Some notes on a Virus spread model: Peter Taylor-March 17 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.

Thinking about virus spreading I send an earlier note using a simple equation from Calculus 1014. There we assumed the key virus spread equation is DY/dt = A*Y*(N-Y), where Y is the number infected and N is the total population. There is no recovery, just continuous infection. It has an analytic solution suited to 1^{st} year calculus! The mathematics gets more complicated when some Y recover but initially there is still exponential growth.

Taking this a bit further one can use the SIR (Susceptible, Infected, Recovered (or dead)) version which seems more realistic. It is well described at https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model and originates from a 1927 paper by Kermack and McKendrick. (Kermack, W.O. and McKendrick, A.G. (1927) Contributions to the Mathematical Theory of Epidemics. Proceedings of the Royal Society of London A, 115, 700-721)

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 $(-1)^{1/2}$ and the governing equations become

din/dt = **b*****s*****in** – **k*****in**; with infections increasing as a result of interactions between infected and susceptible members of the community.

dr/dt = **k*in**; so some infected members recover, and some die. Recovery implies immunity and no longer susceptible.

s = 1 - in - r. The total, normalized population is 1 so s represents the remaining susceptible members I had originally used β for b and γ for k as in some figure titles below.

With t measured in days, k, in the recovery equation is an average recovery rate for an infected individual in days⁻¹ while b is a little more complicated in that in the un-normalized version of the equation it is bS that is in days⁻¹. Thus, b could be interpreted as the number of infection transfers per day from an infected to a susceptible individual. A key parameter is the ratio of b/k. If transmission is fast and recovery slow there will be problems. We may not be able to control k but b can be reduced by reducing "social contacts".

I couldn't get an analytic solution to the non-linear system of equations above, but a simple forward Euler numerical scheme works. In Matlab I used the code below and get sample results as shown, and the same results as the maa web site if I use their input.

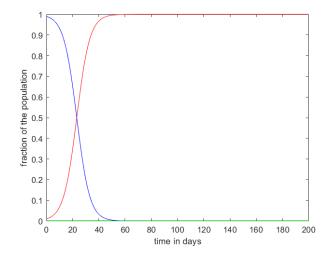
It should be stressed that the results below are numerical solutions to non-linear differential equations and coefficients b and k are taken as constant. In reality there will be significant variations in interaction and transfer rates and in recovery rates but the overall conclusion is that reducing interactions between those infected and those not is the key factor in limiting the eventual spread of the virus, and it may take some time, as most experts and some politicians are telling us.

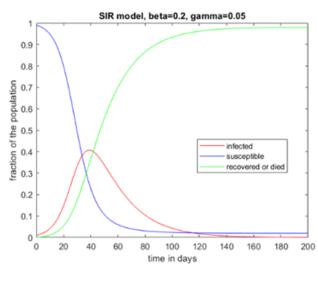
%SIR model t=0:0.1:200; dt=0.1; in=0.01; s = 1-in; r = 0; S(1)= s;IN(1)=in; R(1)= r; for j = 2:2001 [dindt,drdt] = deriv(s,in); in = in + dindt*dt; r = r + drdt*dt; s = 1-in-r; S(j)=s; IN(j)=in; R(j)=r; end plot(t,IN,'r') xlim([0 200]); ylim([0 1]); xlabel('time in days') ylabel('fraction of the population') hold on; plot(t,S,'blue'); plot(t,R,'g')

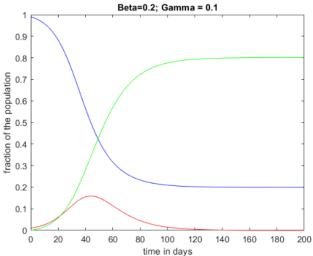
function [dindt,drdt] = deriv(s,in) b=0.2; k=0.1; dindt=b*s*in - k*in; drdt=k*in; end

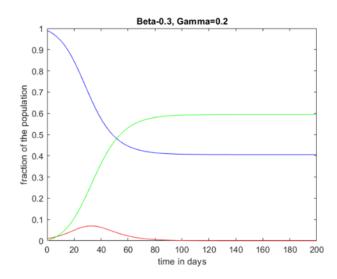
The initial results on the right-hand side looked at the sensitivity to b (beta) and k (gamma).

Changing beta -b and gamma – k one can vary total number who get infected, the height of the peak and maybe prevent some (40% in final figure) from getting it at all. It all depends on contact frequency beta(b) and recovery rate gamma (k). If k=0 all susceptible members of the population will be infected in the end, and r =0, as below, with b = 0.2.





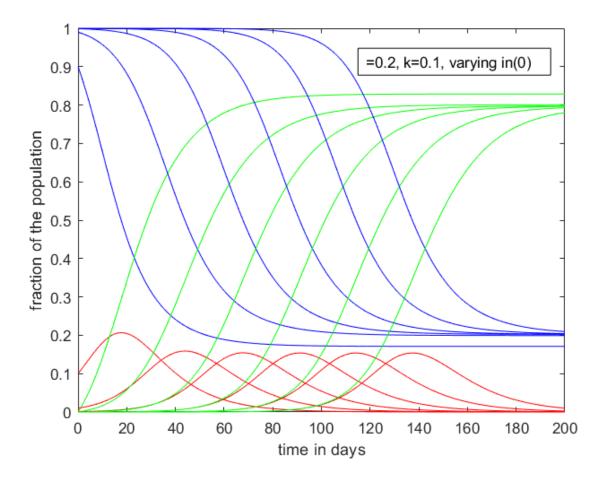




The next step would be to look at estimates related to the current Covid 19 situation. There are infection numbers, but it is not clear that they are at all accurate and it is not clear how long the infection continues until the individual has recovered, or died. I estimate that k⁻¹ is probably in the 5, 10, 20-day range used above.

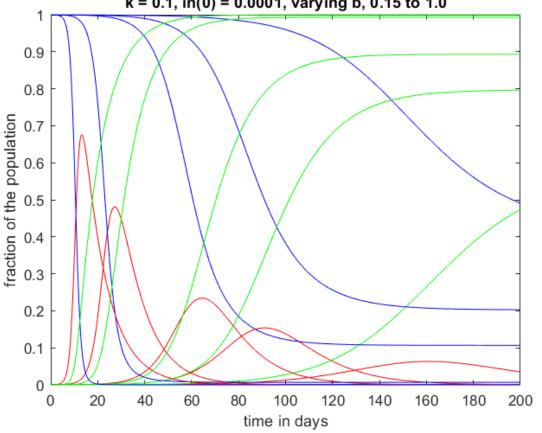
We have also not discussed the initial values used in the code at t=0. What impact does in(0) have? Comparisons below suggest that, provided it is relatively small it just impacts timing and not the final outcome. The in(0) = 0.1 case is rather extreme but even then the impact is not great. What matters is the b/k ratio.

My naieve interpretation of this is that the concern about importing cases from other countries may be excessive at this point. If you keep all out from the start then that would work (if in(0) = 0 the solution is simply in =0!) but once there are a few cases, adding a few more has only a small impact – but this is just a model! Here in(0) has been varies from 0.1 by factors of 10 to 0.000001. Delays are about 25 days per decade change in i(0). Delay is good in that health facilities can be expanded and more will be developed in terms of treatment but the final outcome in terms of the total numbers who have been infected and recovered or died is not significantly changed.



The critical parameter, in this simple model, is the parameter b, and its relationship with k. If we fix in(0) at 10^{-4} and k = 0.1 we can vary b. The figure below uses b = 1.0, 0.5, 0.25, 0.2, 0.15 (from left to right!). The conclusion is that we should limit contacts, and probably do that for an extended period, maybe 6 months. By then it might

be hoped that vaccines might have been developed and treatment refined. Ignoring things and having rapid growth with b=1 would get it over faster but stress hospitals and morgues.





Note that even with b = 0.15 roughly half the population had been infected and recovered (or died). Going to lower values of b the model may be less

reliable. With b = k the equation **din/dt** = b*s*in - k*in leaves the number infected virtually constant while s is very close to 1. Also if b < k then the infection would decrease and eventually cease, as shown here. So, as long as there are not significant numbers initially, the numbers infected will decrease with time if b<k.

Remember that the color code is Red - infected Blue – susceptible Green - recovered or dead.

