Reproductive number of the COVID-19 epidemic in Switzerland with a focus on the Cantons of Basel-Stadt and Basel-Landschaft

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Summary

The WHO declared the COVID-19 outbreak a “Public Health Emergency of International Concern” on January 30, 2020, after rapid spread from a few initial cases to thousands of cases across China and introductions to several other countries. On March 11, 2020, the WHO classified the outbreak as a pandemic. The first cases in Switzerland, Basel-Stadt, and Basel-Landschaft were confirmed on February 25, February 27, and February 28, 2020. As of April 22, 2020, there are 28154 confirmed cases in Switzerland, including 933 and 811 in the Cantons of Basel-Stadt and Basel-Landschaft, respectively. The rapid increase of confirmed cases in March suggests considerable community transmission.

Here, we estimate the reproductive number through time for the whole of Switzerland and its cantons for which sufficient data is available. For this estimation, we use publicly available data on the number of confirmed cases and COVID-related deaths through time, as well as additional data directly obtained from the University Hospital of Basel and the Cantonal Office of Public Health, Economics and Health Directorate of Basel-Landschaft. If the reproductive number is below 1, the epidemic is overall under control for that specific location, with the number of new infections per day decreasing through time. If this number is above 1, the epidemic is exponentially increasing in size.

We find that the reproductive number in Switzerland was between 1.5 - 2 during the first third of March, and has consistently decreased to around 1. After the announcement of the latest strict measure on March 20, 2020, namely that gatherings of more than five people in public spaces are prohibited, the reproductive number dropped significantly below 1, we estimate the reproductive number to be between 0.6 - 0.8 in the first third of April. Our sensitivity analyses address the concern of a decreasing reproductive number being merely an artifact of less intense testing through time.

In summary, our results suggest that from the last week of March onwards, the reproductive number was significantly below 1 in Switzerland and thus, the epidemic was declining. However, our analyses do not allow us to identify a cause for this decline. Going forward, we will provide daily estimates for the reproductive number on our webpage. Important to note in this respect is that estimates of the reproductive number lag about 10 days behind the last date of data collection since confirmation occurs with a delay of around 10 days after infection.

Introduction

The SARS-CoV-2 virus was first identified in China in December 2019 (1). Switzerland recorded its first case on February 25, 2020. As of April 22, 2020, there were 28154, 933, and 811 (2) documented cases in Switzerland, Basel-Stadt, and Basel-Landschaft, respectively. Initial COVID-19 cases had travel links to Italy (3,4), indicating an import of infections from other locations. These imports seeded the initial COVID-19 epidemic in Switzerland. The following rapid increase in the number of newly confirmed cases through time (5) reveals that infection then occurred mainly through so-called community transmission, i.e., transmission within Switzerland.

The reproductive number (6) quantifies the expected number of secondary infections caused by a single infected individual. In particular, the basic reproductive number quantifies the number of secondary infections in a completely susceptible population, while the effective reproductive number quantifies the number of secondary infections at a particular time point of an epidemic. The basic reproductive number for COVID-19 has been estimated to be between 2 and 3.5 for China based on the initial number of confirmed cases through time. For an overview of papers estimating the basic reproductive number, see Liu et al. (7). Estimating the basic reproductive number based on confirmed cases in locations different from China is not straightforward due to early dynamics being driven by imports seeding the epidemic outbreaks. Using genomic sequences of SARS-CoV-2, we confirmed the basic reproductive number to be between 2 and 3.5 for China, as well as for Italy and Washington State (U.S.A.) (8). Several groups (e.g. 9–11) report the effective reproductive number for different countries and regions.

Here, we aim at quantifying the effective reproductive number for the epidemic in Switzerland and in 10 of the 26 cantons forming the Swiss Confederation. The cantons for which we present analyses are among those most affected by COVID-19, as measured by absolute case numbers. We further perform sensitivity analyses for the epidemic in Switzerland and the epidemics in the Cantons of Basel-Stadt and Basel-Landschaft. Hereafter, we refer to the effective reproductive number as the reproductive number or as R(t), with t denoting the time point for which we determine the reproductive number. We will update estimates for R(t) as the epidemic unfolds in the future.

Materials and methods

Datasets

We use data from COVID-19 cases in Basel-Landschaft to estimate the infection time of the disease. We obtained line list information for 166 patients from the Cantonal Office of Public Health, Economics and Health Directorate of Basel-Landschaft. The time of symptom onset and case confirmation for 139 patients and the time of symptom onset and hospitalization for 112 patients was extracted. We summarized these data by calculating the mean and standard deviation of the time between symptom onset and confirmation and the time between symptom onset and hospitalization.

We estimate R(t) based on three different datasets. We obtained the cumulative number of confirmed COVID-19 cases over time for Switzerland and for the Swiss cantons and the cumulative number of deaths over time for Switzerland from the Specialist Unit for Open Government Data of the Canton of Zurich (2). We retrieved this data via an online data repository (5) and accessed all data up until and including April 22, 2020.

We additionally obtained the total number of new COVID-19 cases admitted to the hospital per day for the University Hospital Basel (USB) in Basel-Stadt. This number is smaller than the total number of hospitalizations in Basel-Stadt as also other hospitals admit COVID-19 patients. Further, we obtained the number of new COVID-19 cases admitted to the hospital per day for the Bruderholzspital in Basel-Landschaft with the patients being Basel-Landschaft residents. This number represents the total hospitalizations within the canton among residents of the canton since the Bruderholzspital is the only hospital in Basel-Landschaft admitting COVID-19 patients. This hospitalization data is available until March 31, 2020.

Finally, up until March 31, 2020, we obtained the absolute number of tests performed per day as well as the number of positive tests per day from the two testing centers predominantly performing tests in Basel-Landschaft (Münchenstein and Lausen; open since March 18, 2020 (12)) as well as from the University Hospital in Basel-Stadt (in particular, all the samples from a major cantonal testing center which has been open in its current form since March 9, 2020 (13) are processed in the hospital, together with further samples).

Analyses of confirmed case data, the number of deaths, and the number of hospitalizations

We estimate the reproductive number R(t) as a function of time based on the number of confirmed cases per day. As sensitivity analyses, we additionally estimate R(t) based on the number of deaths per day for Switzerland and the number of new hospitalizations per day for the Basel-Landschaft and Basel-Stadt cantons.

R(t) is the expected number of secondary cases caused by an infected individual at a time point t. R(t) is estimated employing the method from (14) using the implementation in the R package EpiEstim on CRAN (15). It is assumed that an individual who has had a COVID-19 infection for *s* days has an infection intensity w_s. Let the number of newly infected individuals on day *t-s* be *I(t-s)*. Then the expected number of newly infected individuals at time t is $\mathrm{E[I(t)]} = \mathrm{R(t)} \sum_{s=1}^{t} w_s\, I(t-s)$. To estimate the posterior probability distribution of R(t), the full probability distribution for *I(t)* is considered (see Web Appendix 1 in (14)). We use the default prior for R(t) in EpiEstim (mean = 5, standard deviation = 5).

We do not know *I(t)*, but we can measure quantities that are closely related to *I(t)*. Here we first use the number of confirmed cases as a proxy. Second, we use the number of newly admitted COVID-19 patients to a hospital as a proxy. Third, we use the number of deaths as a proxy. Since a case confirmation, a hospitalization, and a death event happen some days after the infection of the patient, for each such event, we need to estimate the corresponding infection time in order to have a proxy which is directly proportional to I(t). Thus, for each observed patient (observed through case confirmation, hospitalization, or death), we simulate their infection time. This is similar to what is also proposed by Abbott et al. (9,16).

To simulate this infection time, we first assume an incubation period, which is gamma-distributed with a mean of 5.3 days (standard deviation = 3.2, (17)). After the incubation period, symptoms appear. We again assume a gamma distribution for the time between symptom onset and the observed event (with an event being case confirmation, hospitalization, or death). The time between symptom onset and case confirmation is estimated from our Basel-Landschaft data (see Results) to be 5.6 days (mean; standard deviation = 4.2). The time between symptom onset and hospitalization is estimated to be 6.6 days (mean; standard deviation = 4.6; see Results). The gamma distribution for the time between symptom onset and death is assumed to have a mean of 15 days (standard deviation = 6.9 (17)).

For each confirmation, hospitalization, or death event, we sample first from the incubation period distribution and then from the distribution of the time interval between symptom onset and the event. We subtract the simulated infection time from the event time to obtain a proxy for the time of infection. This is done 100 times, meaning we obtain 100 time series of infection times.

So far, the simulated time series represent estimated infection times for confirmed patients. However, the number of simulated infections at time *s* days ago may be missing some individuals whose cases have not yet been confirmed but will be confirmed later. Let p_s be the probability of an infection event having been confirmed after *s* days (given the infection will be confirmed eventually). We estimate p_s by simulating waiting times between infection and case confirmation using the same distributions for the incubation period and the time between symptom onset and confirmation as above. p_s is taken to be the fraction of simulated infections confirmed within the first *s* days of infection. Finally, we use our estimates of p_s to correct the time series: the number of infections at *s* days prior to the last day for which we have data is approximated by (# of simulated infections at *s* days prior to today)/p_s. This corrected time series is used for estimating R(t).

For the distribution of w_s, we use the serial interval estimated for COVID-19 infections from (18), with a mean of 4.8 days and a standard deviation of 2.3. Based on this assumption, >90% of onwards transmissions happen within 8 days upon infection of an individual.

We calculate a posterior distribution for R(t) using Bayesian methodology provided in (15) based on each of the 100 time series of infection events obtained above. To reduce the influence of stochastic outliers, we smooth the resulting R(t). The smoothed R(t) is calculated based on assessing the number of new infections at times t, t-1, and t-2 (i.e., for a 3-day window assuming R is constant during that time; see equation above and (15)).

We will report the median of the mean R(t) estimates from the 100 infection time series. Second, we report the median of the first and last 40-quantile of the posterior distribution for

the uncertainty interval (key uncertainty interval approximating the 95% uncertainty interval). Third, we report the first 40-quantile of the 100 obtained first 40-quantiles, and the last 40-quantile of the 100 obtained last 40-quantiles (wide uncertainty interval approximating a 95% uncertainty interval for the bounds of the key uncertainty interval).

Reporting window for the reproductive number

When estimating R(t) from confirmation data, we rely on the testing intensity not changing through time (14). On March 6th, 2020, it was announced that the national strategy to fight COVID-19 changed from finding all COVID-19 positive cases and contact tracing to protecting the population at risk. This policy amounted to not testing every individual with symptoms. The alternative testing strategy was fully implemented starting March 9th, 2020, but was subsequently reverted on April 22nd, 2020. After that date, testing of all individuals with symptoms resumed (19).

More than 90% of individuals transmit within 8 days based on our serial interval assumption. Thus, we can estimate R using comparable testing data from March 17th onwards (March 9 + 8 days). Since we have a reporting delay of about 10 days, this corresponds to R(t) estimates from March 7th onwards. Based on confirmation data until April 22, we can estimate R(t) only until April 12 due to the reporting delay. We therefore show R(t) estimates from March 7 – April 12 for the confirmation data.

In summary, we show R(t) estimates for the time period when Switzerland did not test all symptomatic patients. In our daily updates for the reproductive number provided on our webpage (20), the R(t) for April 13 until at least April 20 may be overestimated due to the change in testing regime. Thus, we will also show results based on hospitalization data on our website in order to obtain robust estimates for April 13-20, 2020.

Assessing potential changes in testing intensity

In addition to the sensitivity analyses regarding the data set mentioned above (i.e., analyses based on cases, hospitalizations, and deaths), we perform a separate analysis assessing the sensitivity of the results to the statistical method. Specifically, we estimate the case reproductive number $R_c(t)$. $R_c(t)$ is defined as the expected number of individuals that an individual becoming infected at time t causes over the period of its infection (21). Thus, $R_c(t)$ takes into account future events. In contrast, R(t) is based on past events; it was defined as the number of secondary infections caused by the individuals who transmit at time t. As a consequence, when calculating $R_c(t)$, a proxy for the number of infections after time t is needed. In fact, since individuals will transmit within 8 days of infection with >90% probability (based on our serial interval assumption), we require data on the number of infections on the interval [t, t+ 8 days] in order to estimate $R_c(t)$. We use the implementation within EpiEstim (15) for calculating $R_c(t)$.

Results

Time between symptom onset and case confirmation or hospitalization

The mean time between symptom onset and a case being confirmed is estimated to be 5.6 days (standard deviation 4.2), see Fig. 1. Based on a mean incubation period of 5.3 days (22), a case is only confirmed around 10.9 days after being infected. Thus we can only quantify the

reproductive number R(t) until about 10 days prior to today. The mean time between symptom onset and hospitalization is estimated to be 6.6 days (standard deviation 4.6).

Quantifying R(t) based on confirmed case data for Switzerland and 10 cantons
In Fig. 2A, we show the cumulative number of confirmed cases (line) and the daily number of new cases (bars) for Switzerland and 10 out of the 11 cantons with the most confirmed cases on March 31, 2020. Graubünden was among the 11 cantons with the most cases; however, we omitted it due to lack of data.

In Fig. 2B, we show in black the R(t) through time based on the confirmed case data for March 7 - April 12. Values of $R(t)>1$ correspond to the exponential growth of the epidemic, while values of $R(t)<1$ imply exponential decline.

Public health policies
In order to compare the R(t) estimates through time to public health policies (23), we highlight changes in policies with dotted vertical lines and a gray area (Fig. 2 and 3). In particular, we display:

- On March 13th, schools were announced to be closed. On March 16th, non-essential shops, bars, and restaurants were announced to be closed. This "Ausserordentliche Lage" (a lockdown) in Switzerland started on March 17th and the "Notlage" (a lockdown) in Basel-Landschaft on March 15th (12). The lockdowns are without curfew.
- On March 20th, the Federal Council prohibited gatherings of more than five people in public spaces (5-people rule).

Sensitivity analysis through employing a different statistical method
As described in the "Materials and methods" section, we performed a sensitivity analysis addressing the statistical method. The blue lines in Fig. 2B are the estimates of the case reproductive number $R_c(t)$. We shifted this plot by 5 days compared to the R(t) plot: 4.8 days is the mean serial interval, which implies that, at any point in time t, new infections are driven by individuals infected on average 4.8 days before time t. Thus, by shifting $R_c(t)$ by 5 days, the R and R_c curves should roughly align. Indeed, we observe the same patterns for R(t) and $R_c(t-5)$, see also (14).

Summary
Overall, we observe a decline in R(t) in the first half of March. R(t) dropped below 1 after the most recent measure (5-people rule) was implemented on March 20. R(t) remained significantly below 1 since. Thus, since the last week of March, the epidemic has been under control ($R(t)<1$). However, our analysis does not allow us to draw conclusions about specific causes for the change in R(t). The dynamics in the cantons follow the same trend; however, the level of uncertainty is larger, as expected.

Analyses with a focus on the epidemic in Switzerland, Basel-Stadt, and Basel-Landschaft
In Fig. 3 we show detailed results for Switzerland and the cantons of Basel-Stadt and Basel-Landschaft. We again show estimates for R from March 7 onwards, until the last date for which we have data on new hospitalizations in the cantons, March 31, 2020.

Again we highlight implementations of public health policies as in Fig. 2. We note one additional measure for Basel-Stadt. As of March 19, the criteria for self-isolation in Basel-Stadt became stricter: individuals with COVID-19 symptoms need to self- quarantine for at

least 10 days (compared to 24 hours after last symptoms up to March 19). People in the same household as a sick person need to self-quarantine for 10 days (compared to 5 days from March 9 - March 19). This intervention was implemented at almost the same time as the 5-people rule, so we only include the dotted line on March 20.

Evaluating potential biases in the results based on the confirmed case data
In Basel-Stadt, the main testing center opened on March 9 (13). Their testing policy was not changed until March 31. Thus our R(t) estimates should not be biased due to changes in testing from March 7 onwards (March 9 + 8 - 10 days, see above). In Basel-Landschaft, the two testing centers predominantly performing tests in that canton opened on March 18 (12). Their testing policies were not changed until March 31, meaning we are confident in our R(t) estimates from March 16 onwards (dashed line).

The testing intensity between March 9 and March 31 may have changed throughout the time course of this COVID-19 epidemic in Switzerland, despite official recommendations (including the policies of the testing centers in Basel-Stadt and Basel-Landschaft) not having changed until March 31. For example, a decrease in testing through time due to a shortage of tests and swabs could, in principle, cause the observed decrease in estimated R(t) through time.

Sensitivity analyses based on hospitalization and death data
In order to address this potential confounding factor, for Switzerland, we compare the estimates of R(t) based on the number of confirmed cases through time to the R(t) based on the number of deaths due to COVID-19 through time. We argue that although the chance of a COVID-19 case being confirmed depends on the testing intensity at that time, the chance of death due to COVID-19 being reported does not change through time. Fig. 3A (bottom) shows the number of confirmed cases and the number of deaths through time (cumulative: lines; per day: bars). Fig. 3B (bottom) reveals that both data sources indicate the same trend; however, the estimates based on the death data are much more uncertain, which is expected as the deaths are a subset of the number of confirmed cases.

For the cantons of Basel-Stadt and Basel-Landschaft, we compare the number of confirmed cases through time and the number of newly hospitalized COVID-19 patients. Again, until March 31, there were no changes in the guidelines for when to hospitalize a patient. Thus we have no reason to suspect that the chance of a COVID-19 case being hospitalized changed through time. In Fig. 3A (top and middle), we show the number of confirmed cases and the number of hospitalizations. Fig. 3B (top & middle) shows the estimates of R(t).

For both cantons, the uncertainty intervals for the hospitalization data are very wide due to the number of hospitalizations being rather small. Basel-Landschaft estimates based on hospitalizations show the same trend in R(t) as the estimates based on confirmed cases. For Basel-Stadt, we obtain a very minor signal for a decrease in R(t) and have very wide uncertainty intervals, indicating that the data do not contain much information.

Testing intensity in the cantons
Finally, we looked at the ratio of the number of positive tests to the total number of tests per day for the University Hospital in Basel-Stadt (in particular, all the samples from the main cantonal testing center which is open in its current form since March 9 are tested at this hospital), and for the two testing centers in Basel-Landschaft (open since March 18), see Fig. 4. The correlation between time and ratio was not significant for either canton (p-value for

Basel-Stadt: 0.21; for Basel-Landschaft 0.57). We want to highlight that these testing centers do not only test people from the respective canton. Further, some people from the respective canton may be tested elsewhere. Nevertheless, being the major testing centers of the cantons, the relative numbers should indicate the trend of testing intensity for the respective canton.

Discussion

Data on the spread of COVID-19 through time are of utmost importance to control this pandemic. An important measure obtained from the data is the reproductive number through time. Here, we investigated if changes in testing intensity could bias the reported reproductive number, and see no indication for major biases based on comparing confirmed case data and death data.

We see a continuous decline of the reproductive number through time in the second and third weeks of March. From the last week of March onwards, the reproductive number was significantly below 1, which corresponds to a decline in the epidemic. A similar trend was estimated in (16,10,24; accessed on April 24). Importantly, while we can look at the correlation between the reproductive number and public health measures, we cannot assess causation using our tools. Some approaches (11,25) aim at identifying the causes of R(t) changes. In general, as different measures were introduced very rapidly, it is hard to disentangle the effect of different measures.

Nevertheless, monitoring of R(t) can help health officials to evaluate if the epidemic is under control. In response to indications of a growing epidemic ($R(t)>1$), officials could implement more protective measures in advance to prevent overload of hospital capacity. Conversely, in response to indications of a shrinking epidemic ($R(t)<1$) officials could carefully relax protective measures in combination with wide-spread testing, contact-tracing, and isolation to avoid a rebound (26). Important in this respect is that the reporting has a delay of about 10 days, as new infections are reported with a delay of about 10 days. This also holds for the related approach described in (16). Only approaches making extra assumptions in order to extrapolate from the time interval covered by the data points can provide more recent predictions, see e.g. (24). Such predictions are not on a daily basis, though.

For estimating the R(t), we use the method presented in (14). We see one main caveat when using this method. This method assumes that all infections are included in the analysis. However, in Switzerland, mainly individuals belonging to risk groups were tested for COVID-19 during the considered time period. If the proportion of non-reported cases is constant, then in expectation, the underlying theory is still correct as the proportion cancels out from the equation given above. In (14), it is shown in a simulation study that the R(t) estimates are also robust to underreporting when the full probability distribution is considered.

At the start of the Swiss epidemic, new infections were imports from other locations rather than community transmissions (4). The imports can lead to an overestimation of R at the start of the outbreak. Thus we refrain from interpreting the estimated R(t) values at the beginning of March 2020. Further, migration between cantons may bias the within-canton estimates. Future phylodynamic analyses may be able to refine the reproductive values for the early epidemic in Switzerland and the epidemics in the cantons based on genomic sequencing data using the concept proposed in (8).

In conclusion, monitoring an epidemic through modelling is an essential part to guide prevention measures for the society as well as for hospitals. We will update R(t) in real-time throughout the course of the epidemic on our website (20). In this way, we intend to provide up-to-date information on the transmission dynamics of SARS-CoV-2 in Switzerland and its cantons.

Code and data availability

All code for performing the analyses and all data compiled for this study is available on https://github.com/jscire/Swiss_covid_Re.

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Disclosure statement

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Author contributions

TS conceived the idea of the study. JS and TS designed and performed the analyses. SN and TV provided feedback on the analysis design. GB assisted in analyses. TS and JS interpreted the results. RM, LM, TG, TE, CQ, MS, STS, MB, RB, WK, KSR, CHN, SB, HHH, AE, RK, AW, CAM, MM, TB, AM designed the testing procedures in their cantons and provided data. SF, KNK, and JS provided data. TS wrote the first draft of the manuscript. All authors critically revised the manuscript and contributed to the final version.

References

1. Chen L, Liu W, Zhang Q, Xu K, Ye G, Wu W, et al. RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak. Emerg Microbes Infect. 2020 Jan 1;9(1):313–9.

2. openZH/covid_19 [Internet]. Specialist Unit for Open Government Data Canton of Zurich; 2020 [cited 2020 Mar 30]. Available from: https://github.com/openZH/covid_19

3. New Coronavirus 2019-nCoV: first confirmed case in Switzerland [Internet]. [cited 2020 Apr 27]. Available from: https://www.bag.admin.ch/bag/en/home/das-bag/aktuell/medienmitteilungen.msg-id-78233.html

4. Federal Office of Public Health (BAG). New coronavirus Covid-19: three new confirmed cases in Switzerland [Internet]. [cited 2020 Apr 2]. Available from: https://www.bag.admin.ch/bag/en/home/das-bag/aktuell/medienmitteilungen.msg-id-78268.html

5. corona-data.ch for Switzerland [Internet]. [cited 2020 Mar 30]. Available from: https://github.com/daenuprobst/covid19-cases-switzerland

6. Anderson RM, May RM. Population biology of infectious diseases: Part I. Nature. 1979 Aug;280(5721):361–7.

7. Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med. 2020 13;27(2).

8. Vaughan T, Nadeau S, Scire J, Stadler T. Phylodynamic Analyses of outbreaks in China, Italy, Washington State (USA), and the Diamond Princess [Internet]. Virological. 2020 [cited 2020 Mar 30]. Available from: http://virological.org/t/phylodynamic-analyses-of-outbreaks-in-china-italy-washington-state-usa-and-the-diamond-princess/439

9. Abbott S, Hellewell J, Munday JD, Chun JY, Thompson RN, Bosse NI, et al. Temporal variation in transmission during the COVID-19 outbreak | CMMID Repository [Internet]. [cited 2020 Apr 7]. Available from: https://cmmid.github.io/topics/covid19/current-patterns-transmission/global-time-varying-transmission.html

10. Lemaitre J, Perez-Saez J, Azman A, Rinaldo A, Fellay J. Switzerland COVID-19 Scenario Report [Internet]. Available from: https://jcblemai.github.io/

11. Flaxman S, Mishra S, Unwin J, Coupland H, Mellan TA, Zhu H, et al. Report 13 Imperial College London - Estimating the number of infections and the impact of non-pharmaceutical interventions on COVID-19 in 11 European countries [Internet]. Imperial College London. [cited 2020 Apr 3]. Available from: http://www.imperial.ac.uk/medicine/departments/school-public-health/infectious-disease-epidemiology/mrc-global-infectious-disease-analysis/covid-19/report-13-europe-npi-impact/

12. Basel-Landschaft Media release. Notlage Basel-Landschaft [Internet]. [cited 2020 Apr 2]. Available from: https://www.baselland.ch/politik-und-behorden/regierungsrat/medienmitteilungen/regierungsrat-beschliesst-weitergehende-massnahmen-um-die-ausbreitung-des-coronavirus-einzudaemmen

13. University Hospital Basel. COVID-19 Testing Center Predigerkirche [Internet]. Unispital Basel. [cited 2020 Apr 2]. Available from: https://www.unispital-basel.ch/patienten-besucher/notfall/coronavirus/

14. Cori A, Ferguson NM, Fraser C, Cauchemez S. A new framework and software to estimate time-varying reproduction numbers during epidemics. Am J Epidemiol. 2013 Nov 1;178(9):1505–12.

15. Cori A, Cauchemez S, Ferguson NM, Fraser C, Dahlqwist E, Demarsh PA, et al. EpiEstim: Estimate Time Varying Reproduction Numbers from Epidemic Curves [Internet]. 2019 [cited 2020 Mar 30]. Available from: https://CRAN.R-project.org/package=EpiEstim

16. Abbott S, Hellewell J, Thompson RN, Bosse NI, Meakin S, Munday JD. Covid-19: Estimates for Switzerland [Internet]. Covid-19. [cited 2020 Apr 24]. Available from: https://epiforecasts.io/covid/posts/national/switzerland/

17. Linton NM, Kobayashi T, Yang Y, Hayashi K, Akhmetzhanov AR, Jung S, et al. Incubation Period and Other Epidemiological Characteristics of 2019 Novel Coronavirus Infections with Right Truncation: A Statistical Analysis of Publicly Available Case Data. J Clin Med. 2020 Feb;9(2):538.

18. Nishiura H, Linton NM, Akhmetzhanov AR. Serial interval of novel coronavirus (COVID-19) infections. Int J Infect Dis. 2020 Apr 1;93:284–6.

19. Neue Strategie - BAG empfiehlt viel mehr Corona-Tests [Internet]. Schweizer Radio und Fernsehen (SRF). 2020 [cited 2020 Apr 24]. Available from: https://www.srf.ch/news/schweiz/neue-strategie-bag-empfiehlt-viel-mehr-corona-tests

20. Stadler T. Website Computational Evolution Group, ETH Zürich [Internet]. [cited 2020 Mar 31]. Available from: https://bsse.ethz.ch/cevo/research/sars-cov-2.html

21. Wallinga J, Teunis P. Different Epidemic Curves for Severe Acute Respiratory Syndrome Reveal Similar Impacts of Control Measures. Am J Epidemiol. 2004 Sep 15;160(6):509–16.

22. Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, et al. Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia. N Engl J Med. 2020 26;382(13):1199–207.

23. Federal Office of Public Health (BAG). Media releases [Internet]. [cited 2020 Apr 2]. Available from: https://www.bag.admin.ch/bag/de/home/das-bag/aktuell/medienmitteilungen.html?dyn_startDate=01.01.2016

24. Flaxman S, Mishra S, Unwin J, Coupland H, Mellan TA, Zhu H, et al. Report 13 Imperial College London - Real time update of the results for Switzerland [Internet]. Imperial College London. [cited 2020 Apr 3]. Available from: https://mrc-ide.github.io/covid19estimates/#/details/Switzerland

25. Banholzer N, Weenen E van, Kratzwald B, Seeliger A, Tschernutter D, Bottrighi P, et al. Estimating the impact of non-pharmaceutical interventions on documented infections with COVID-19: A cross-country analysis. medRxiv. 2020 Apr 21;2020.04.16.20062141.

26. Salathé M, Althaus CL, Neher R, Stringhini S, Hodcroft E, Fellay J, et al. COVID-19 epidemic in Switzerland: on the importance of testing, contact tracing and isolation. Swiss Med Wkly [Internet]. 2020 Mar 19 [cited 2020 Apr 6];150(1112). Available from: https://smw.ch/article/doi/smw.2020.20225

Figure legends

Figure 1. Time between COVID-19 symptom onset and case confirmation. Histogram of the time between symptom onset and case confirmation for 139 patients from Basel-Landschaft.

Figure 2. Reproductive number of COVID-19 in Switzerland and 10 cantons. A: The line shows the cumulative number of confirmed COVID-19 cases in Switzerland and 10 cantons. The bars show the number of newly confirmed cases for a particular day. Note that the y-axis is on a log scale. **B**: The reproductive number through time estimated based on the confirmed case data. In black, we show the median of means for R(t) and the lighter areas correspond to the two uncertainty intervals. In blue, we show the estimated values for $R_c(t)$ as a sensitivity analysis. The vertical dotted lines are public health measures. In particular, the right of the gray interval is the time of the "Ausserordentliche Lage" (a lockdown) with non-essential shops and schools being closed. The dashed horizontal line highlights the threshold value R(t)=1.

Figure 3. Reproductive number of COVID-19 in Switzerland and the Cantons Basel-Stadt and Basel-Landschaft including sensitivity analyses. A: The black line shows the cumulative number of confirmed COVID-19 cases in Switzerland as well as the Cantons of Basel-Stadt and Basel-Landschaft. The black bars show the number of newly confirmed cases for a particular day. The red line shows the cumulative number of deaths for Switzerland and the blue line shows the cumulative number of hospitalizations for the cantons. The bars again show the number of new deaths or hospitalizations for a particular day. Note that the y-axis is on a log scale (thus no bar means 1 case and a bar from 1 down means 0 cases).
B: The estimates for R(t) based on the confirmed case data for the Cantons of Basel-Landschaft (top, black), Basel-Stadt (middle, black), and Switzerland (bottom, black) and the estimates for R(t) based on the number of COVID-19 related hospitalizations in Basel-Landschaft (top, blue), at the University Hospital Basel-Stadt (middle, blue), and the number of COVID-19 related deaths in Switzerland (bottom, red). Again, the solid lines are the median of means and the lighter areas are the two uncertainty intervals. The R(t) values to the right of the dashed line for Basel-Landschaft are obtained based on confirmed data collected under the same testing policy (in the other two plots, testing policy did not change). The vertical dotted lines are public health measures. In particular, the right of the gray interval is the time of the "Ausserordentliche Lage" (a lockdown) with non-essential shops and schools being closed. The dashed horizontal line highlights the threshold value R(t)=1.

Figure 4. Proportion of COVID-19 positive tests per day in testing centers of Basel-Stadt and Basel-Landschaft. We show the ratio of # positive tests and # tests per day performed (i) at the University Hospital Basel-Stadt and (ii) the two testing centers in Basel-Landschaft. If testing intensity decreased since the testing centers opened, we would expect an increase in this ratio as we would expect a trend towards testing individuals with stronger symptoms. We plot the regression line and the 95% confidence interval. However, the correlation between time and ratio is not significant.

Figures

Figure 1:

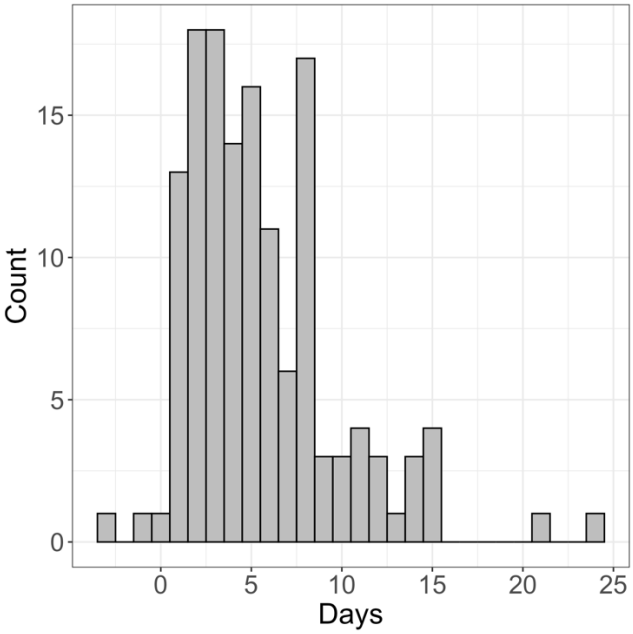

Figure 2:

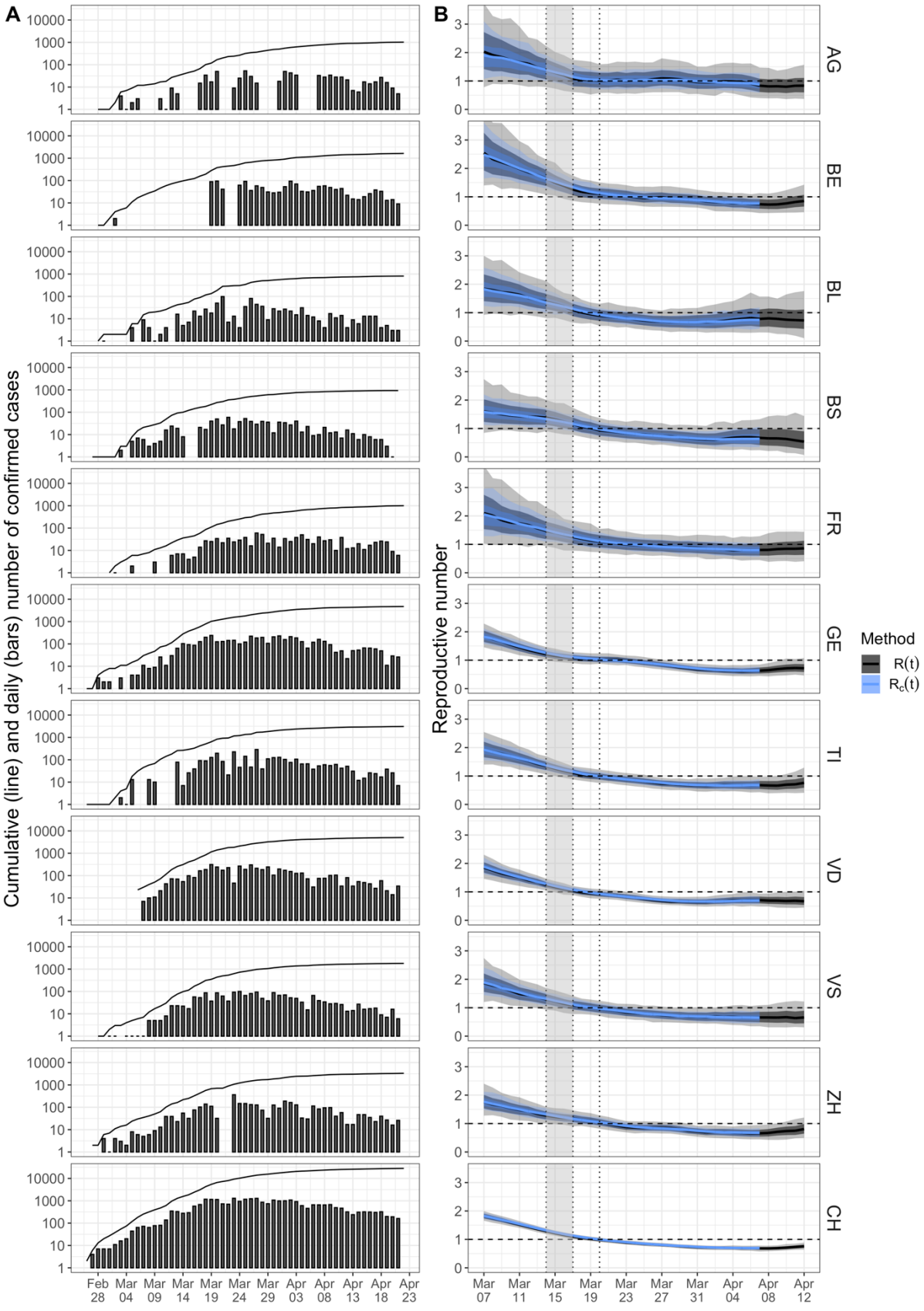
A
B
Cumulative (line) and daily (bars) number of confirmed cases
Reproductive number
AG
BE
BL
BS
FR
GE
TI
VD
VS
ZH
CH
Method
R(t)
$R_c(t)$
Feb 28
Mar 04
Mar 09
Mar 14
Mar 19
Mar 24
Mar 29
Apr 03
Apr 08
Apr 13
Apr 18
Apr 23
Mar 07
Mar 11
Mar 15
Mar 19
Mar 23
Mar 27
Mar 31
Apr 04
Apr 08
Apr 12

Figure 3:

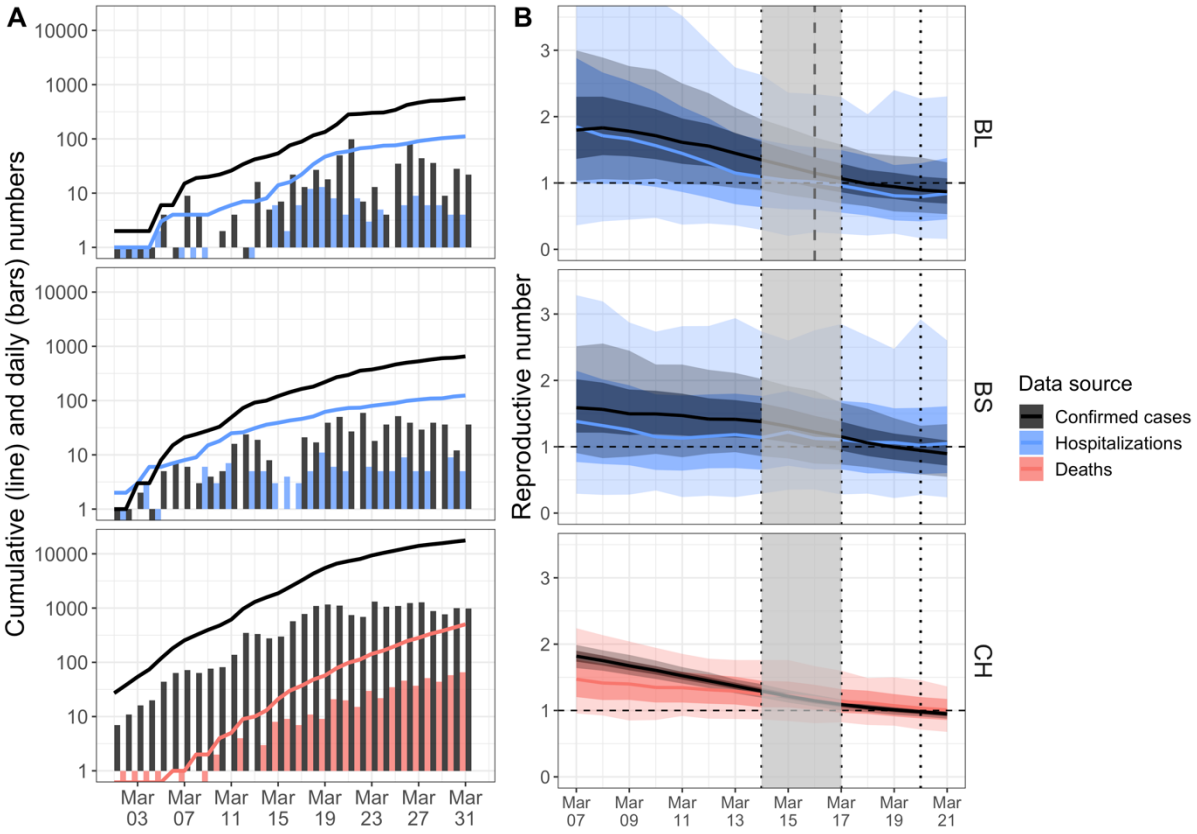

Figure 4: