

Supplementary Material: transmission and infected population indicators

Standard mechanistic epidemiological models rely on SIR (Susceptible-Infected-Removed) systems of ordinary differential equations and their extensions (for examples of application to the COVID-19 epidemic, see [5, 6]). Assume here that the dynamics of the epidemic are described by the following SIRD compartmental model:

$$\begin{cases} S'(t) = -\frac{\alpha(t)}{N} S(t) I(t), \\ I'(t) = \frac{\alpha(t)}{N} S(t) I(t) - (\beta + \gamma) I(t), \\ R'(t) = \beta I(t), \\ D'(t) = \gamma I(t), \end{cases} \quad (1)$$

with S the susceptible population, I the infectious population, R the recovered population, D the number of deaths due to the epidemic and N the total population (which is assumed to be constant, thereby neglecting the effect of death on the total population size). The time-dependent coefficient $\alpha(t)$ is the contact rate and $1/\beta$ is the mean time until an infectious becomes recovered. The results in [1] indicate that infectiousness starts 2 to 3 days before symptom onset and declines significantly 8 days after symptom onset. Based on these observations we assume here that the mean duration of the infectiousness period is $1/\beta = 10$ days. In [2], the duration of the incubation period was estimated to have a mean of 5.2 days. Thus, the mean duration of the non-infectious exposed period is relatively short (about 2 to 3 days), and can be neglected without much differences on the results, as shown in [3]. The parameter γ corresponds to the death rate of the infectious, which has been estimated in [5, 6], based on French data: $\gamma = 8 \cdot 10^{-4}$ (corresponding to an infection fatality rate of $\gamma/(\gamma + \beta) \approx 0.8\%$).

Computation of R_0 based on the number of observed deaths. To compute the basic reproduction number, we assume that the contact rate α is constant at the beginning of the epidemic, during a period (t_0, t_1) . The date t_0 is defined as the first day such that the observed number of deaths \hat{D}_{t_0} exceeds 10, and t_1 is the first date where the number of deaths \hat{D}_{t_1} crosses the value 100. The basic reproduction number can be computed as [4]:

$$R_0 = \frac{\alpha}{\beta + \gamma}.$$

As $S \approx N$ at the early stage of the epidemics and since $\beta + \gamma \approx \beta$, we have:

$$I'(t) = I \left(\alpha \frac{S}{N} - (\beta + \gamma) \right) \approx I \beta (R_0 - 1),$$

which can be solved explicitly, leading to

$$\begin{cases} I(t) = I_0 e^{\beta (R_0 - 1) (t - t_0)}, \\ R(t) = \frac{I_0}{R_0 - 1} \left(e^{\beta (R_0 - 1) (t - t_0)} - 1 \right), \\ D(t) = \hat{D}(t_0) + \frac{\gamma}{\beta} \frac{I_0}{R_0 - 1} \left(e^{\beta (R_0 - 1) (t - t_0)} - 1 \right), \end{cases}$$

with $R(t_0) = 0$, $I(t_0) = I_0$ and $D(t_0) = \hat{D}_{t_0}$.

Fixing the value \hat{D}_{t_1} (cumulated number of recorded deaths on day t_1), we get:

$$I_0 = \frac{\beta (R_0 - 1) (\hat{D}_{t_1} - \hat{D}_{t_0})}{\gamma e^{\beta (R_0 - 1) (t_1 - t_0)} - 1}.$$

Finally,

$$D_t = \hat{D}_{t_0} + (\hat{D}_{t_1} - \hat{D}_{t_0}) \frac{e^{\beta (R_0 - 1) (t - t_0)} - 1}{e^{\beta (R_0 - 1) (t_1 - t_0)} - 1}, \quad (2)$$

for all $t \in (t_0, t_1)$. R_0 is then computed by fitting the above formula to the data \hat{D}_t with a standard nonlinear curve fitting procedure (using Matlab[®] Curve Fitting Toolbox[®]), over the period (t_0, t_1) .

Computation of R_t based on the number of observed deaths. The effective reproduction number is defined as:

$$R_t = \frac{\alpha}{\beta + \gamma} \frac{S(t)}{N}.$$

The value of R_t is computed with the same procedure as R_0 (we use the same approximations as above: $S \approx N$ and $\beta + \gamma \approx \beta$), but instead of fitting (2) over a fixed period (t_0, t_1) , we apply the fitting procedure over a dynamical time period $(t - \tau, t)$. Thus, R_t is computed by fitting to the data \hat{D}_s for $s \in (t - \tau, t)$ (same fitting procedure as above) the formula:

$$D_s = \hat{D}_{t-\tau} + (\hat{D}_t - \hat{D}_{t-\tau}) \frac{e^{\beta(R_t-1)(s-(t-\tau))} - 1}{e^{\beta\tau(R_t-1)} - 1}. \quad (3)$$

In the illustrations presented in the main text, the size of the window was $\tau = 15$ days.

Computation of the actual number of cases. We use the above procedure to compute R_t , and to deduce $\alpha(t) \approx \beta R_t$. The computation of the number of cases begins at some time t_0 defined again as the first day such that the observed number of deaths \hat{D}_{t_0} exceeds 10. To initialise the number of infectious $I_0 = I(t_0)$, we use the equation $D'(t) = \gamma I(t)$, and we define I_0 as $1/\gamma \times$ (mean number of deaths over the period ranging from 5 days before t_0 to 5 days after t_0). $S(t_0) = N$ corresponds to the population size in the considered country.

Then, the solution of the system (1) can be computed with a standard numerical algorithm, using e.g. Matlab[®] *ode45* solver. The daily number of cases is computed as $S(t-1) - S(t)$, the variation in the number of susceptibles between two consecutive days.

References

- [1] Xi He, Eric HY Lau, Peng Wu, Xilong Deng, Jian Wang, Xinxin Hao, Yiu Chung Lau, Jessica Y Wong, Yujuan Guan, Xinghua Tan, et al. Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nature Medicine*, pages 1–4, August 2020.
- [2] Qun Li, Xuhua Guan, Peng Wu, Xiaoye Wang, Lei Zhou, Yeqing Tong, Ruiqi Ren, Kathy SM Leung, Eric HY Lau, Jessica Y Wong, et al. Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia. *New England Journal of Medicine*, 382:1199–1207, 2020.
- [3] Z Liu, P Magal, Ousmane Seydi, and Glenn Webb. A COVID-19 epidemic model with latency period. *Infectious Disease Modelling*, 2020.
- [4] J D Murray. *Mathematical Biology*. Third edition, Interdisciplinary Applied Mathematics 17, Springer-Verlag, New York, 2002.
- [5] Lionel Roques, Etienne Klein, Julien Papaix, Antoine Sar, and Samuel Soubeyrand. Using early data to estimate the actual infection fatality ratio from COVID-19 in France. *MDPI Biology*, 9(5):97, 2020.
- [6] Lionel Roques, Etienne K Klein, Julien Papaix, Antoine Sar, and Samuel Soubeyrand. Impact of lockdown on the epidemic dynamics of COVID-19 in France. *Frontiers in Medicine*, 2020, DOI: 10.3389/fmed.2020.00274.