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A pitfall in estimating the effective reproductive number R_t for COVID-19

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Background

The effective reproductive number R_t of COVID-19 is determined indirectly from data that are only incompletely known (fig. 1). Approaches based on reconstructing these data by sampling time lags from suitable distributions introduce noise effects that can result in distorted estimates of R_t. This, in turn, may lead to misleading interpretations of the efficacy of the various measures taken to limit COVID-19 transmission. We discuss in some detail a study used for real time monitoring of the reproductive number in Switzerland [2].

We argue that the method used to derive the above curve is systematically flawed and leads to an underestimation of the efficacy of the lockdown. The method adopted by the Robert Koch Institute suffers from similar deficiencies, their impact is however smaller.

Introduction

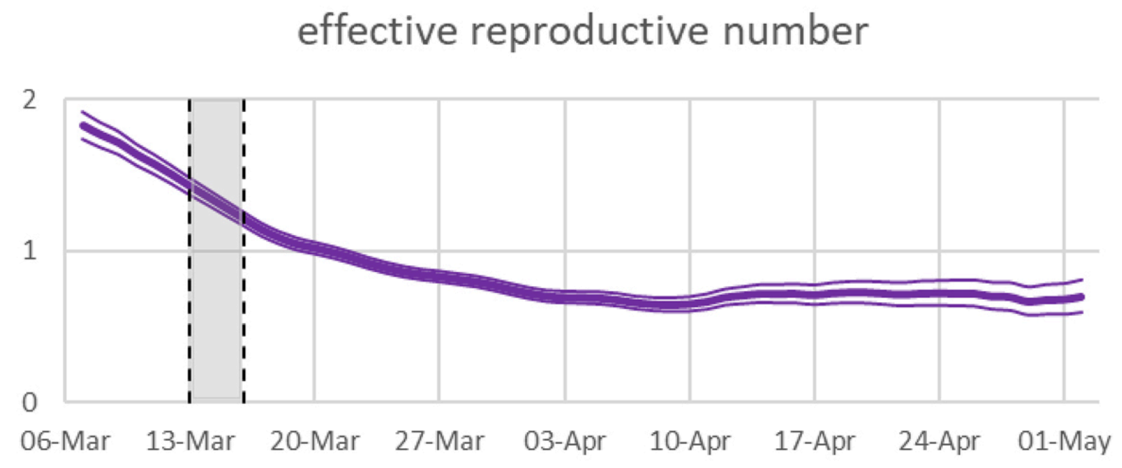
The daily varying effective reproductive number R_t is often used to monitor the spread of epidemic diseases such as COVID-19. It measures the expected number of secondary infections on day t due to a single infected individual and is given by

$$R_t = \frac{I_t}{\sum_{n>0} I_{t-n} w_n}$$

where I_t is the number of new infections on day t (and equally I_{t-n} the number of infections on day $t - n$ and so on), and the w_n are the infection intensities, i.e. w_n is the probability that a secondary infection was contracted from a person who got infected n days earlier. Whereas the infection intensities can be fitted to available data, the I_t are not observable directly, unless representative proportions of the population were tested on a daily basis. Therefore, they need to be inferred indirectly from some other data.

There are different schemes to reconstruct the I_t from the data, such as the classical statistical inference methods. In the present article we concentrate on schemes that are based on the idea of a “mechanical” reconstruction of the infection data by sampling time lags of observed data from suitable distributions. In the context of the current COVID-19 pandemic, such schemes have been implemented in different ways by various groups in different countries.

Figure 1: Effective reproductive numbers in Switzerland as shown in the real time monitoring on 13 May 2020. Mean and 95% uncertainty intervals are estimated on confirmed cases [1]. The shaded region is the onset of strong public health measures.



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In the following section, we present these schemes and show how they systematically introduce noise into the true data. In the remaining sections we examine the impact of the noise on the reproductive numbers calculated from these data.

The reconstruction scheme and its smoothing effect

We exemplify the scheme and how it introduces noise into the data by the version implemented by Scire et al. [3], which is very similar to the implementation by Abbott et al [4]. For the sake of clarity, we limit our exposition of the scheme to the observables C_t, the number of confirmed cases on day t. The other observables used analogously by the group are hospitalisations and deaths. Moreover, as our focus is on the days around 17 March, when the lockdown started, and as more than 2 months have passed since then, we restrict our exposition to those days of infection where all infections can be assumed to be confirmed by the actual date of the monitoring. According to the parameters used by the group, 95% of the cases are confirmed within 20 days after infection. For their method of extending the reconstruction to later days we refer again to their article.

Now, let X denote the incubation time of a randomly drawn case, i.e. the time between infection and symptom onset, and analogously Y the time between symptom onset and confirmation. The distributions of X and Y result from fitting to available data; see [2] and references therein. Then for every confirmed case α one samples independently a x'_a from the distribution of X and a y'_a from the distribution of Y.

The *reconstructed* infection day i'_a of this case a is then simply the day when the virus infection was confirmed minus $(x'_a + y'_a)$. Counting the number of cases that fall now on day t gives the reconstructed I_t, that we denote by I'_t. The reproductive numbers calculated from these I'_t are denoted by R'_t.

That this scheme introduces noise into the true data is seen as follows. We denote the true infection day by i_α, the true incubation period by x_a and the true time between symptom onset and confirmation by y_a. Then we have $i'_a = i_a + x_a + y_a - x'_a - y'_a$. As the sampled x'_a and y'_a are independent of the true x_a and y_a (because we don't know these; we just know that they are approximately distributed like X and Y, respectively), the reconstructed i'_a equals the true "signal" i_a plus some "noise" $d'_a = x_a + y_a - x'_a - y'_a$.

As we will see in the following examples, this results in a smoothing of the infection number statistics, which in turn, under certain circumstances, has a significant impact on the reproductive numbers calculated from it. (From a mathematical point of view, this is clear: If all the I_t are large, then we have $C \cong I * p$, where $p_n = P(X + Y = n)$, and $I' \cong C * \tilde{p}$, where $\tilde{p}_n = p - n$, i.e. $I' \cong I * p * \tilde{p}$.)

An illustrative example

The following example illustrates the effect of this scheme on the reconstructed reproductive number. Assume that $I_1 = 128$ and $R_t = 2$ for $t \leq 6$ and $R_t = 0.8$ for $t \geq 7$, and that infectiousness is limited to the day after infection, i.e. $w_1 = 1$. This yields the "true" infection numbers and reproductive numbers which are illustrated by the red curves in figure 2. For the *reconstructed* data we take X and Y both to be Gaussian with mean 5 and standard deviation 1. Thus, the "noise" is also Gaussian with mean 0 and standard deviation 2. With this "noise", the scheme results in the average in the corresponding blue curves.

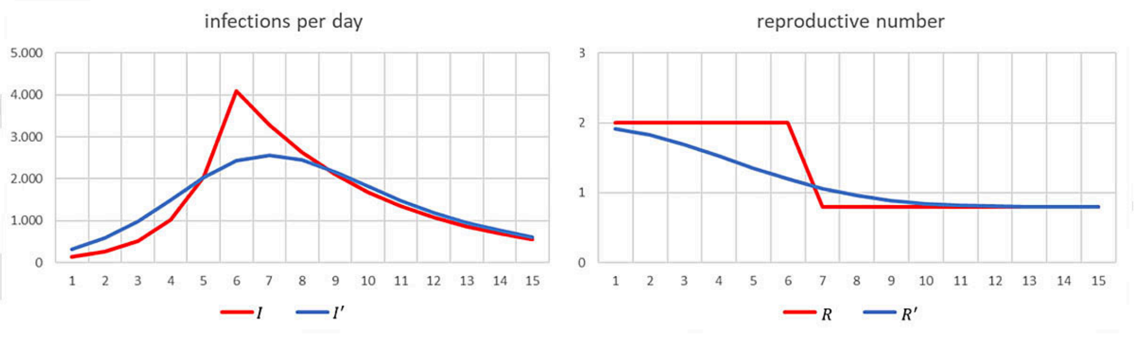
Of course, the blue curve R' is prone to lead to wrong decisions: If a lockdown caused the sharp decline in R from day 6 to day 7, then the blue curve may suggest that its impact was much less important and that most of the reduction was already achieved before the lockdown. It might even lead to the conclusion that the lockdown was not needed at all and that softer measures in already force before day 6 have had a sufficient effect, whereas in reality they had no effect at all. This in turn could lead to the conclusion that the pandemic can be kept under control by adhering to soft measures only.

The reproductive number in Switzerland around 17 March

We now turn to the situation in Switzerland around 17 March 2020. A calculation based on distributions for the time lags X and Y and the infection intensity as described in [3] yields the following result (fig. 3).

Unlike in the illustrative example above, we cannot start from "true" numbers of new infections. We instead choose the numbers of new infections, denoted by I^{fit} (red curve), in such a way that the resulting expected numbers of confirmed cases C^{av} (solid black curve) fit well the black dots C^{true} which show the actually reported data of confirmed cases [5]. Here, to get C^{av} from the numbers of new infections, we shift forward the infection day of each such case

Figure 2: "True" (red) and reconstructed (blue) infection and reproductive numbers.



by sampling independently from X and Y. (See appendix 1 for the algorithm used to infer I^{fit}.)

Given I^{fit}, we proceed as in the illustrative example, but, of course, with “noise” according to these X and Y instead of the Gaussian’s used there. This gives the *reconstructed* numbers of new infections I' (blue curve). Using the infection intensities w_n from [3], we calculate the corresponding reproductive numbers R^{fit} and R'. The latter matches well the green curve R^{TF} that shows the estimated mean reproductive numbers, as published on the website [1] on 13 May.

The remarks made above on the illustrative example apply also here. We note also that our red curve of reproductive numbers is in quite good agreement with the results of the inference analysis reported in [6, 7].

An alternative approach to reconstruction

Contrary to Switzerland, where, as far as we know, the date of symptom onset of the single cases is not collected systematically, this information is available for the majority of the cases in Germany. For the sake of clarity, we assume here that it is known for all cases. (We refer to [8] for the method applied to the cases with no known date of symptom onset.) Then, the Robert Koch Institute applies the following simpler scheme [8]: The reconstructed infection day i_a'' of a case a is the day of its symptom onset minus m, where m is the average incubation time. Counting the number of cases that fall now on day t gives the reconstructed I_t that we denote by I_t''. The reproductive numbers calculated from these $I_t''$are denoted by R_t''. (As our focus is again on the days around 17 March, we restrict our exposition to those days of infection where all infections can be assumed to be confirmed by the actual date of the monitoring. For a method to extend the reconstruction to later days we refer to [8].)

Of course we can view the subtracted value m as sample from the distribution of the constant time lag $X = m$. Therefore, this scheme is at least formally very similar to the one adopted by [3].

From the above discussion it is now clear that the so reconstructed infection times $i_a'' = i_{a\,+}\, d_a$ with ”noise” $d_a'' = x_a - m$ lead also to a smoothing of the infection number statistics and thus to misleading reproductive numbers. But it is also intuitively clear, that the impact is significantly smaller. This is confirmed by the following calculation.

Assume that the above I^{fit} are the true new infections per day, and that the distribution of the incubation time X is as above. Denote by S_t^{av} the resulting expected number of cases with symptom onset on day t. Then $I_t'' = S_{t+m}^{av}$. Assuming moreover that also the infection intensities are as above, we get the following result (fig. 4):

We stress that the knowledge of the dates of symptom onset is an advantage, as adopting the same scheme but with dates of confirmation instead of symptom onset, would introduce the ”noise” $x_a + y_a - m'$, where m' is the average time between infection and confirmation, into the true data, and this is clearly more ”noise” than in the scheme based on dates of symptom onset.

Figure 3: Cases and reproductive numbers in Switzerland around 17 March. See text below for the definition of the curves.

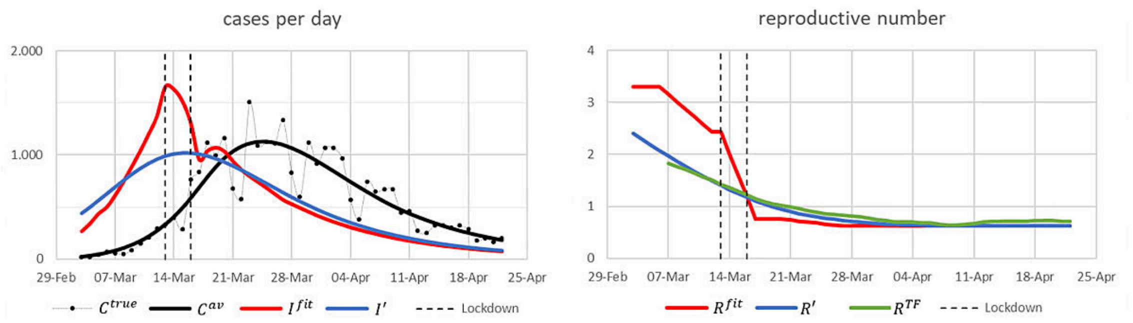
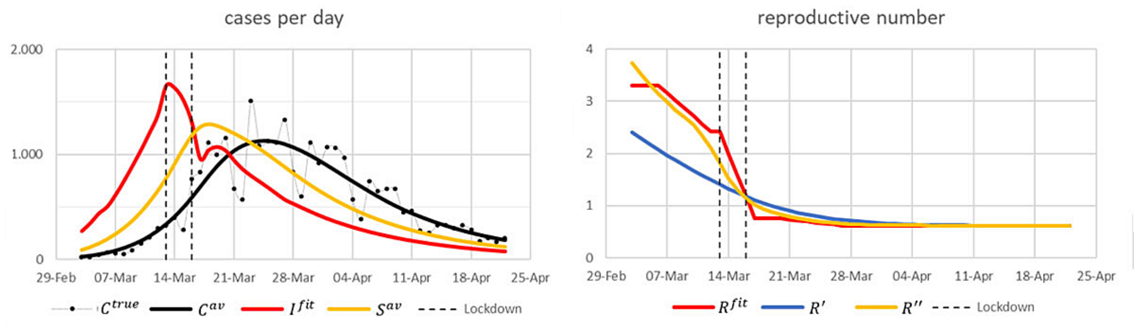


Figure 4: Left: “True” infection numbers (red) and their corresponding expected numbers of cases with symptom onset per day (yellow) and of confirmed cases per day (black). Right: The corresponding ’true’ reproductive numbers (red) and their reconstructions according to the schemes [8] (yellow) and [3] (blue).



Conclusion

In this article we have re-examined a type of scheme used to estimate the effective reproductive numbers R_t for COVID-19 with examples of two versions currently in use [3, 8]. These schemes are based on reconstruction of not directly observable data by sampling time lags of observed data from suitable distributions. Noise effects inherent in these schemes smooth the number statistics of the true data. The analysis of thus smoothed number statistics yields stable results and is easier to handle than classical inference methods as applied in [6, 7]. However, under certain circumstances like the current COVID-19 pandemic, the introduced noise effects dominate the information contained in the true data and lead to erroneous interpretations. The simpler approach adopted by [8] performs better than the one used in [3]. Moreover, we point out that adequate knowledge of the date of symptom onset is an advantage.

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Appendix 1

Fitting algorithm

Appendix 2

Suggested improvements to the analysis

The appendices are available as a separate file for downloading at https://smw.ch/article/doi/smw.2020.20307.