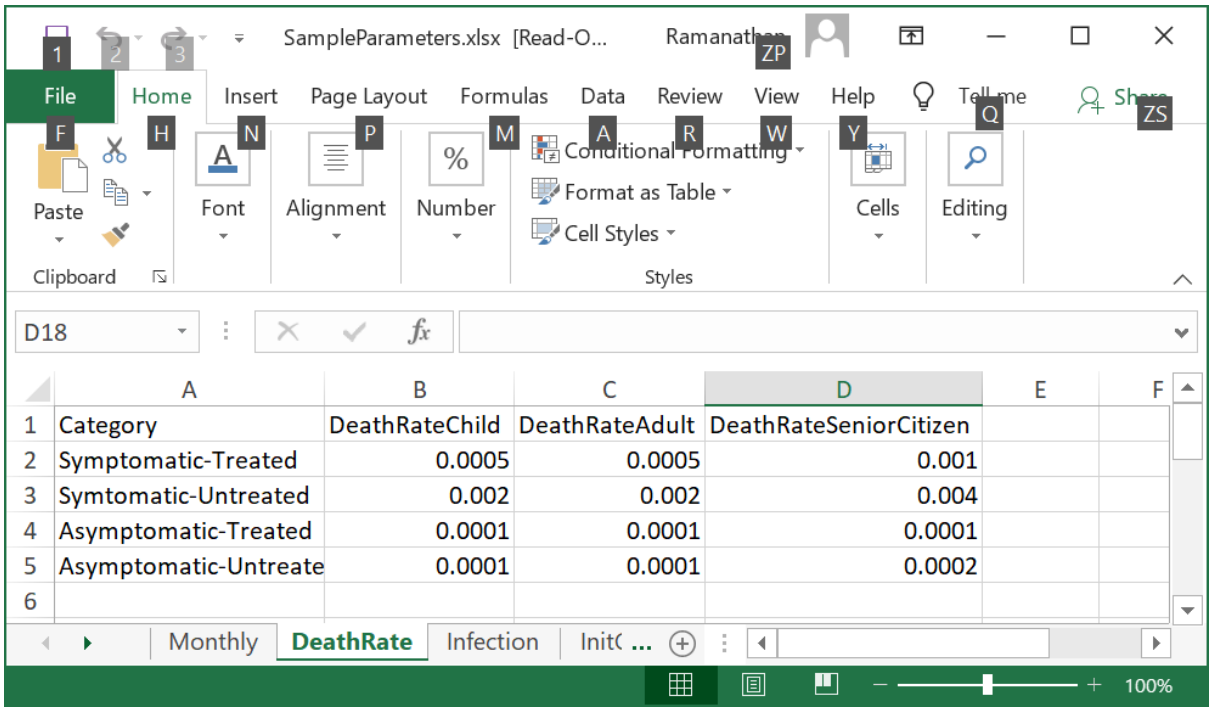
It will open a read-only file called 'SampleParameters.xlsx'. You can save that in a different name, in a suitable directory. There are four worksheets in this SampleParameters.xlsx file.

In the tab named 'Monthly' you can give the spreading and vaccination details.

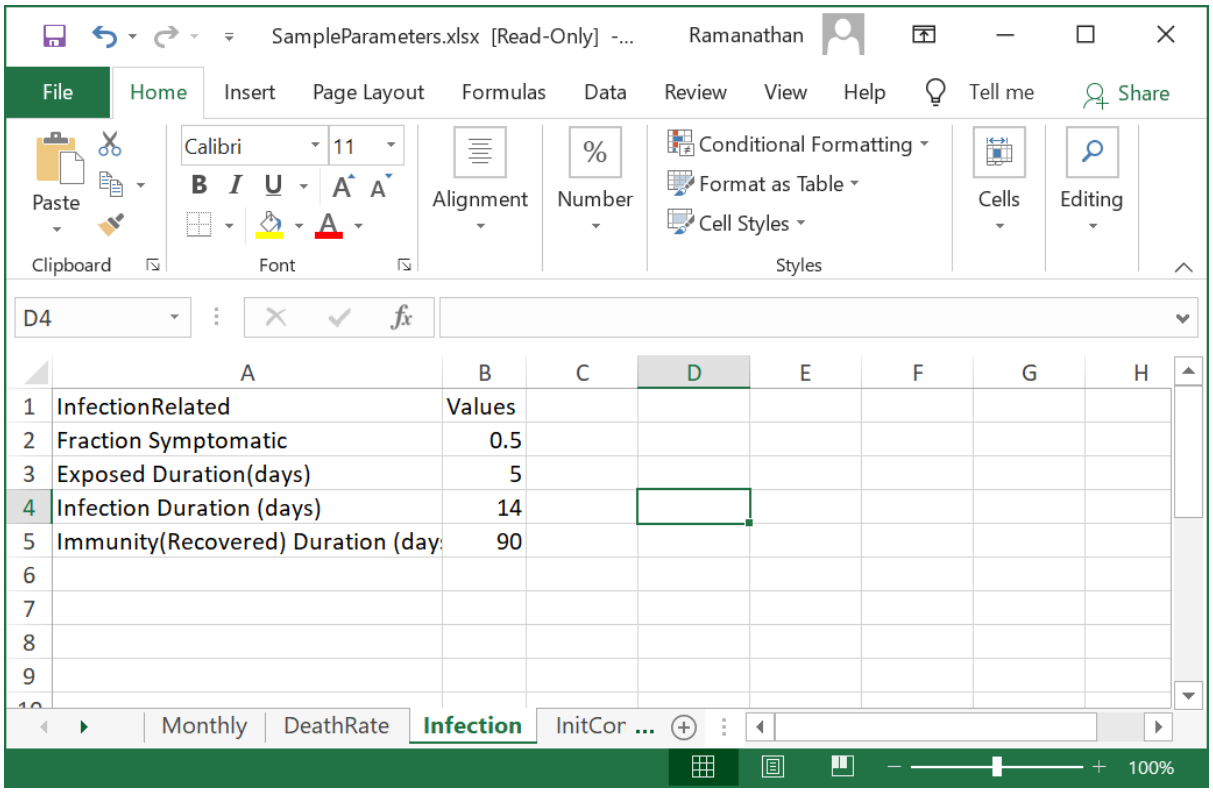


	A	B	C	D	E	F	G
1	Month-Year	R0Symptomatic	R0Asymptomatic	SymptomaticFractionTreated	AsymptomaticFractionTreated	R0FracAduVac	R0FracSenVac
2	Mar-20	2.5	2.8	0.7	0.1	0	0
3	Apr-20	2.5	2.8	0.7	0.1	0	0
4	May-20	2.5	2.8	0.7	0.1	0	0
5	Jun-20	2.5	2.8	0.7	0.1	0	0
6	Jul-20	2.5	2.8	0.7	0.1	0	0
7	Aug-20	2.5	2.8	0.7	0.1	0	0
8	Sep-20	2.5	2.8	0.7	0.1	0	0
9	Oct-20	2.5	2.8	0.7	0.1	0	0
10	Nov-20	2.5	2.8	0.7	0.1	0	0
11	Dec-20	2.5	2.8	0.7	0.1	0.01	0.01
12	Jan-21	2.5	2.8	0.7	0.1	0.01	0.01
13	Feb-21	2.5	2.8	0.7	0.1	0.01	0.01
14	Mar-21	2.5	2.8	0.7	0.1	0.01	0.01
15	Apr-21	2.5	2.8	0.7	0.1	0.01	0.01
16	May-21	2.5	2.8	0.7	0.1	0.01	0.01
17	Jun-21	2.5	2.8	0.7	0.1	0.01	0.01
18	Jul-21	2.5	2.8	0.7	0.1	0.01	0.01
19	Aug-21	2.5	2.8	0.7	0.1	0.01	0.01
20	Sep-21	2.5	2.8	0.7	0.1	0.01	0.01
21	Oct-21	2.5	2.8	0.7	0.1	0.01	0.01
22	Nov-21	2.5	2.8	0.7	0.1	0.01	0.01
23	Dec-21	2.5	2.8	0.7	0.1	0.01	0.01

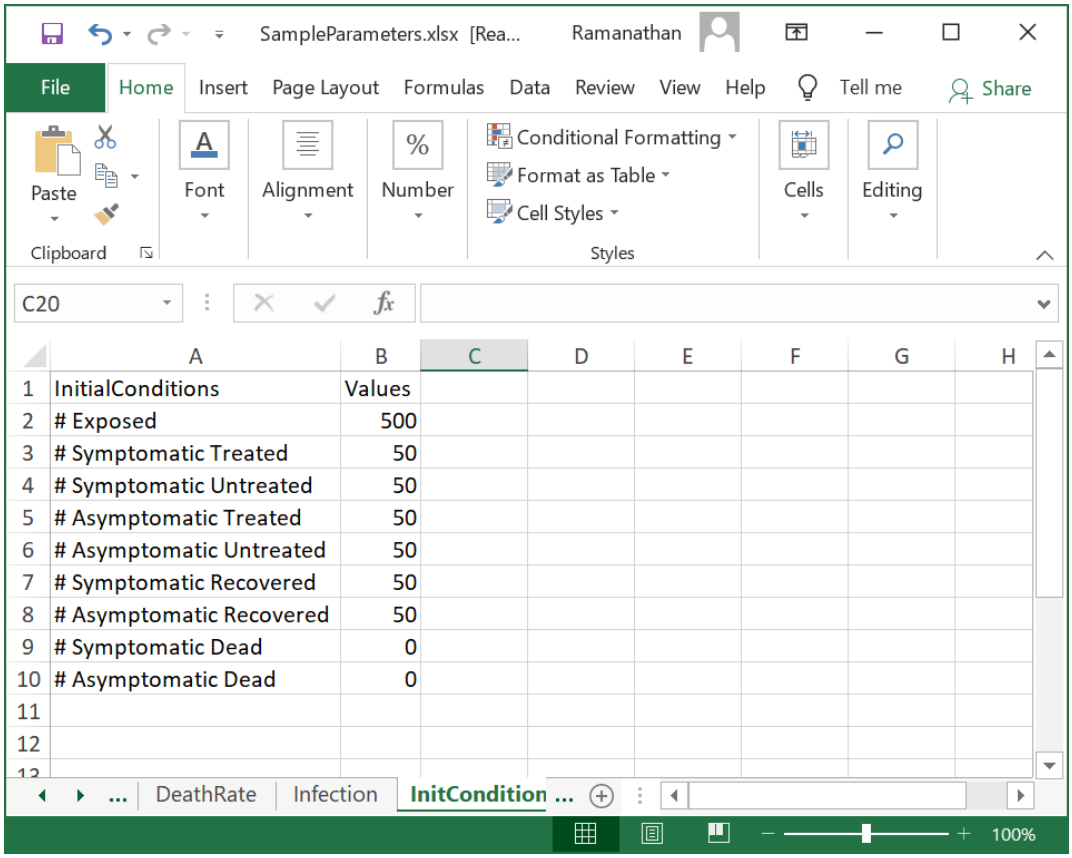
In the worksheet named ‘DeathRate’, you can give the deathrate values.



In the worksheet named ‘Infection’, you can give infection related information

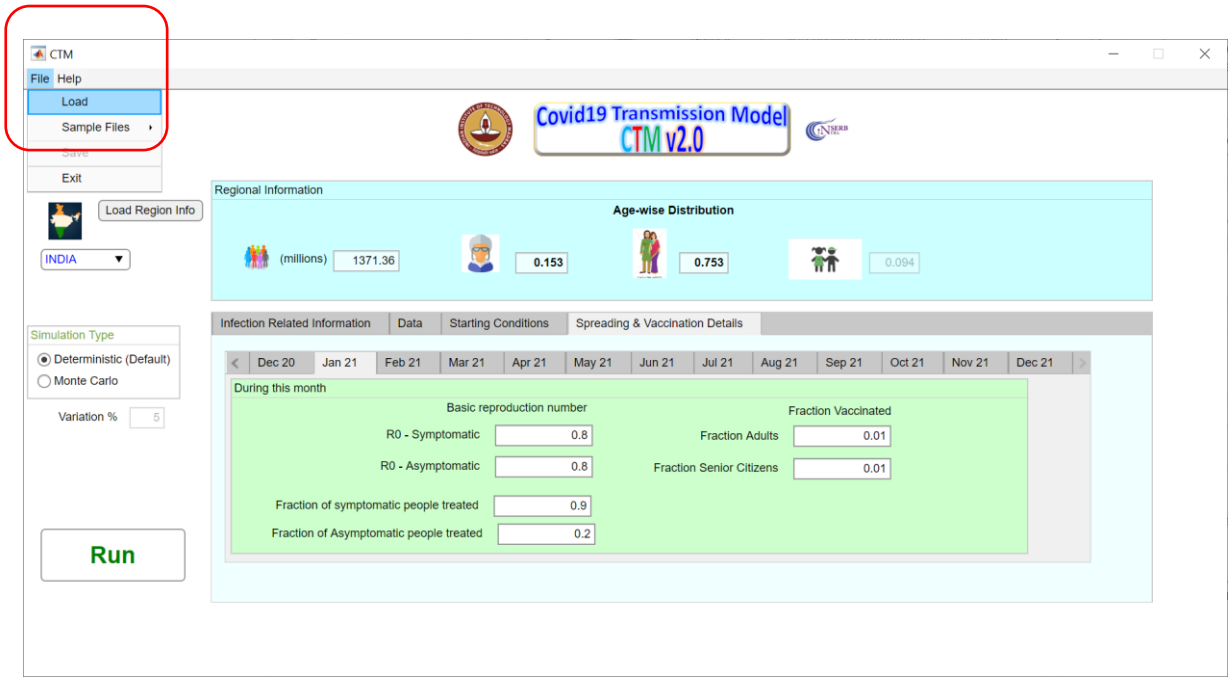


Finally, in the worksheet named ‘InitConditions’, you can give the starting conditions



	A	B
1	InitialConditions	Values
2	# Exposed	500
3	# Symptomatic Treated	50
4	# Symptomatic Untreated	50
5	# Asymptomatic Treated	50
6	# Asymptomatic Untreated	50
7	# Symptomatic Recovered	50
8	# Asymptomatic Recovered	50
9	# Symptomatic Dead	0
10	# Asymptomatic Dead	0
11		
12		

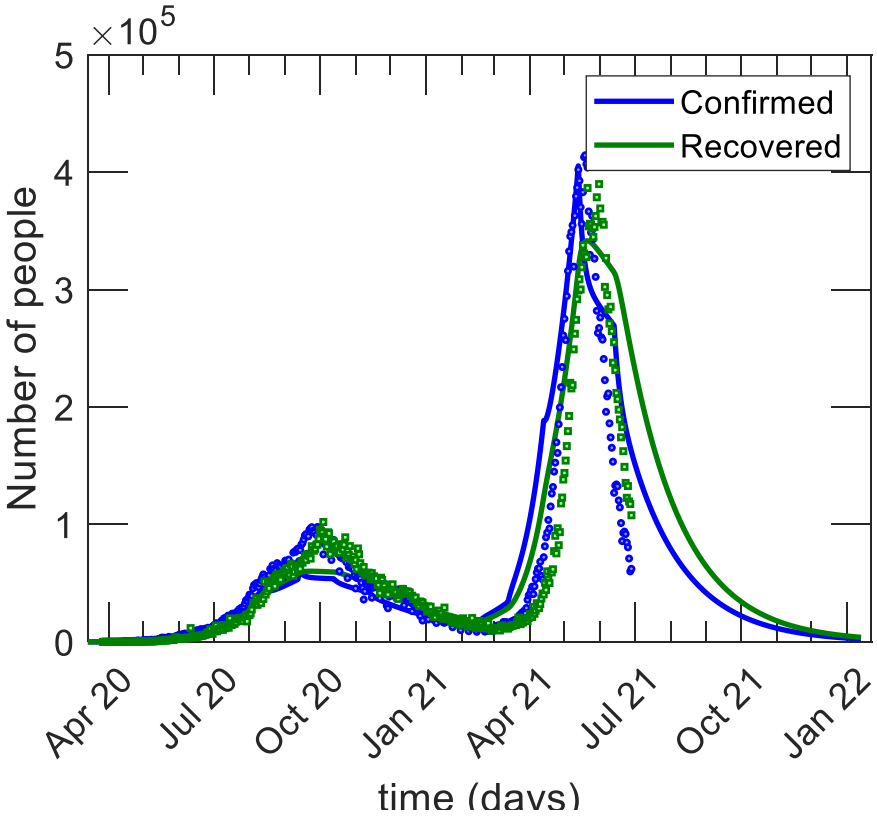
You should save the file in a different name, and then you can load this file using ‘File→Load’ menu.



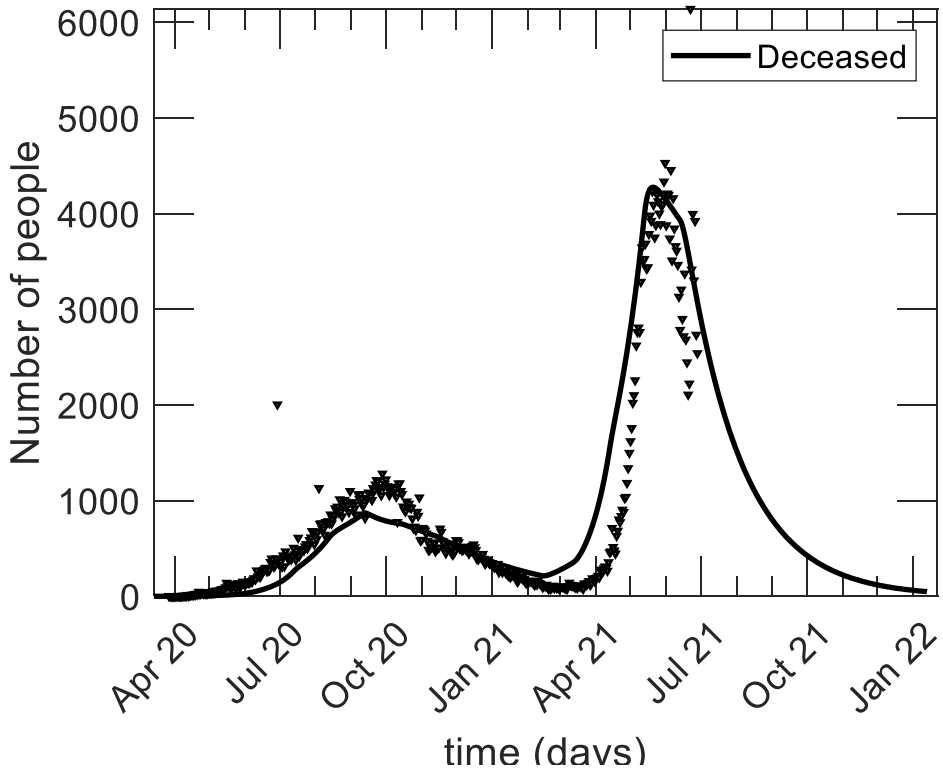
A file open dialog will appear. You should select the appropriate excel file, and click ‘Open’. The software will open the parameter file and populate the fields using the parameters.

Saving the results

After choosing the correct region, and typing in the appropriate parameter values (or using a parameter file to fill these values), you should click the ’Run’ button at the bottom left side of the software. In a few seconds, the simulation would be completed and the results will be shown as graphs. Two figures will appear. One of them will show ‘Confirmed’ and ‘Recovered’.



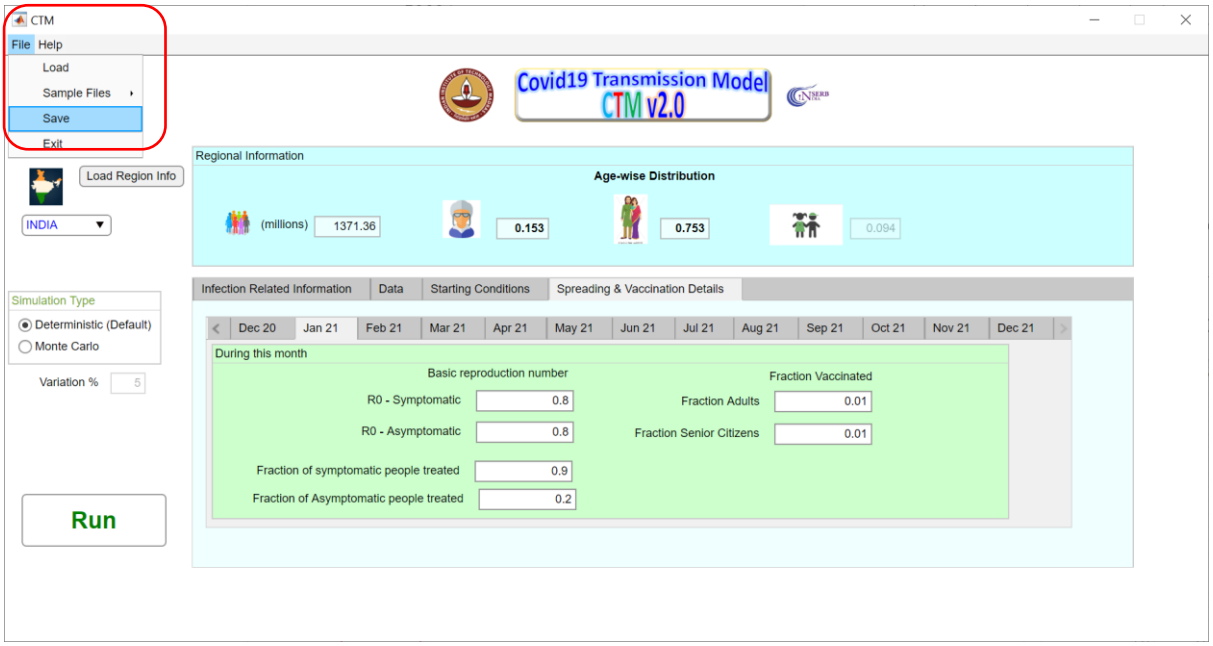
The second figure will show the number of deceased.



Again, note that 1st Mar 2020 is the first day in the model. In the above example, 'real data' is shown as points, while the model results are shown as lines. The shaded regions show the 'upper and lower limits' of the estimates, based on Monte Carlo simulations.

The plots show only the symptomatic patients. For example, 'Confirmed' here means, the number of confirmed patients with symptom. This combines children, adults and senior citizens, who exhibited symptoms. The idea is that only those who exhibited symptoms are likely to be counted in the 'Confirmed Covid19 patients' list generated, and this may serve as a fair comparison.

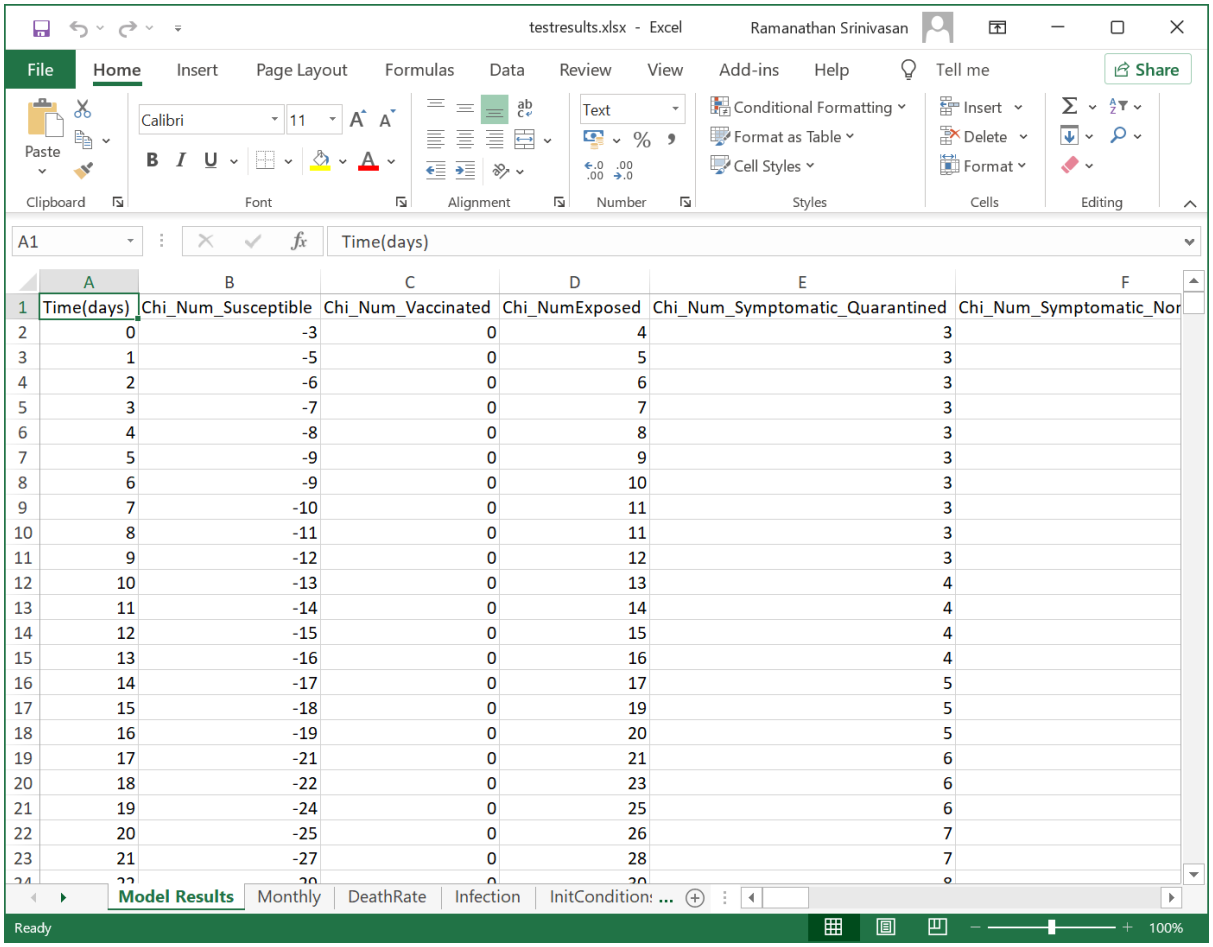
We can save all the results in an excel file. You should click ‘File→Save’. This will open a save file dialog box. Choose a file name and save it in the desired folder.



Please note that only after a run is completed, the save option is available.

The individual classifications are stored separately. i.e., # of symptomatic children infected, # of asymptomatic children infected, and likewise for all other groups (adults/senior citizens, symptomatic/ asymptomatic, susceptible/exposed/infected-treated/ infected-untreated/ recovered / deceased). There are 34 columns in total. The first column is time. The remaining 33 columns correspond to the # of new individuals added to each variable in the 33 equations.

A screenshot of the results file is shown here. This corresponds to deterministic simulations.



	A	B	C	D	E	F
1	Time(days)	Chi_Num_Susceptible	Chi_Num_Vaccinated	Chi_NumExposed	Chi_Num_Symptomatic_Quarantined	Chi_Num_Symptomatic_Nor
2	0	-3	0	4	3	
3	1	-5	0	5	3	
4	2	-6	0	6	3	
5	3	-7	0	7	3	
6	4	-8	0	8	3	
7	5	-9	0	9	3	
8	6	-9	0	10	3	
9	7	-10	0	11	3	
10	8	-11	0	11	3	
11	9	-12	0	12	3	
12	10	-13	0	13	4	
13	11	-14	0	14	4	
14	12	-15	0	15	4	
15	13	-16	0	16	4	
16	14	-17	0	17	5	
17	15	-18	0	19	5	
18	16	-19	0	20	5	
19	17	-21	0	21	6	
20	18	-22	0	23	6	
21	19	-24	0	25	6	
22	20	-25	0	26	7	
23	21	-27	0	28	7	

The result excel file contains 6 work sheets. The worksheet named ‘Model Results’ contain the results. The worksheet named ‘Region’ contains the region information used in the simulation (Population and age distribution). The other four worksheets are ‘Monthly’, ‘DeathRate’, ‘Infection’ and ‘InitConditions’. They contain the parameters used in the simulation to get that particular set of results.

If ‘Monte Carlo’ type simulation is used, another worksheet called ‘ResultsStdev’ will also be included in the file.

BUGS

We believe that there are no bugs in the code but then we might be wrong! If you find any issue or bugs, please let us know by sending an email (srinivar AT iitm.ac.in). Thank you.

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