Estimating $\mathcal{R}_t$ from Covid-19 case counts

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Abstract

Here we give an interpretation of the *effective reproduction number*, $\mathcal{R}_t$ that arises from the Susceptible-Infectious (SI) model for the spread of infectious disease. We also outline a simple scheme for estimating $\mathcal{R}_t$ from daily case counts.

1 The standard SI model

The Susceptible-Infectious (SI) model [3] is often used to study the spread of infectious disease by tracking the number (S) of people susceptible to the disease and the number (I) of people infectious with the disease.

Based on the model, the only way that a person can leave the susceptible group is to be infected and become immediately infectious, and the only way that a person can leave the infectious group is to recover or die. It is further assumed that those who have recovered or died from the disease are no longer susceptible.

It is also assumed that all those who have not had the disease are equally susceptible and that the probability of their contracting the disease at time $t+1$ is proportional to the product of S and I at time t.

These assumptions lead us to a pair of difference equations for S and I, where the unit of time t is one day:

$$S_{t+1} = S_t - \beta \frac{S_t I_t}{N} \tag{1}$$

$$I_{t+1} = I_t + \beta \frac{S_t I_t}{N} - \gamma I_t \tag{2}$$

Here the parameter $\beta \geq 0$ controls the rate at which the susceptible become infected and the parameter $\gamma \geq 0$ controls the rate at which the

infectious recover or die. The parameter N is the size of the **initial** susceptible population and is usually assumed constant. The number of infected persons who are no longer infectious is given by $N - (S_t + I_t)$.

The susceptible time series (S) is a monotonically decreasing sequence starting at $S_0 = N$ just before the outbreak of the disease whilst the infectious group I starts at $I_0 = 0$ just before the outbreak but then climbs and falls depending on interventions but eventually dies out to zero when the disease has run its course.

With this model the trajectories of S_t and I_t are pre-determined at the outset by the parameters, β, γ and N. See Figure 1 for an example trajectory.

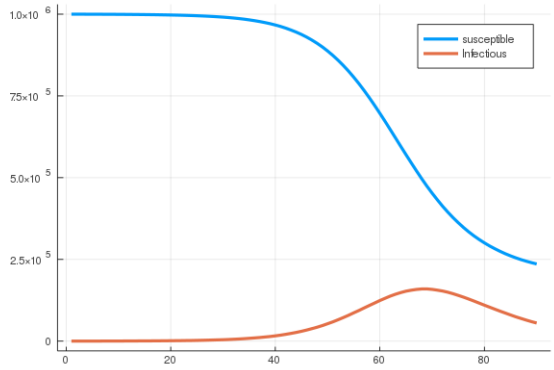

Figure 1: Susceptible and Infectious time series for user defined parameters, $\gamma = \frac{1}{7}$, $N = 10^6$ and $\beta = 2\frac{\gamma}{N}$.

2 Introducing $\mathcal{R}_t$

To gain some *control* over an epidemic, authorities can enforce quarantine or social distancing measures which may affect some of the model parameters. The parameter γ cannot be manipulated through such measures as it is the reciprocal of the length of the infectious period which in the case of Covid-19 is estimated to be about one week, so $\gamma = \frac{1}{7}$.

The other two parameters, β and N, can be manipulated via interventions and it is a common practice to define a quantity called the *effective* reproduction number, $\mathcal{R}_t$ as follows:

$$\mathcal{R}_t = \frac{\beta}{\gamma}\frac{S_t}{N} \tag{3}$$

and then recast the discrete SI model as:

$$S_{t+1} = S_t - \gamma \mathcal{R}_t I_t \tag{4}$$
$$I_{t+1} = I_t + \gamma I_t(\mathcal{R}_t - 1) \tag{5}$$

Note that $\mathcal{R}_0 = \frac{\beta}{\gamma}$ which is called the **basic** reproduction number and tells us how many persons an infected person will infect during their infectious period at the start of an epidemic and before any interventions can be mounted. In the case depicted in figure 1, the basic reproduction number is $\mathcal{R}_0 = \frac{\beta}{\gamma} S_0 = 2$.

Note that if no interventions are put in place during the course of the epidemic then $\mathcal{R}_t$ will decrease monotonically as S_t decreases. The goal of interventions is to decrease $\mathcal{R}_t$ faster than its natural decline induced by the diminishing pool of susceptible persons. In particular it is desirable to force $\mathcal{R}_t < 1$ so that the pool of infectious is smaller when a person leaves the pool than when he enters it.

To see if an intervention is successful or not we must have some way of estimating the current value of $\mathcal{R}_t$ from case counts.

3 Estimating $\mathcal{R}_t$ from case count data

An estimate for yesterday's $\mathcal{R}_t$ value can be obtained by comparing the size of yesterday's infectious pool with the size of today's infectious pool by rewriting equation 5 as follows.

$$\mathcal{R}_t = 1 + \frac{1}{\gamma}\left(\frac{I_{t+1} - I_t}{I_t}\right) \tag{6}$$

$\gamma \mathcal{R}_t \geq 0$ measures the likelihood of transmitting the disease when an infected and a susceptible come in contact. Hence $\mathcal{R}_t$ is the number of transmissions caused by an infected person during his infectious period.

From the figure, one can see that if $(\beta/k)S(0)$ is much greater than 1, then the entire population quickly becomes infected and then recovered/dead. For $(\beta/k)S(0)$ less than 1, the infection seems to die out after

only a small percentage of the population has been infected. For values somewhat greater than 1, the number infected and hence later recovered/dead seems to be a larger fraction but not necessarily all of the population. The Matlab code used to produce these plots can be found in Appendix A.

4 Conclusions

The results of this simple model look fairly reasonable and so they might be used to decide on a strategy for curtailing an epidemic through vaccinations, quarantines, etc. Many enhancements to the model can be made. For a discussion of some of these, see, for example, [3].

A Matlab Code for Producing Plots

```
global betaglob  % Global variables to be supplied to function sirdot.
global kglob     % Give them funny names so they won't be used elsewhere.

kglob = 0.1;               % Set k.
betas = [.005; .0005; .0002; .0001];
for kase=1:4,
  betaglob = betas(kase);  % Set beta.
  tfinal = 50;  if kase > 2, tfinal = 500; end;
  [tout,sout] = ode45('sirdot',[0 tfinal], [990; 10; 0]); % Solve with ode45.

  subplot(2,2,kase)
  plot(tout,sout(:,1),'-', tout,sout(:,2),'--', tout,sout(:,3),'-.');
  xlabel('t'), ylabel('population')
  if kase==1,
    title('beta = 0.005, k = 0.1, (beta/k)*S0 = 49.5');
  elseif kase==2,
    title('beta = 0.0005, k = 0.1, (beta/k)*S0 = 4.95');
  elseif kase==3,
    title('beta = 0.0002, k = 0.1, (beta/k)*S0 = 1.98');
  else
    title('beta = 0.00005, k = 0.1, (beta/k)*S0 = 0.495');
  end;
end;

function sirprime = sirdot(t,sir)
global betaglob
global kglob
beta = betaglob;  k = kglob;

sirprime(1,1) = -beta*sir(1)*sir(2);
sirprime(2,1) = beta*sir(1)*sir(2) - k*sir(2);
sirprime(3,1) = k*sir(2);
```

References

[1] Johnson, Teri, *Mathematical Modeling of Diseases: Susceptible-Infected-Recovered (SIR) Model*, Math 4901 Senior Seminar, University of Minnesota, Spring 2009. http://www.morris.umn.edu/academic/math/Ma4901/Sp09/Final/Teri-Johnson-Final.pdf .

[2] Tung, K. K., *Topics in Mathematical Modeling*, Princeton University Press, 2007.

[3] Wikipedia, *Compartmental models in epidemiology*, http://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology .