Epidemiology in the force field of mathematics and politics

Jürg Fröhlich* and Daniel Wyler**

1. Introduction

Since its outbreak, the COVID-19 pandemic occupies a central position in the public discourse, pushing aside debates on other more dangerous global threats, such as climate change, nuclear proliferation, and growing tensions, internationally and within our societies. Governments have resorted to unprecedented and disputed measures in the name of public health, using or refuting 'Science'. With the media playing an important role, some scientists have risen to 'stardom', while others are ignored.

The COVID-19 pandemic illustrates how mathematics and science can be used – or abused – concretely. The present crisis also sheds some light on how science and science policy are reacting to external pressure and urgency in times of a dangerous pandemic. Cases in point are the fast retraction of two hastily written papers which turned out to be flawed (Rabin) and the so-called "covidization" of science (Woolston, Pai 1), which may threaten the diversity of research.

That invoking scientific arguments to help political decision-making is not without problems and dangers (for all parties involved) is well known. During the past several months, various problems have surfaced, such as inconsistent communication of 'scientific' findings by political bodies, inconsistent predictions based on simplistic mathematical models, all contributing to some unnecessary confusion and fear. Considerable pressure exerted by politicians, the media and, more

generally, the public upon scientists to come up with quick, ready-made statements and advice is creating a situation that may prevent a serious search for trustworthy and stable results, predictions and recommendations (for an overview of different government responses, see Hale et al). As the great British mathematician Sir Michael Atiyah put it: "Too often we [scientists] have to react to external events, to short-term crises, to financial cuts or to ministerial changes. In this semi-political world in which the scientific community has to operate we are in danger of losing our way and our identity. The scientific ethos becomes increasingly hard to discern." (Atiyah).

When communicating insights and results of their work to the public, which is often not familiar with the scientific methods that have led to those insights and results, scientists should respect some basic rules and principles. The most important one is to be completely open and honest about the scope and range of one's insights and results. For, otherwise, one may raise unjustified hopes and exaggerated expectations. Another important aspect to remember is that almost all predictions of future trends based on reliable scientific methods are *probabilistic*; they can assign a certain likelihood to certain events; but one can not exclude that different events might happen. To find out how and when to communicate uncertain predictions of future events requires considerable wisdom. Unfortunately, this fact, too, is often ignored. It is to be expected that violations of these rules and principles tend to have very unde-

* ETH Zürich, Theoretische Physik, HIT K 42.3, Wolfgang-Pauli-Strasse 27, 8093 Zürich.

E-mail: *juerg@phys.ethz.ch*
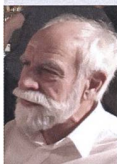
Jürg Fröhlich, Dr. sc. nat., born in 1946 in Schaffhausen; classical education at the "Kantonsschule"; studied physics at ETH Zurich (1965–1972, PhD in theoretical physics). After appointments at the University of Geneva, Harvard University, Princeton University, and the Institut des Hautes Etudes Scientifiques (IHES) at Bures-sur-Yvette, France, he joined the Physics faculty of the ETH Zurich in 1982, founded the "Center for Theoretical Studies" at the ETH Institute of theoretical physics in 1985, and served as Head of the Department of Physics for five years. For his scientific work in theoretical and mathematical physics he received various recognitions. Since his retirement in 2011, he has continued his scientific studies and held visiting positions at Bielefeld, Princeton, and at the IHES.

** Universität Zürich, Winterthurerstrasse 190, 8057 Zürich.

E-mail: *wyler@physik.uzh.ch*

Daniel Wyler, PhD (Physik), 1949 in Jerusalem geboren, besuchte die Kantonsschule in Aarau, studierte Physik an der ETH Zürich (1969–1974). PhD 1977 Carnegie-Mellon University, Pittsburgh, USA. Postdoc-Anstellungen an der Rockefeller University, an der Universität Bonn und am CERN. Ab 1987 Professor für theoretische Physik an der Universität Zürich, Dekan, Prorektor 2010–2015. Hauptarbeitsgebiet: Theoretische Elementarteilchenphysik. Seit der Emeritierung 2015 verschiedene Aktivitäten in «Open Science» (insbesondere Open Access, Citizen Science) und internationaler Zusammenarbeit; Fortführung der Arbeit in theoretischer Physik.

sirable longterm consequences for the public's trust in science and scientists (and for the funding of science).

In fact, the communication of some implausible claims kindled the interest of the authors in mathematical epidemiology and its methods. The official curves showing the temporal behavior of the 'effective reproductive number' R (see below) around lockdown in Switzerland (March 17, 2020) seemed to contradict naive expectations (see SNTF). Instead of a sudden falloff around March 17 (a total lockdown for everyone would have resulted in a jump of R to zero), the published curve began to fall smoothly considerably earlier. In this contribution, we report on some of the things we believe we have learned. We think that our considerations are important in a time when an alarmingly high percentage of the population appears to be turning away from scientific reasoning (examples are the "non-vaccinators", deniers of climate change and followers of various conspiracy theories). See (Phalkey, Pai 2) for thoughts about how to inform the public.

In the following, we try to limit the use of mathematical language, but we might not always succeed. In any event, we are convinced that using mathematics properly prevents one from falling into various traps originating from too cavalier a treatment.

2. What data may tell us, and how to interpret them – examples

The data concerning a subject of wide interest and relevance, such as a pandemic or climate change, should be provided in a consistent, easy to use form. The present drive for open access and open data (often referred to as FAIR data) should encourage the creation of data hubs to replace the present plethora of data sites and providers; digital tools to enable this transition will have to be developed.

When dealing with data and using them to predict or estimate certain developments it is important to bear in mind the following guidelines.

(a) Determine which data among a large set of data are *directly measurable/observable*, and which data have to be reconstructed from a basic set of directly observable data and hence are only indirectly and usually only *approximately* known. An example of data that can be measured (or inferred) directly on a certain day numbered t is the number of patients who have carried the Sars-CoV-2 virus and have died in Switzerland on day $t - 2$. An example of data that cannot be measured directly and have to be reconstructed from other data are the reproductive number R_t on a certain day t, and the total number of people who, on day t, are infected from the Sars-CoV-2 virus

in a country like Switzerland. If, for certain purposes, one uses data that are *not* directly measurable, then it is crucial to disclose which *directly measurable* data are used and which algorithms are applied to estimate them, and in particular, give an honest estimate of the uncertainties that are thereby generated.

(b) Typically, there are more data available than might possibly be useful (but most often are not) to predict certain developments, such as the evolution of an epidemic. It is thus crucial to:

– Determine the subset of a possibly huge set of data that is relevant to carry out a certain task. For this purpose, one could assign *weights* to data and keep only those that have a fairly large weight. For example, the colour of the hair of a COVID-19 patient is very unlikely to be relevant when one tries to estimate his/her probability to be cured. However, his/her age and the answer to the question whether she or he has diabetes are evidently relevant data and hence must be of large weight.

– Determine how reliable the data are one uses to carry out a certain task. Answer the following questions: Are the sources of one's data trustworthy? What are the likely *error margins* of the data one works with?

(c) As mentioned, the statistical and systematic errors of the data and the methods of analysis should be treated with great care. Often times, these errors can neither be determined very precisely, nor can they be neglected. Furthermore, the models and the mathematical algorithms one uses to extract estimates and predictions of certain developments from a given set of data tend to have some intrinsic flaws and/or the data available to us may not suffice to make unambiguous predictions on the basis of the models in use.

A famous example illustrating, a posteriori, why it may take a long time to discover a basic law of nature enabling one to predict certain developments over long stretches of time concerns the prediction of positions of the planets in the night sky. Ptolemy's model of the solar system (Earth-centred, around 100 AD), involving epicycles, had some serious intrinsic flaws built into it, although it could actually be used to predict, fairly reliably, the positions of planets some years into the future. It took considerably more than one thousand years until Kepler (heliocentric, around 1600) found more fundamental and reliable laws of planetary motion. Still there were (numerically rather small) intrinsic shortcomings, because the perturbations of the planets' orbits caused by their mutual gravitational attraction were neglected. It took another century

until Newton discovered laws of planetary motion and gravitation more fundamental than Kepler's that enable people who are very strong at calculating or use large computers to make astonishingly accurate predictions for the motion of planets in the solar system over long stretches of time. It then took another three hundred years until Einstein discovered a law that is even more fundamental and precise than Newton's, that enabled him to explain an observed minute deviation of the motion of Mercury from the Newtonian prediction, which, before Einstein, was a mystery. This illustrates the fact that it takes much dedication and time to discover laws describing the time evolution of certain phenomena and to then build models expressing such laws that are simple enough to be practical, but sufficiently precise to be trustworthy.

Predictions brought forward on the basis of a scientific reasoning process are almost always afflicted with smaller or larger uncertainties. They are of the kind that a process will happen with a certain positive likelihood (not rarely difficult to estimate); but with a different likelihood, a different development will be observed. Unfortunately, *firm* predictions that are almost certain to come true are rare. It is crucial to communicate *honestly and transparently* how certain and believable one's prediction of a certain development is, with what probability something else might happen, and how reliable/believable the model and the algorithms are one has used to arrive at one's predictions.

Next, we sketch some concrete examples of how data, typically time series, can be used to come up with estimates or predictions of future developments. Our examples are expected to be relevant in connection with the COVID-19 pandemic. We start with a straightforward and intuitive

Example 1 (extrapolation of data). Suppose we are given a time series of length N consisting of the numbers, $k_{tot}(t)$, $t = t_0, ..., t_0 + N$ of patients in Swiss hospitals carrying the Sars-CoV-2 virus on day t. Here t_0 is the time when tests for Sars-CoV-2 were first made on all patients admitted to Swiss hospitals, and N is at least twice or thrice the estimated incubation time of the disease.

What could we try to do with this particular set of data? The most straightforward use is to fit a smooth curve, $\kappa(t)$, $t_0 \leq t \leq t_0 + M$, $M > N + 1$, using, for example, *Gauss' method* of least squares. (How to choose the ansatz for this curve requires some experience; naïve choices, such as a polynomial of degree $\leq N$, often do not work very well.) This curve enables us to define a set of non-negative integers, $k_{tot}(t)$, $t = t_0 + N + 1$, $t_0 + 1$, ..., $t_0 + M$, by setting

(1)
$$k_{tot}(t) \cong \kappa(t), t = t_0 + N + 1, ..., t_0 + M, M > N + 1.$$

If $k_{tot}(t)$ is well below the number of hospital beds available to treat patients carrying the Sars-CoV-2 virus, for all days $t = t_0 + N, ..., t_0 + M$, then the situation looks safe from the point of view of hospitalization. If, however, it is larger than the number of such hospital beds, for some $t > N$, then there are reasons to worry, and new measures to lower the infection rate should be introduced.

In this case (and possibly in many other instances) simple considerations may yield useful results, and one does not have to resort to very sophisticated methods. Errors in the predictions can be estimated using well-known methods of statistics.

Example 2. Often, one is facing questions about quantities that are not directly observable and must be reconstructed from available information. This procedure invariably introduces (possibly large) errors. As an example, let us assume that we would like to make an educated guess of the true number $n(t)$, of people living in Switzerland who carry the virus on some day t. Obviously, the numbers $n(t)$, $t = t_0, t_1, ...$ are *not* directly measurable. But we can assume that we know the number, $m(t)$, of people in Switzerland who are *known* to be infected on day t, *because* they have been tested for the virus on some day $t' \leq t$ and are still being treated on day t. Clearly, $m(t) \leq n(t)$. We might want to look for a relation of the kind

(2)
$$n(t) = H(t)^{-1} m(t) + \mu(t),$$

where $H(t)$ is a number smaller than 1 representing the expected ratio between $m(t)$ and $n(t)$, and $\mu(t)$ describes *noise* (including statistical errors) in the data. Our task is to estimate $H(t)$ and make a guess for the form of $\mu(t)$. This is the type of question one is often faced with in epidemics. Of course, if we could test everybody within a very short period of time, we would know $n(t)$. Without this option, we aim to find representative groups of people, some of whom have been tested positive and control how they develop. Using suitably chosen observable data and statistical methods (and their uncertainties!) this may allow one to estimate the total number of infected people.

To proceed, we note that the following data are measurable: The average number, τ, of days people remain infectious after having been infected with the SARS-CoV-2 virus; the average delay, δ, between the infection of a patient with the SARS-CoV-2 virus and a possible hospitalization; the total number, $h(t)$, of people hospitalised in Switzerland on day t among

those people who had previously tested positive for the SARS-CoV-2 virus on some day $t' \leq t$, before being hospitalised, and are known to be ill on day t; clearly $h(t) \leq m(t)$; finally the *total* number, $k(t)$, of people who are hospitalized in a Swiss hospital on day t and are tested positive. To summarize, the following data would seem to be directly measurable:

(3)
τ, δ, and the time series $m(t)$, $h(t)$, $k(t)$, with $t_0 \leq t \leq T$,

where t_0 is the time when one started to record these directly observable data (after the tests for the SARS-CoV-2 virus were first made available), and T is the present time, minus a few days.

We claim that using the directly observable data in Eq. (3) one can make an educated guess of the total number $n(t)$ of people in Switzerland who, on day t, are infected. Since this requires taking time averages and smoothing of data, our guess is afflicted with statistical errors that depend on quantities such as τ and δ; they are not easy to determine precisely.

To be a bit more precise, we suppose that, on average, people infected with the SARS-CoV-2 virus are infectious for τ days. We assume that, for several weeks, namely on days $t = t_1, ..., t_2$, with $2\tau \leq t_2 - t_1 \approx 20$ to 30, $m(t)$ people have been tested to carry the virus on day t in Switzerland during recent weeks. We require that every person tested for SARS-CoV-2 on any day between t_1 and t_2 is tested only once, so that the samples of tested people on different days $t = t_1, ..., t_2$ are disjoint from one another. It is important to carry out tests on samples of people that are statistically typical, for example have a typical age distribution and whose various health conditions are typical. Every (statistically typical) sample of $m(t)$ infected people taken on day t is monitored after day t, for at least 2τ consecutive days after day t. In particular, one takes data of how many among those infected have to be hospitalized on day t– this number is denoted by $h(t)$ – and of how many days δ, on average, after a positive test hospitalization takes place (if necessary, one could record more accurate data rather than only an average delay). Apart from $m(t)$ and $h(t)$, we need also the total number, $k(t)$, of patients who are hospitalized on day t and are tested positive. Thus the accessible data are the time series

(4)
$m(t)$, $h(t + \delta)$, $k(t + \delta)$, $t_1 \leq t \leq t_2$,

and the delay time δ. We set $T = \frac{(t_1 + t_2)}{2}$ and define the average value, $\overline{m}(T)$, of $m(t)$ by the sum of the $m(t)$ over the interval $t_1 \leq t \leq t_2$, divided by $t_2 - t_1$, and $\overline{h}(T)$, $\overline{k}(T)$ are defined accordingly. We then define

$$H(T) := \frac{\overline{h}(T + \delta)}{\overline{k}(T + \delta)}$$

and expect that

$$\overline{n}(t) \simeq H(t)^{-1}\overline{m}(t).$$

Taking various time averages to eliminate fluctuations on short time scales and introducing a noise function $\mu(t)$ in Eq. (2), describing fluctuations and noise in the data, is crucial. The noise function can be estimated by comparing the actual data, $m(t)$, to their averages, $\overline{m}(t)$, for sufficiently many days t. This will yield information about the variance of $\mu(t)$. If this variance is fairly small, as compared to $m(t)$, (meaning that the epidemic evolves quite smoothly in time, and the number of new infections does not fluctuate very much), then one may take $\mu(t)$ to be Gaussian.

The data reconstructed from the time series in Eq. (3), in particular $H(t)$ and $\mu(t)$, along with a (hopefully plausible) ansatz of an evolution equation for $n(t)$, can now be fed into a filter, such as a *Kalman filter* (Kim, Bang). This will yield an educated guess – but not more than that(!) – of the true evolution of, for example, daily infection numbers. From this one might infer the values of some *not directly observable* quantities, such as the reproductive number, R_t, and estimate the error bars within which these quantities can be predicted. It adds to the confusion that, in public communications, indirectly known quantities, such as R_t, are used as if they were easily accessible, and without sufficient discussion of error bars.

3. Modelling the evolution of epidemics
So far, we have discussed two aspects of how to work with available data. One is, of course, interested in the causal chain of evolution that regulates the epidemics. Phenomenological modelling of epidemics (or similar phenomena, such as insects or diseases) has of course a long history. In passing, we mention here only the important series of papers that set the scene for many epidemiological studies, namely the work of Kermack and McKendrick, starting in1927 (Kermack, McKenndrick), extending earlier work in (Ross and Hudson, 1917), which led to evolutionary models such as the well known SIR Models (Luchsinger).

We continue with some basic observations. In order to come up with an intelligent prediction of the evolution of the COVID-19 epidemic in Switzerland, we look for approximate laws of evolution of quantities such as the total number $n(t)$ of people who are infected with the Sars-CoV-2 virus on day t. In general, it is necessary to include additional variables next to $n(t)$ when looking for a proper characterisation of the 'state', $x(t)$, of the epidemic on day t.

A (possibly inadequate) first guess of how one might define $x(t)$ is as follows: $x(t)$ is a vector with many components all of which have values in the non-negative integers; it is given by

(5)
$$x(t) := (n(t), n(t-1), \ldots, n(t-\tau), k(t), \ldots, k(t-\tau), p(t), \ldots, p(t-\tau)).$$

Here, $k(t)$ is the number of patients who are hospitalised on day t and test positive for SARS-CoV-2; $p(t)$ is the number of infected people who have passed away on day t (recall that τ is an estimate for the number of days a patient is sick with COVID-19 after having been infected with the SARS-CoV-2 virus, before he or she is cured or has died). If needed, the quantity $n(t)$ can be split into relevant subclasses, for instance risk classes. Defining factors of risk classes are the patients' age, their medical condition, a record of how their immune system tends to react, etc.

In our definition of the state $x(t)$ of the COVID-19 epidemic, we are obviously neglecting the geographic distribution and connectedness of people infected with Sars-CoV-2. This might often be an unacceptable simplification, corresponding to what physicists call a "mean field ansatz". Taking into account the spatial inhomogeneities of $n(t)$ increases the computational complexity of the evolution equations considerably. There is a rich literature on this issue in a variety of contexts, see, e.g., (Luchsinger)

As the propagation of infections is stochastic, the simplest ansatz is a linear stochastic evolution equation for the state $x(t)$ of the epidemic:

(6)
$$x(t) = \Gamma_\omega(t) \cdot x(t-1) + w(t-1),$$

where ω is a random variable afflicting all the parameters in the equation (such as the randomness in the infection process), Γ_ω is a (random) transition matrix depending on ω, and $w(t)$ describes statistical noise in the data, originating from, among other sources of noise, fluctuations due to people entering or leaving Switzerland.

For Eq. (6) to be useful in making predictions we ought to know something about the law of the random matrix $\Gamma_\omega(t)$. Often, people guess the mean values of its matrix elements

(7)
$$G(t) := \langle \Gamma_\omega(t) \rangle,$$

where $\langle (\cdot) \rangle$ denotes an average (mean) over the random variable ω. Taking subsequently an average over ω on both sides of equation (6), one arrives at a deterministic evolution equation. But averaging leads to a simple linear equation only if $\Gamma_\omega(t)$ and $x(t-1)$ are **independent** random variables, which is a property that often remains unchecked. Note that if one assumes a non-linear stochastic evolution equation, taking means would usually not make sense at all, unless one knows a lot about the law of the random matrix Γ_ω. More material on the convergence of stochastic to deterministic equations can be found, e.g., in (Luchsinger).

Taking the stochastic nature of the evolution equation (6) seriously will enable one to guess the statistical distribution, i.e., the error bars, of one's predictions. Reliable estimates of error bars appear to be rare in analyses publicly debated in recent months.

For (5) to be useful, at all, one has to relate the state $x(t)$, which is **not** directly observable, to observable data with the help of relations of the kind of (2) or generalizations thereof. One is then ready to feed one's data into a filter equation, such as the *Kalman filter*. Here, we will not elaborate on this method; but it would be useful if authors disclosed more transparently what they are doing in their analyses. This would induce some confidence in the reliability of their results.

To conclude we mention the three most important questions to be reckoned with:
(*a*). Is the model one uses (that is the evolution equations) trustworthy/reliable? As the example of planetary motion shows, this is usually difficult to assess and can lead to considerable uncertainties.
(*b*). What are the values and errors of parameters used in the model? This is actually a core topic of statistics.
(*c*). What are the stochastic uncertainties, what is the law or randomness (for stochastic models)?

4. The effective reproductive number R_t
"*...of course, everyone in the universe and their dog knows about the R-number now...*"
www.bbc.co.uk/sounds/play/m000l267, ca. at 10:15 min

Loosely speaking, the reproductive number is the expected number of secondary infections produced by one primary infection. If the reproductive number exceeds 1, public measures may be called for in order to keep control of an epidemic. This simple interpretation explains why the reproductive number has attracted wide attention. Within the SIR model, the basic reproductive number R_0 describes the initial increase of infected individuals.

During an epidemic, one works with time dependent quantities, such as the "case reproductive number", or, alternatively, the "effective reproductive number". The case-reproductive number at time t is defined as the

average number of secondary cases that a primary case infected at time t will eventually infect, thereby taking into account the impact of control measures and depletion of susceptible persons during the epidemic (Wallinga). The effective reproductive number R_t at time t, is defined as the ratio of new infections on day t, to the infectivity-weighted average of infected cases of the days prior to day t (Cori). While the case reproductive number is simpler to understand and conceptually easy to define, it is difficult to estimate and is measurable only much later. On the other hand, while the meaning of the effective reproductive number is not obvious, it is more amenable to quasi-instantaneous estimation.

A major problem here is that the number of infected people at time t is **not** known at that time and cannot be measured directly. In fact, only a fraction of infected people will be detected, namely those who later show symptoms and, even later, are tested positive (after 10 days or so, say). Thus, we are confronted with the need to calculate 'backwards', not knowing precisely the time and place of infection. We now understand why Example 2 discussed above is important.

The determination of R_t is thus highly indirect, involving various statistical tools. Further, as shown in Example 1 of Section 3, important information can be gained directly from data, without knowledge of R. Nevertheless, as the various choices of R have gained a high visibility and play such a prominent role in communicating to the public any necessary measures to contain the pandemic, it seems worthwhile to look at this quantity in some more detail.

We start by commenting on the determination of R_t. Consider the following evolution equation featuring R_t:

$$I_t = R_t \sum I_{t-n} w_n,$$

where I_t is the number of people newly infected on day t etc. and w_n, the infectivity, is the probability that a secondary infection was contracted from a person who got infected n days earlier. Whereas the infectivities 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 (see Example 2 of Section 3). Therefore, they need to be inferred indirectly from some other data. For example, R_t can be thought of as the ratio between the number of true and expected infections.

Because of the stochastic character of the infection process, the time spans X from the infection to the onset of symptoms (incubation time), and from there to a test (confirmation), Y, are distributed with a characteristic time lag. The distributions (laws) of X and Y are obtained by fitting these quantities to avail-

able data; see (SNTF) and references therein. Then, for every confirmed case a one samples a number x'_a from the distribution of X and a number y'_a from the distribution of Y.

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

The scheme sketched here introduces *noise* into the true data (Petermann). We denote the true infection day by i_a, 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 values of x'_a and y'_a are independent of the true values of x_a and y_a (because we don't know these; we just know that they are approximately distributed in the same way as X and Y, respectively), the reconstructed infection day i'_a equals the true "signal" i_a plus some "noise" given by $d'_a = x_a + y_a - x'_a - y'_a$.

This noise results in a smoothing of the behaviour of R'_t. As a result, the effects of 'sudden' measures, such as a lockdown, are less visible in the reported behaviour of R_t. Furthermore the errors introduced in R_t are underestimated.

There are of course ways to avoid this artificial smoothing. A natural way is to assume that R_t is constant, except for steps at 'points of change' where abrupt new measures (lockdown, limits on gatherings, etc.) are imposed (Flaxman). The height of the steps is fitted to account for observed data. This procedure, applied to times of new social measures, also gives a picture of the effectiveness of the measures imposed. Of course, model assumptions must be checked and uncertainties estimated. Illustrative examples show that errors less than about 20% are unrealistic.

Concluding this section, we note that R_t may not be particularly useful for monitoring the pandemic and communicating its course to the public, because of the large uncertainties in this quantity's determination and meaning.

5. Conclusions

The present pandemic has given rise to an enormous amount of activity in COVID-19-related research. Special grants have been offered, and many people have redirected their research efforts into areas promising some impact on the handling of the crisis. It has also raised the interest of the authors of this contribution to look more closely at the situation, in particular at

mathematical issues related to modelling and understanding the crisis, but also thinking about strategies to control the damage done to the economy by the pandemic and about the well-being of Swiss society.

The urgency of taking appropriate measures has led to the inclusion of scientists into policy-making bodies, such as national task forces. The hunger of the mass media for good stories has propelled some scientists to star status. This may have contributed to the fact that the media have not offered an accurate, balanced and critical picture of the status of our understanding of the crisis.

Time constraints and policy pressures have often been responsible of the circumstance that advisory groups have not been assembled with the required breadth of expertise. Error-awareness and critical assessment of results (to be made before results are released into the public domain) appear to have suffered in the course of this crisis. As a result, some communications may have conveyed the impression that no (or only very tiny) errors are involved in the results that are being communicated, leading to unrealistic expectations and, as a consequence, to a lack of credibility of scientists.

There are lots of data published every day on several websites; but there does not appear to exist much coordination and consistency between them. We feel that, in view of this situation, plans to establish a Swiss data centre – considered in connection with the trend towards open access and open (FAIR) data – deserve to be strongly promoted.

Despite the plethora of data, it is not clear to us whether the data are treated in adequate ways (see Example 1, above), and whether reliable use is made of them.

In particular, we have studied communications connected to the reproductive number R. We think that there has been a lack of bona-fide statistics and a certain hesitation on the side of the 'official' task-force scientists to include outsiders. Indeed a reliable derivation of R is far from obvious.

There is a tendency in the medical literature to relegate technical 'details' such as mathematical formulae into 'supplementary material'. While this is understandable from the viewpoint of improved readability, it hides the mathematical methodology needed to properly assess the reliability of the results. It might be cumbersome to list all definitions and assumptions (such as the statistical independence of random variables) but doing a careful job will make the situation more sustainable. The use of prefabricated statistics packages presents similar dangers.

The emphasis on research tightly or vaguely connected to COVID-19 has led to a certain "covidisation" of research, resulting in a lack of fundamental research on this and other related diseases. While hoping that this is a short-term phenomenon, we fear that this trend might end up in a certain depletion of the diversity of research and, in the long term, will not help to overcome crises such as COVID-19. ∎

References

Atiyah M. "Farewell Address by Sir Michael Atiyah to the Royal Society", Suppl. Royal Soc. News, vol. 8, No. 6, pp xv–xxii, 1995.

Cori A., Ferguson N.M., Fraser C., Cauchemez S. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. 2013.

Flaxman S., Mishra S., Gandy A. et al. Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe. Nature 584, 257–261 (2020). *https://doi.org/10.1038/s41586-020-2405-7*.

Hale Th., Angrist N., Kira B., Petherick A., Phillips T., Webster S. "Variation in Government Responses to COVID-19" Version 6.0. Blavatnik School of Government Working Paper. May 25, 2020. Available: *www.bsg.ox.ac.uk/covidtracker*.

Kermack W.O., McKendrick A.G. A Contribution to the Mathematical Theory of Epidemics Proc Royal Soc London A 115, 700–721 (1927).

Kim J. and Bang H. Introduction to Kalman Filter and Its Applications, *https://www.intechopen.com/books/introduction-and-implementations-of-the-kalman-filter/introduction-to-kalman-filter-and-its-applications*.

Luchsinger Ch. Lectures and notes on mathematical epidemiology, see e.g. *http://www.luchsinger-mathematics.ch/Diss01.pdf*, *http://www.luchsinger-mathematics.ch/me.html*.

Pai M.1 Covidization of research: what are the risks?. Nat Med 26, 1159 (2020). *https://doi.org/10.1038/s41591-020-1015-0*.

Pai M.2 Journalists Need To Get It Right: Epidemiology Training Can Help. *https://www.forbes.com/sites/madhukarpai/2020/08/09/journalists-need-to-get-it-right-epidemiology-training-can-help/*.

Petermann M., Wyler D. A pitfall in estimating the effective reproductive number Rt for covid-19, Swiss Med Wkly 2020; 150:w20307.

Phalkey J. The pandemic: What should the public know? *https://www.natureasia.com/en/nindia/article/10.1038/nindia.2020.112*.

Rabin R.C. The Pandemic Claims New Victims: Prestigious Medical Journals. *https://www.nytimes.com/2020/06/14/health/virus-journals.html*.

Scire J. Swiss Med Wkly. 2020;150:w20271.

SNTF: Swiss National COVID-19 Science Task force. Available at *https://doi.org/10.4414/smw.2020.20307*.

Wallinga J., Teunis P. Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures. Am J Epidemiol. 160(6),509–516 (2004).

Woolston C. 'It's like we're going back 30 years': how the coronavirus is gutting diversity in science. *https://www.nature.com/articles/d41586-020-02288-3*.