

SIR model and additions

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1 The model

In the SIR model for the spread of a epidemic in a population with N members we use the set of susceptible people S , the recovered ones R and those infected I . The set of coupled differential equations is:

$$\begin{aligned}S(n+1) &= S(n) - S(n)\frac{I(n)}{N}\beta, \\I(n+1) &= I(n) + S(n)\frac{I(n)}{N}\beta - I(n)\lambda, \\R(n+1) &= R(n) + I(n)\lambda,\end{aligned}\tag{1.1}$$

where λ is the inverse of the time needed to recover from the illness and β is the chance that a person could infect others while being ill. The reproducibility parameter R is $R = \beta/\lambda$, the average number of people that could get sick from one infected.

At any time

$$N = S + I + R.\tag{1.2}$$

This is required by the differential equations as can be easily checked.

It is interesting to divide by N all the equations in Eq. (1.1), so that $s = S/N$, $r = R/N$ and $i = I/N$ and this equation becomes

$$\begin{aligned}s(n+1) &= s(n) - s(n)i(n)\beta, \\i(n+1) &= i(n) + s(n)i(n)\beta - i(n)\lambda, \\r(n+1) &= r(n) + i(n)\lambda, \\s(n) + i(n) + r(n) &= 1.\end{aligned}\tag{1.3}$$

In simulations where the number of infected and recovered people detected from tests is a number much less than the total population of the region/country, one can make the approximation $s(n) \simeq 1$. We then get the linearized system of

differential equations:

$$\begin{aligned} s(n+1) &= s(n) - i(n)\beta , \\ i(n+1) &= i(n) + i(n)\beta - i(n)\lambda , \\ r(n+1) &= r(n) + i(n)\lambda , \\ s(n) + i(n) + r(n) &= 1 . \end{aligned} \tag{1.4}$$

Notice that still the conservation rule is fulfilled.

We focus on the differential equations for $i(n)$ and $r(n)$, which can be solved easily and we obtain:

$$\begin{aligned} i(n) &= i(n_0)e^{\lambda(R-1)(n-n_0)} , \\ r(n) &= \frac{i(n_0)}{R-1}e^{\lambda(R-1)(n-n_0)} . \end{aligned} \tag{1.5}$$

• In the case in which $s \simeq 1$ the solution for $i(n)$ and $r(n)$ is scale invariant. Therefore, the use of partial epidemiologic data, as the one obtained from making tests that only cover part of the population, is a good approach for calculating the reproducibility parameter for the actual spreading of the epidemic in the population.

2 Abrupt change of test rates

Notation: i infected people, r recovered people, s susceptible people to get infected, being all of them normalized by the total population. In addition, $\lambda = 1/14$ [days] $^{-1}$.

Let us assume that the numbers of infected and active cases are much larger than their variations. Let us consider the situation in which there is a sharp variation in the number of tests, so that one could think that this drives to an increasing amount of detected cases, roughly proportional to the increase in tests. Let us denote by $\delta i'$ the actual rate of detection and δi the one that would happen if the rate of testing were stayed fixed. We also need to include the total number of positive cases c , so that $\delta i = \delta c - \delta r$ and $\delta i' = \delta c' - \delta r$. Then,

$$\begin{aligned}\frac{\delta i'}{\lambda} &= \frac{\delta c' - \delta r}{\lambda} = i(R' - 1) , \\ \frac{\delta i}{\lambda} &= \frac{\delta c - \delta r}{\lambda} = i(R - 1) ,\end{aligned}\tag{2.6}$$

with R' the actual reproducibility parameter for the new situation and R the one that would had occurred if the situation did not change. In addition we have assumed that $s \simeq 1$, which is the case for i and $r \ll 1$. Taking the ratio of these equations:

$$\frac{\delta c' - \delta r}{\delta c - \delta r} = \frac{R' - 1}{R - 1} .\tag{2.7}$$

With $\delta c = \delta c'/\nu$ then

$$\frac{\delta c' - \delta r}{\delta c'/\nu - \delta r} = \frac{R' - 1}{R - 1} .\tag{2.8}$$

The solution is

$$R - 1 = (R' - 1) \frac{\delta c'/\nu - \delta r}{\delta c' - \delta r} .\tag{2.9}$$

The critical behavior happens when $\delta c'/\nu \lesssim \delta r$, in which case there is a change of sign in $R - 1$ with respect to $R' - 1$ ($\nu > 1$).

On 2020/04/23 $\delta c' = 4635$, $\delta r = 3335$, and then $\delta c'/\delta r = 1.39$. On the other hand the variation in the number of tests of immunology is $\delta_s = 1656$, while the increase in PCR tests is $\delta_p = 2881$. Then, we could estimate ν by $\nu \simeq (\delta_p + \delta_s)/\delta_p = \delta c'/\delta_p = 1.57$ and with this number applied to Eq. (2.9)

$$\frac{R - 1}{R' - 1} = -0.30 .\tag{2.10}$$

- If the evolution were smoother there would not be a mismatch between detection of infection cases and the relative increase in the number of recovered people and this effect would not be so drastic. Notice that here we have taken in Eq. (2.6) that the rate of recovered people is the same for both detection rates.

Indeed, after some days (between 1-2 weeks) one would expect that the increase in testing also implies an increase in the rate of recovered people, so that after this time one also has to distinguish between the actual rate $\delta r'$ and δr so that $\delta r = \delta r'/\nu$. In such circumstances, $R - 1$ and $R' - 1$ have the same sign because then

$$\begin{aligned}\frac{\delta i'}{\lambda} &= \frac{\delta c' - \delta r'}{\lambda} = si(R' - 1) , \\ \frac{\delta i}{\lambda} &= \frac{\delta c'/\nu - \delta r'/\nu}{\lambda} = si(R - 1) , \\ \frac{R' - 1}{R - 1} &= \nu ,\end{aligned}\tag{2.11}$$

after dividing the first line by the second one. Of course, after some time since the sharp rise in the detection of positive cases has occurred, it would become an increasingly bad assumption to take that $i' = i$.