A (simplified) Covid-19 model

A (simplified) Covid-19 model. The so-called SEIR model is a standard way to model the spread of infectious diseases. It is an example of a compartmental model. We will look at this model in its most basic form, and solve it numerically for various parameters.

The population of N individuals is assigned to different compartments, and individuals can move between compartments. The SEIR model uses four compartments, S,E,I,R, representing segments of the population, so S+E+I+R=N (a simplification, meaning the total population is constant, with some leeway in interpreting the term "total population").

- S. Susceptible individuals. Those are healthy, and not immune individuals who may become infected upon contact with an infected individual.
- E. Exposed individuals. These are individuals who have been infected, but because of the incubation period of the virus are not yet infectious themselves. They will transition to the infected group;
- I. Infected individuals. These are individuals who have been infected, and can pass on the infection to susceptible individuals.
- R. Removed individuals. (In an optimistic scenario referred to as recovered individuals.) These include people who have recovered and are now immune, and people who have died.

Note that for Covid-19 we do not know yet whether recovered people are immune, and if so, for how long. This model assumes they become immune. Interactions between people in compartments are proportional to the number of people in each compartment – this gives a "quadratic" term. Transfers from one compartment to another that do not involve interactions are assumed to occur proportional to the number of people in one compartment, corresponding to linear terms. The equations are as follows (the variable t is time, say measured in days):

$$\begin{array}{ll} \frac{dS}{dt} = -\beta S \frac{I}{N} & \text{susceptibles become exposed due to interaction with } I, \text{ contact rate of } \beta \\ \frac{dE}{dt} = +\beta S \frac{I}{N} - \alpha E & \text{incoming } S \text{ minus exposed moving to } I, \ \alpha = 1/\text{incubation period} \\ \frac{dI}{dt} = \alpha E - \gamma I & \text{incoming exposed - "removed"}, \ \gamma = 1/\text{infectious period} \\ \frac{dR}{dt} = +\gamma I & \text{incoming exposed - "removed"}, \ \gamma = 1/\text{infectious period} \\ \end{array}$$

Now the interesting part is, that some of these parameters will also be time dependent – the effect of physical distancing

and lockdown or reopening. You probably have heard about the now infamous parameter R_0 , the reproduction numbers. For our model we have $R_0 = \beta/\gamma$. (Given that we have "removed" individuals R, the R_0 naming convention is somewhat unfortunate.)

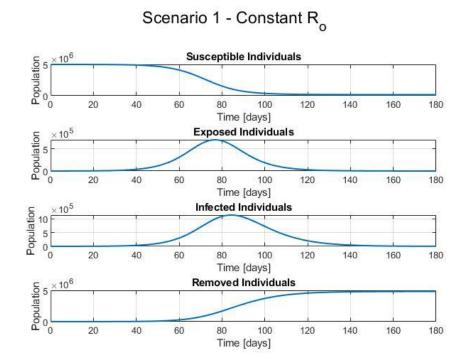
A reasonable set of parameters is

1. = 1/5.2, incubation period of roughly 5 days.

- 2. = 1/10, infectious period of 10 days. The actual period is probably longer, but this value considers that sick people go to hospital or stay home, rather than continuing to circulate among the general population).
- 3. R_0 = 3.5, for now assumed constant (which would be bad news).

Results with constant R_0

In the first scenario, we consider that R_0 is constant and its value is equal to 3.5. The result for this is shown below.



As it can be seen, in this scenario, all of the population gets removed from the model, and this model has the highest number of infections that is possible. If the value of R_0 is reduced from 3.5 to 2.5, 1.25, 0.9, then the number of infections also decreases, but the infection rate also decreases. This means that, it takes more time for the population to get infected and the maximum number of infected individuals is lower that it is for 3.5.

Note that the parameter $\beta = R_0 \Upsilon$.

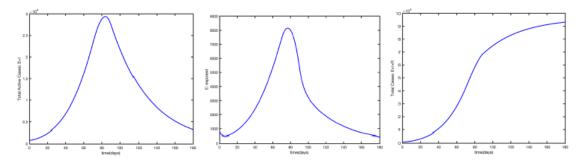
When things become interesting is when we work with time-varying parameters, in particular $R_0 = R_0(t)$ (and, by association, $\beta = \beta(t)$). When you look at the model, _ is the contact rate, which can be controlled. If we all stayed in a remote log cabin by ourselves, _ = $R_0 = 0$; if we practice physical distancing and wear masks when physical distancing is not possible, then R_0 might stay below 1; if we hang out in bars or at large gatherings, then _ and R_0 will go through the roof – leading to large numbers of I_0 , infected and infectious people. We could model the effect of intervention with data for R_0 as follows (three profiles are given):

Days (since outbreak)	120	2170	7184	8590	91110	1111000	after 1000
R_0	3.5	2.6	1.9	1.0	0.55	0.55	0.5
R_0	3	2.2	0.7	0.8	1.00	0.90	0.5
R_0	3	2.2	0.9	2.5	3.20	0.85	0.5

For British Columbia we use N = 5 Million.

We also need initial conditions with I(0) and/or E(0) non-zero. So, "to get started" let us take I(0) = 40; E(0) = 20 I(0); R(0) = 0, S(0) = N - I(0) - E(0) - R(0).

Once again, R(0) is the initial value of R(t), and is nor related to the reproductive number R_0 . Last point: we run the simulation for 6 months, so take $T_{final} = 180$. Sample output:



Results with changing R_0

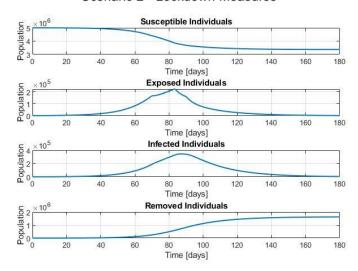
Now we have three more scenarios:

- 1. Lockdown measures
- 2. Effective measures
- 3. Preventive Measures

The results for all 3 are shown below.

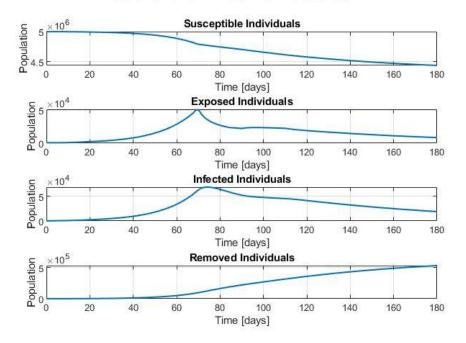
The results for all 3 are shown below.

Scenario 2 - Lockdown Measures



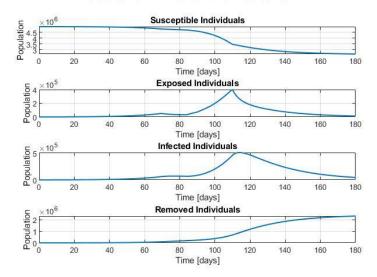
In lockdown measure, we see that that it takes time for people to get infected. The time that it takes for maximum number of people to get infected is almost same as scenario 1.

Scenario 3 - Effective Measures



For effective measure, we see that we get the lowest number of exposed and infected individuals. In this scenario, it takes time to recover from infected individuals, but then again, the number of cases in this scenario is much less than other 3 cases.

Scenario 4 - Preventive Measures



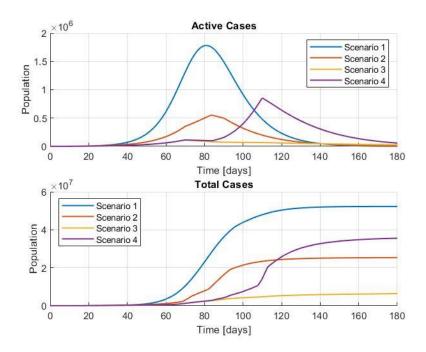
From the plots above, it can be seen that effective measures result in lowest total infections, but it takes more time for the infection to go. The highest infected people are in preventive measures, but it takes more time to reach the peak. For lockdown measures, the pandemic overs quickly then rest of the 2 scenarios.

The deaths per million for each of the 4 scenarios is given below:

Scenario 1	11.3947 deaths per million	
Scenario 2	3.3750 deaths per million	
Scenario 3	1.0021 deaths per million	
Scenario 4	3.5937 deaths per million	

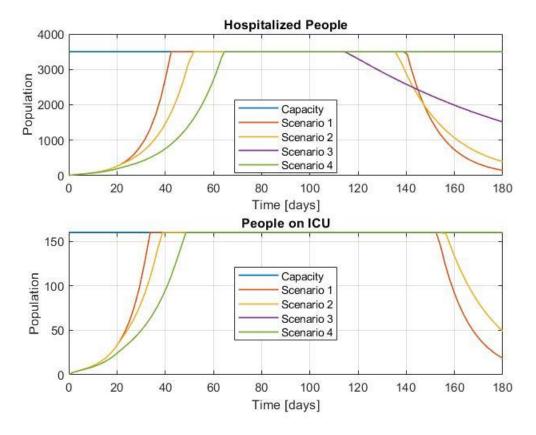
Active and Total Cases

The plot below shows the active and total cases for all 4 scenarios.



As it can be seen from graph above, in the scenario 1, where we have constant R_0 , the number of active cases is most, whereas, for scenario 3, in which effective measures are taken, we get the lowest number of people for active cases. For the total cases scenario, we get lowest with scenario 3, and for each of the 4 scenarios, we get a constant value of total cases after 180 days, meaning that after 180 days, for each of the 4 cases, the pandemic is almost over.

The plot below shows a plot for patients in hospital and patients on ICU.



We see that for all 4 cases, at peak times, between 60 to 120 days, the capacity of hospitalized people and people on ICU are at maximum. For all scenarios, except scenario 4, we see that after a certain time, the number of people in hospital decreases. For scenario 4, both the patients on ICU and people in hospital are still at maximum and are taking full capacity.