

The epidemiological model which is proposed here can be described by the following formula of epidemic growth:

$$N_t = N_0 2^{\frac{t}{T_d}}$$

where  $T_d$  is the doubling time in days,  $t$  number of days,  $N_0$  the number of currently infected, and  $N_t$  the number of infected after  $t$  days.

We can adjust the formula to reflect a part of the general population by dividing the left and the right elements of the equation by the total population  $P_{total}$ .

$$P_t = P_0 2^{\frac{t}{T_d}} \quad (1)$$

The share of the population involved in an epidemic is limited so it is necessary to incorporate this limitation in the calculations. For this goal, we will use the effective reproduction number  $R_t$ , which can be calculated with the following formula derived from the basic reproduction number  $R_0$ :

$$R_t = R_0(1 - P_t) \quad (2)$$

Taking the simplified SEIR model <sup>[2]</sup> and making some assumptions we can derive the value of the growth rate

$$G_r = \frac{R_t - 1}{D}$$

where  $D$  is infectious time (for Covid-19 was taken 10 days <sup>[1]</sup>).

The dependence between the doubling time and the growth rate is defined in the following equation

$$T_d = \frac{\ln(2)}{G_r}$$

From this, the following dependence can be derived:

$$T_d = \frac{D \ln(2)}{R_t - 1}$$

Inserting the resulting doubling time into (1) we obtain

$$P_t = P_0 2^{\frac{t(R_t-1)}{D \ln(2)}}$$

or, after the simplification,

$$P_t = P_0 e^{\frac{t(R_t-1)}{D}}$$

In case we want to calculate the value for the following day  $t = 1$

$$P_1 = P_0 e^{\frac{R_t-1}{D}}$$

The effective reproduction number can be calculated from (2) with the known  $P_{current}$  from the previous step

$$P_{next} = P_{current} e^{\frac{R_0(1-P_{current})-1}{D}}$$

This final formula has only one user-defined parameter and allows us to calculate all other characteristics of the epidemic, including saturation level, days to the end, and the shape of the curve at any selected point.

We also can modify some values with help of the parameter  $\mu \in [0; 1]$  to see how restrictive actions change the development of an epidemic.

$$P_{next} = P_{current} e^{\frac{\mu R_0(1-P_{current})-1}{D}}$$

To make it even simpler, we can define the “restrictive” basic reproduction number with following equation:

$$R'_0 = \mu R_0$$

Since we have only very limited opportunity to influence epidemic development by changing the  $R'$  we can build the model and estimate all epidemic parameters including the total level of exposure and make projection into the future with all possible actions. Initial  $R_0$  can be calculated at the beginning of an epidemic directly from doubling time: in the case of Covid-19 it has been estimated at 3,5 for Germany.

All intervention points and adapted values  $R'_0$  can be calculated with help of the regression or corrected manually.

With the help of this method it is possible to calculate

- Epidemic time with and without restrictions
- Predict fatalities
- Impact of restrictive actions
- Population immunity at any given point by known rate to detected cases

## References

- [1] Xi He, Eric H. Y. Lau et al. Temporal dynamics in viral shedding and transmissibility of COVID-19. <https://www.nature.com/articles/s41591-020-0869-5> Nature (2020)
- [2] J. M. Heffernan et al. Perspectives on the basic reproductive ratio. <https://doi.org/10.1098/rsif.2005.0042> J. R. Soc. Interface 2005 2, 281–293 (2005)