$$S \rightarrow I \rightarrow R$$

S - susceptible individuals

I - individuals suffering from a disease and spreading the infection

R – recovered

Let's make this assumption:
1. the increase in the group of individuals sought is proportional to
the number of individuals released and the number of susceptible individuals - rIS
2. the increase in healed individuals is directly proportional to the number
online patients - aI, where $a > 0$.
3. the incubation period is so short that it can be neglected - the individual
susceptible who got infected get sick immediately.
4. the population is thoroughly mixed - each type of individual has the same place and an individual of a different type.
With these assumptions, let's formulate the equations (Kermack-McKendrick (1972)):

$$\begin{aligned} \dot{S} &= -rSI \\ \dot{I} &= rSI - aI \\ \dot{R} &= aI \end{aligned}$$

Note that this model has a built-in assumption of constant-count:

$$\dot{S} + \dot{I} + \dot{R} = 0$$

Meaningful baseline data for the epidemiological model are:

$$S(0) = S_0 > 0, I(0) = I_0 > 0, R(0) = 0$$

The critical parameter $\rho = a / r$ is called the relative coefficient
recovery and is the inverse of the contact ratio $\sigma = r / a$. Associated with it is the so-called base reproduction rate for a given infection:

$$R_B = \frac{rS_0}{a}$$

It describes the number of individuals newly infected by one currently infected. If RB> 1, the disease spreads. One of the ways
the reduction of the RB is the reduction of the S0 or the number of susceptible individuals. The baseline reproductive rate is a key controlled parameter
e.g. by vaccination.

We have to fit this:

$$\frac{dR}{dt} = aI = a\left(N - R - S\right) = a\left(N - R - S_0 e^{-R/\rho}\right)$$

dR/dt are recovered + deaths per day

We have everything except a and ρ. We can get this by fitting our data. Then we get Rb and we can compare Rb for different periods of time (for different restrictions).