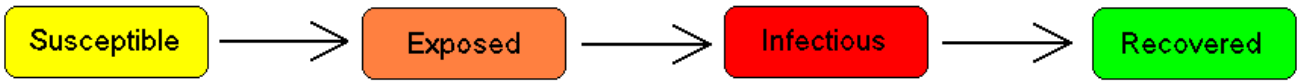
More notes on a Virus spread model: **Peter Taylor-March 20, 2020:** **First let me emphasize that I am not an expert in epidemiology or related areas - this is just a simple application of some basic Applied Math.**

The basic SIR equations set up in Kermack and McKendrick (1927) relate, S(t)-the number of susceptible individuals, I(t)-the number of infected individuals, and R(t)-the number of recovered (or deceased) individuals. The total population N = S + I + R, and N is considered constant. S, I and R can be normalized by N, s = S/N, in = I/N etc., using "in" to avoid confusion with $(-1)^{1/2}$.

This has been extended in various ways, see for example,



https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology#The_SEIR_model

This was with the addition of an exposed category who may or may not be infectious. It is currently believed (see ECDC note below) that they can transmit the virus. We will interpret Infectious as symptomatic and "exposed" as those who have the virus but no symptoms. In many ways they are the most dangerous since they will not necessarily self-isolate. We will also add a Deceased category. For some applications a birth rate and regular death rate can be added, see Earn et al (2010), but here we assume them to be equal and our Deceased category will just be those dying as a result of the infection.

So we add e = E/N and d = D/N as our variables and modify the equations to become,

de/dt = bi*s*in + be*s*e – (c+ke+me)*e ; with "exposeds" increasing as a result of interactions between both infectious and exposed with susceptible members of the community, at rates bi and be. Exposeds can then move to being infected, at rate c, recover, at rate ke or die, at rate me.

din/dt = c*e – (ki + mi)*in ; exposeds become infecteds at rate c, who then recover at rate ki and die at rate mi.

dr/dt = ki*in + ke*e; some infected and some exposed members recover. Recovery implies immunity and no longer susceptible.

dd/dt = me*e + mi*in; some exposed and some infectious members could die from the virus, but initially we will set me = 0.

Finally

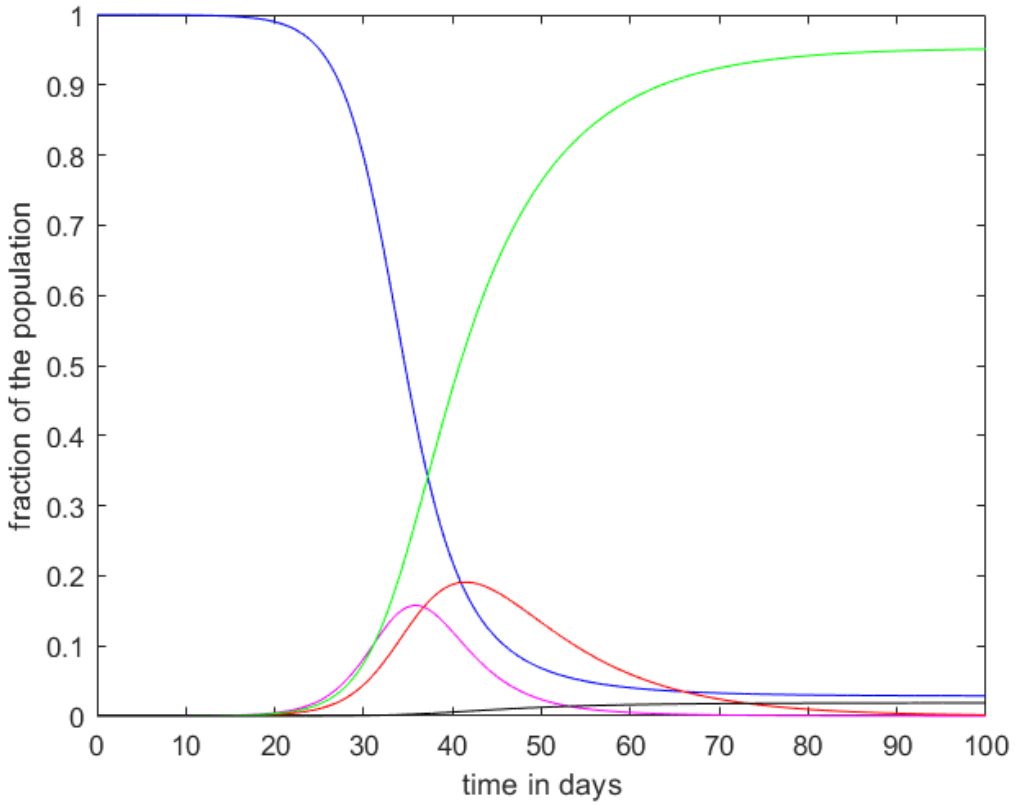
s = 1 – e – in -r- d. The total, normalized population is 1 so s represents the remaining susceptible members.

With t measured in days, ke and ki, in the recovery equation are average recovery rates for exposed and infected individuals in $days^{-1}$ while in the de/dt equation, be and bi are a little more complicated in

that in the un-normalized version it is b*S that is in days^{-1}. As in the SIR model, the bs could be interpreted as the numbers of infection transfers per day from exposed or infected members to a susceptible individual. Key parameter are the ratios of be/ke and bi/ki. If transmission is fast and recovery slow there will be problems. We may not be able to control the ks but the bs can be modulated by reducing "social contacts".

Some initial results are shown below, with be=0.5; bi=0.5; ki=0.1; c=0.2; ke=0.2 ; me=0.00; mi=0.004; and at t =0, e = 0.00001; in = 0.0; s = 1-e; r = 0; d=0;

The colour code is Susceptible – blue, Exposed – magneta, Infected – red, Recovered – green and Deceased – black.



The initial number of exposed but not symptomatic individuals is 0.00001 x the population. We could apply the model to any relatively isolated community provided there was not too much exchange with the outside world. So for the Greater Toronto area with a population of 6 million that is 60 "exposed" individuals. With 153 confirmed (so infectious) cases we are way ahead of that now (March 20, 2020). Running the model with e=10^{-4} at t = 0 moves things back by about 7 days. **WITH THE PARAMERS** USED the peak infectious numbers are about 18% of the population and if 14% of those need hospitalization (WHO numbers) we would need 150,000 beds. Ontario has 1700 ICU beds. Final numbers deceased in this **SIMULATION** are 1.8% of the population.

With no vaccine and no current cure most of the population will be infected at some stage UNLESS the interaction rates between exposed and susceptible are drastically reduced. This can be done but needs to be maintained until a vaccine can be developed and "herd immunity" has a chance.

As with the SIR model one can play with parameters, which could be allowed to be varied with time or other criteria. We can play with the parameter values but as a first guess these seem plausible. Code is below but should be checked!!!

From https://www.ecdc.europa.eu/sites/default/files/documents/RRA-sixth-update-Outbreak-of-novel-coronavirus-disease-2019-COVID-19.pdf
Transmission in pre-symptomatic stage of infection: In addition to case reports, pre-symptomatic transmission has been inferred through modelling, and the proportion of pre-symptomatic transmission was estimated to be around 48% and 62% [41]. Pre-symptomatic transmission was deemed likely based on a shorter serial interval of COVID-19 (4.0 to 4.6 days) than the mean incubation period (five days) with the authors indicating that many secondary transmissions would have already occurred at the time when symptomatic cases are detected and isolated [42]. Major uncertainties remain in assessing the influence of pre-symptomatic transmission on the overall transmission dynamics of the pandemic.

```
%SEIRD2 model in matlab - Peter Taylor
t=0:0.05:100;
dt=0.05; e = 0.00001; in = 0.0; s = 1-e; r = 0; d=0;
S(1)= s;IN(1)=in; R(1)= r; E(1)=e;
for j = 2:2001
   [dedt, dindt,drdt,dddt] = deriv(s,in,e);
   e=e+dedt*dt; in = in + dindt*dt;
   r = r + drdt*dt; d = d+dddt*dt; s = 1-e-in-r-d;
   E(j)=e; IN(j)=in; R(j)=r; S(j)=s; D(j)= d;
end
figure
plot(t,S,'blue')
xlim([0 100]); ylim([0 1]); xlabel('time in days')
ylabel('fraction of the population')
hold on; plot(t,E,'m');plot(t,IN,'r'); plot(t,R,'g');
plot(t,D,'black');

function [dedt,dindt,drdt,dddt] = deriv(s,in,e)
be=0.5; bi=0.5; c=0.2; ke=0.2 ; ki=0.1; me=0.00;
mi=0.004; dedt=bi*in*s +be*e*s-(c+ke+me)*e;
dindt=c*e-(ki+mi)*in;
drdt=ki*in+ke*e;
dddt=me*e+mi*in;
end
```

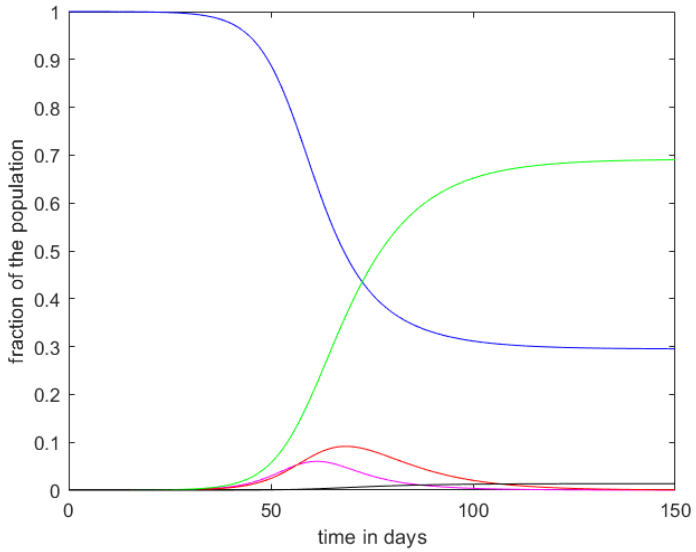
```
## I get "plot.new" errors sometimes!
#SEIRD2 model in R - Peter Taylor
t<-seq(0, 200, by=.1); S<-t;IN<-t; R<-t;E<-t;D<-t;
dt=0.1; e = 0.00001; inf = 0.0; s = 1-e; r = 0; d=0;
S[1]<-s;IN[1]<-inf;R[1]=r;E[1]=e;D[1]=d;
be=0.5;bi=0.5;ki=0.1;c=0.2;ke=0.2;me=0.00;
   mi=0.004;

        for (j in 2:2001){
        dedt=bi*inf*s +be*e*s-(c+ke+me)*e;
        dindt=c*e-(ki+mi)*inf; drdt=ki*inf+ke*e;
        dddt=me*e+mi*inf;
        e=e+dedt*dt; inf = inf + dindt*dt;
        r = r + drdt*dt; d = d+dddt*dt;
        s = 1-e-inf-r-d; E[j]=e;IN[j]=inf;
        R[j]=r;S[j]=s;D[j]= d;}

plot(t,S,type='l',col='blue',xlim=range(0,100),
        ylim=range(0,1), xlab='time in days',
        ylab='fraction of the population');
lines(t,E,type='l',col='purple');
lines(t,IN,type='l',col='red');
lines(t,R,type='l',col='green');
lines(t,D,type='l',col='black');
#plots should the same as those with matlab#
```

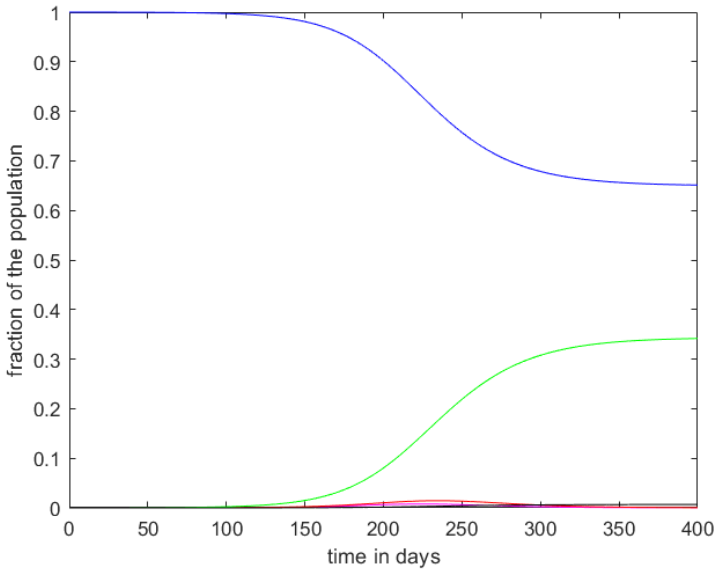
Parameter variation.

If we can reduce interaction between infected and susceptible community members we can slow things down and reduce extremes. The plot below and has all parameters the same as above except that bi is reduced to 0.1.

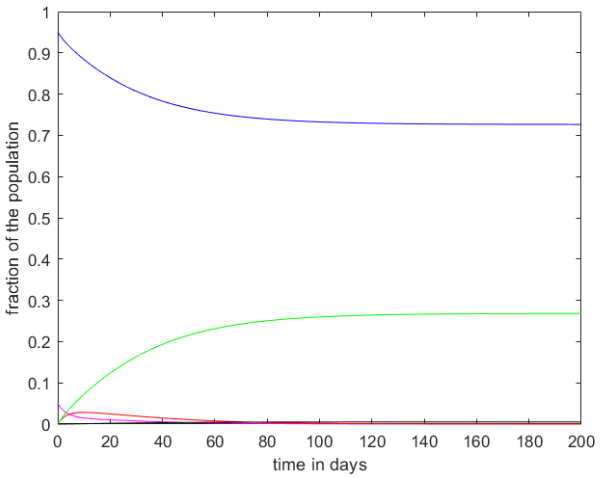


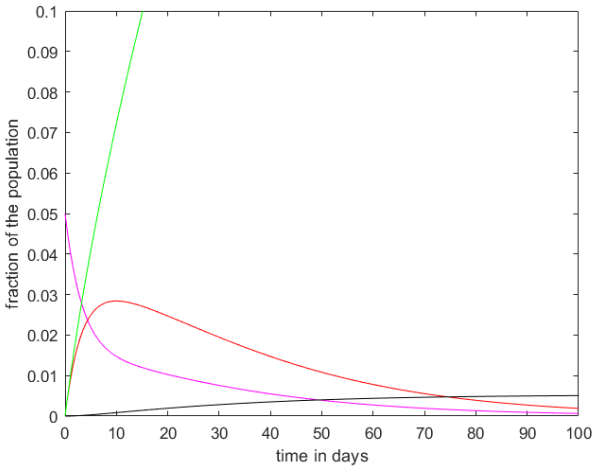
The peak infectious numbers are now about 9% of the population and if 14% of those need hospitalization (WHO numbers) we would “only” need 75,000 beds. Final numbers deceased in this **SIMULATION** are 1.3% of the population and 30% of the population manages to avoid being infected.

Reducing be as well, to 0.3, we get the plot below, with a longer time scale. The time scale is longer, total death rates are down below 0.7% and the peak infected percentage of the population is down to about 1.4%, so maybe manageable.



IF we can reduce be and bi even further then the initial growth does not occur and there is no exponential growth. To illustrate this we can put in a significant number of infected individuals at t = 0 and watch numbers decay. So we start with in = 0.05 and see how numbers change with time if be = 0.2, bi=0.1 to simulate a low contact environment with an influx of exposed but asymptomatic individuals from outside the community, e(0) = 0.05, an extreme value for illustration





There will be infections and deaths but with a decay rate faster than the growth rate the numbers infected decay after an initial growth (transfer from exposed) and life goes back to normal after a couple of months. **IF we can keep interaction rates low from now on this might be achievable!**

As noted several times this is just a simple model, but it can give guidance on potential impacts of different courses of action. The central requirement is to keep infection rates below recovery rates. If we can improve recovery rates through medication and treatment that is one aspect but the urgent thing to do is to reduce infection rates by limiting interactions between infectious individuals (infected and exposed) to the rest of the population who are susceptible. At present that is most of us but if things go on the eventual limit is when the majority of the population have been infected and recovered so that “herd immunity” starts to apply.

We are at a very early stage in Canada and reducing interactions should be possible. This has to go on until an effective vaccine is developed, so many months. Reducing interactions for a few weeks will slow things down but the growth can go back to exponential if infection rates exceed recovery rates at any time.

Play with the code and convince yourself! Note SIR has 3 variables, 2 parameters, SEIRD has 5 variables, 7 parameters, so still moderately simple.

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