

Mathematical Epidemiology - Effective Reproduction Number

Lecture series at Faculty of Mathematics and Physics, CUNI in Prague

Tomáš Rosa, Ph.D.

Head of Cryptology and Biometrics Competence Centre of Raiffeisen BANK International in Prague



Effective Reproduction Number $R_e(t)$

- **Do not mix R_0 and $R_e(t)$**
 - **R_0 describes qualitative characteristics, $R_e(t)$ shows local dynamics**
 - **$R_e(t)$ captures actual countermeasures, seasonality, immunity status, etc.**
 - **their relative influence is hard to distinguish, but the overall picture is valid**
 - **in particular, we are just crossing herd immunity threshold (in given context!) when $R_e(t) = 1$**
 - **$R_e(t)$ indicates how the epidemic would spread during outbreaks**
 - **this is regardless if there actually is or is not such an outbreak, it is sort of a potential**
 - **we shall be careful about estimates of $R_e(t)$, however; do not forget on confidence intervals**
 - **many different methods, all of them having certain assumptions - this has to be considered**

OurWorldInData Engine for “Reproduction Rate”

$$gr(I_t) = \frac{I_t - I_{t-1}}{I_{t-1}}$$

$$gr(I_t) = \gamma(R_t - 1) + \varepsilon_t, \quad \varepsilon_t \sim \text{i.i.d. } N(0, \delta_e^2)$$

$$R_t = R_{t-1} + \eta_t, \quad \eta_t \sim \text{i.i.d. } N(0, \delta_\eta^2)$$

- SIR-based
observable
internal state
function and
internal state
update

PLOS ONE

RESEARCH ARTICLE

Tracking \mathcal{R} of COVID-19: A new real-time estimation using the Kalman filter

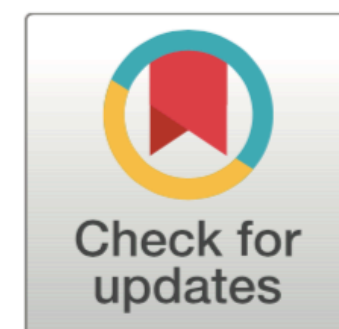
Francisco Arroyo-Marioli¹, Francisco Bullano¹, Simas Kucinkas^{ID 2*}, Carlos Rondón-Moreno^{ID 1}

¹ Central Bank of Chile, Santiago, Chile, ² Humboldt University of Berlin, Berlin, Germany

* simas.kucinkas@hu-berlin.de

Abstract

We develop a new method for estimating the effective reproduction number of an infectious disease (\mathcal{R}) and apply it to track the dynamics of COVID-19. The method is based on the fact that in the SIR model, \mathcal{R} is linearly related to the growth rate of the number of infected individuals. This time-varying growth rate is estimated using the Kalman filter from data on new cases. The method is easy to implement in standard statistical software, and it performs



EpiEstim Package for CRAN-R Engine



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Practice of Epidemiology

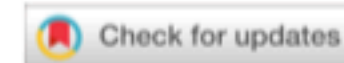
A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics

Anne Cori*, Neil M. Ferguson, Christophe Fraser, and Simon Cauchemez

* Correspondence to Dr. Anne Cori, Department of Infectious Disease Epidemiology, MRC Centre for Outbreak Analysis and Modelling, Imperial College London, St Mary's Campus, Norfolk Place, London W2 1PG, United Kingdom (e-mail: a.cor@imperial.ac.uk).

Initially submitted November 26, 2012; accepted for publication May 23, 2013.

The quantification of transmissibility during epidemics is essential to designing and adjusting public health responses. Transmissibility can be measured by the reproduction number R , the average number of secondary cases caused by an infected individual. Several methods have been proposed to estimate R over the course of an



RESEARCH ARTICLE

UPDATE Estimating the time-varying reproduction number of SARS-CoV-2 using national and subnational case counts

[version 2; peer review: 1 approved with reservations]

Sam Abbott ^{1*}, Joel Hellewell ^{1*}, Robin N. Thompson¹, Katharine Sherratt ¹, Hamish P. Gibbs¹, Nikos I. Bosse ¹, James D. Munday ¹, Sophie Meakin ¹, Emma L. Doughty², June Young Chun ³, Yung-Wai Desmond Chan¹, Flavio Finger ⁴, Paul Campbell ⁴, Akira Endo ¹, Carl A. B. Pearson ¹, Amy Gimma ¹, Tim Russell ¹, CMMID COVID modelling group, Stefan Flasche ¹, Adam J. Kucharski¹, Rosalind M. Eggo¹, Sebastian Funk ¹

¹Center for the Mathematical Modelling of Infectious Diseases, London School of Hygiene & Tropical Medicine, London, WC1E 7HT, UK

²Institute of Microbiology and Infection, University of Birmingham, Birmingham, UK

³Division of Infectious Diseases, Department of Internal Medicine, National Cancer Center, Goyang, South Korea

⁴Epicentre, Médecins Sans Frontières, Paris, France

* Equal contributors

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<https://doi.org/10.12688/wellcomeopenres.16006.1>

Latest published: 08 Dec 2020, 5:112
<https://doi.org/10.12688/wellcomeopenres.16006.2>

Abstract

Background: Assessing temporal variations in transmission in different countries is essential for monitoring the epidemic, evaluating the effectiveness of public health interventions and estimating the impact of changes in policy.

Methods: We use case and death notification data to generate daily estimates of the time-varying reproduction number globally, regionally, nationally, and subnationally over a 12-week rolling window. Our modelling framework, based on open source tooling, accounts for uncertainty in reporting delays, so that the reproduction number is estimated based on underlying latent infections.

Results: Estimates of the reproduction number, trajectories of infections, and forecasts are displayed on a dedicated website as both maps and time series, and made available to download in tabular form.

Conclusions: This decision-support tool can be used to assess changes in virus transmission both globally, regionally, nationally, and

Open Peer Review**Reviewer Status** ?

Invited Reviewers

1

version 2(update)
08 Dec 2020

?

report

version 1

01 Jun 2020

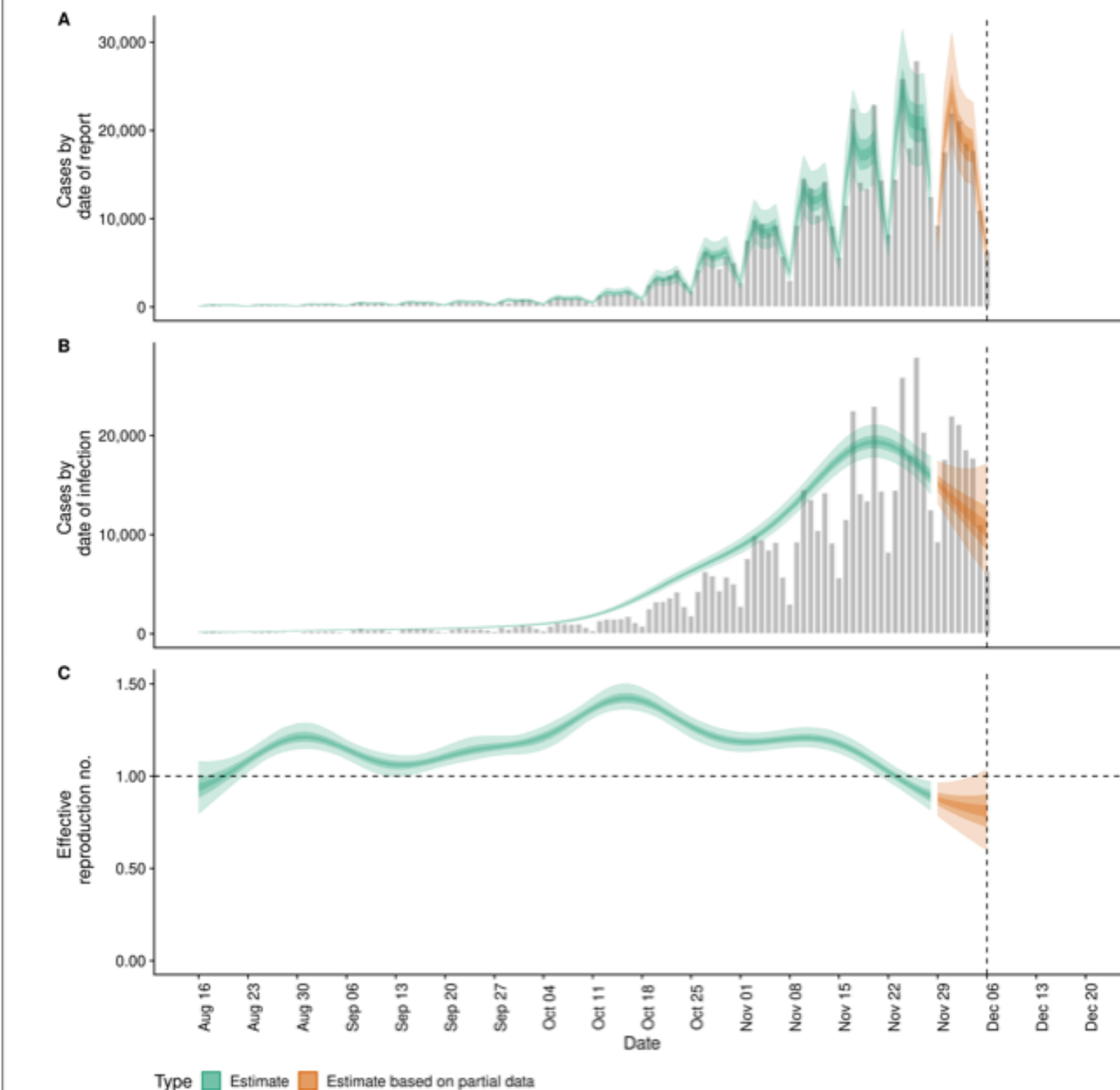
1. **Francesco Chirico** , Post-graduate School of Occupational Health, Università Cattolica del Sacro Cuore, Roma, Italy

Any reports and responses or comments on the article can be found at the end of the article.

Summary (estimates as of the 2021-12-06)

Table 1: Latest estimates (as of the 2021-12-06) of the number of confirmed cases by date of infection, the expected change in daily confirmed cases, the effective reproduction number, the growth rate, and the doubling time (when negative this corresponds to the halving time). The median and 90% credible interval is shown for each numeric estimate.

	Estimate
New confirmed cases by infection date	10451 (6023 – 17175)
Expected change in daily cases	Likely decreasing
Effective reproduction no.	0.81 (0.6 – 1)
Rate of growth	-0.054 (-0.12 – 0.0092)
Doubling/halving time (days)	-13 (75 – -5.9)

Confirmed cases, their estimated date of report, date of infection, and time-varying reproduction number estimates

Schätzung der aktuellen Entwicklung der SARS-CoV-2-Epidemie in Deutschland – Nowcasting

Erläuterung zu den verwendeten Daten

Es besteht ein großes Interesse daran das aktuelle Infektionsgeschehen und die zeitnahe Entwicklung von SARS-CoV-2-Infektionen und Covid-19-Erkrankungsfällen in Deutschland darzustellen und zu verstehen. Naturgemäß kann niemand die tatsächliche Anzahl der heute oder in der vergangenen Woche erfolgten Infektionen genau wissen oder be-

In Deutschland werden gemäß der Meldepflicht nach Infektionsschutzgesetz (IfSG) Infektionen mit SARS-CoV-2 von den Ärzten und Laboren an die zuständigen Gesundheitsämter gemeldet und von diesen über die zuständigen Landesbehörden an das [Robert Koch-Institut \(RKI\)](#) übermittelt.

Zum aktuellen Datenstand (13.4.2020, 00:00 Uhr)

Fatal Infections Trajectory and Model-Based $R(t)$ Inference

Odhad průběhu epidemie SARS-CoV-2 v ČR na základě počtu úmrtí: Statistické modelování pomocí reálných dat

Received: 19 December 2020

Revised: 3 March 2021

Accepted: 17 March 2021

DOI: 10.1111/biom.13462

BIOMETRIC PRACTICE

Biometrics WILEY
A JOURNAL OF THE INTERNATIONAL BIOMETRIC SOCIETY

Inferring UK COVID-19 fatal infection trajectories from daily mortality data: Were infections already in decline before the UK lockdowns?

Simon N. Wood 

School of Mathematics, University of Edinburgh, UK

Correspondence

Simon N. Wood, School of Mathematics, University of Edinburgh, UK.

Email: simon.wood@ed.ac.uk

Abstract

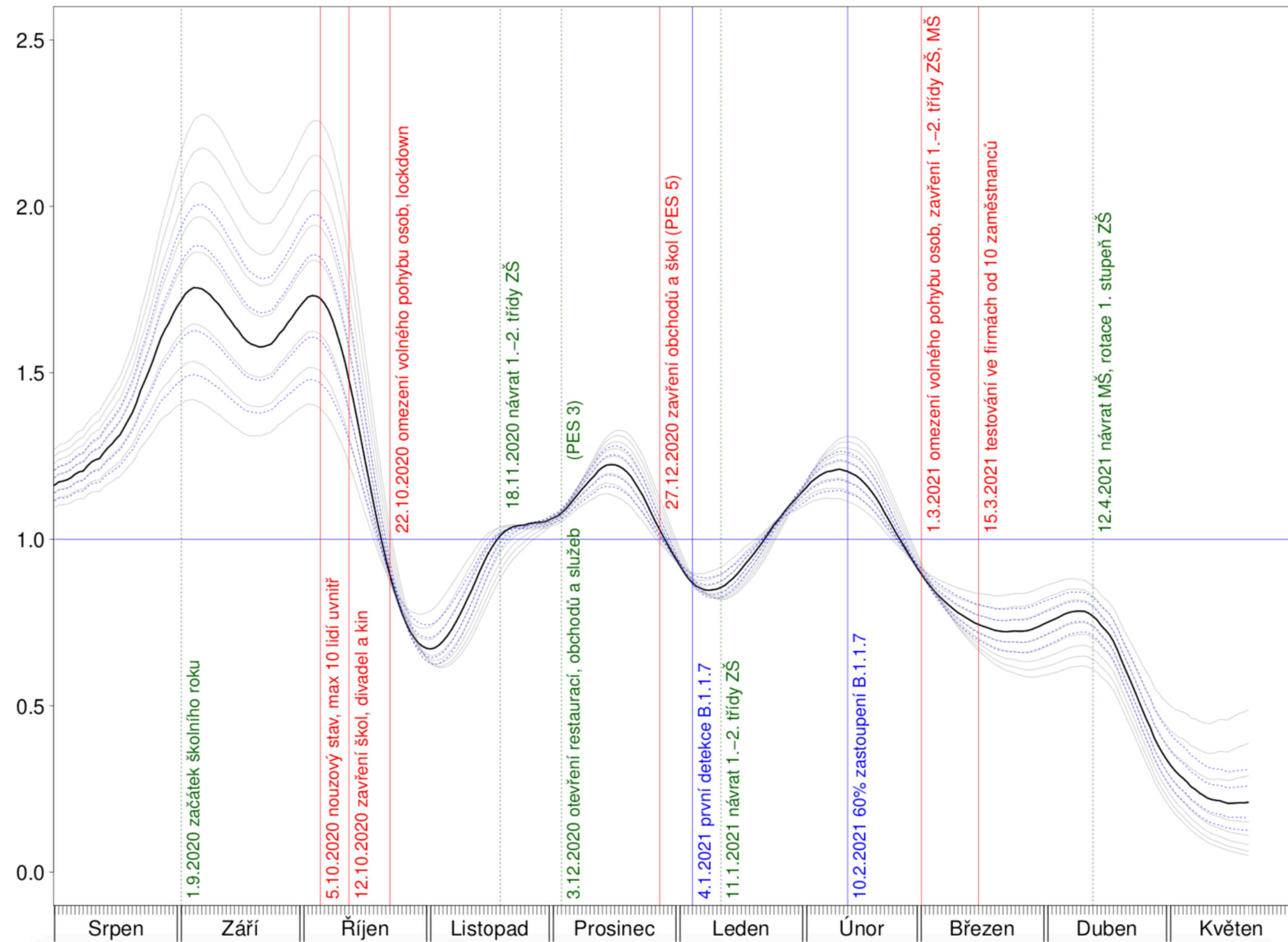
The number of new infections per day is a key quantity for effective epidemic management. It can be estimated relatively directly by testing of random population samples. Without such direct epidemiological measurement, other approaches are required to infer whether the number of new cases is likely to be increasing or decreasing: for example, estimating the pathogen-effective reproduction number, R , using data gathered from the clinical response to the dis-

Robert Straka^{1,2}, Arnošt Komárek³

7. června 2021

chniki Ciepłej i Ochrony Środowiska, Wydział Inżynierii Metali i Przemysłowej, Akademia Górniczo Hutnicza im. Stanisława Staszica w raka@metal.agh.edu.pl
tematiki, Fakulta jaderná a fyzikálně inženýrská, České vysoké učení
traze
avděpodobnosti a matematické statistiky, Matematicko-fyzikální fakulta
arlovy, komarek@karlin.mff.cuni.cz

GAM Fatality Incidence vs Kalman-Filtered General Incidence $R_e(t)$ Engines



[Straka, Komárek] featuring [Wood]

Estimate of the effective reproduction rate (R_e) of COVID-19

Our World in Data

The reproduction rate represents the average number of new infections caused by a single infected individual. If the rate is greater than 1, the infection is able to spread in the population. If it is below 1, the number of cases occurring in the population will gradually decrease to zero.



Source: Arroyo-Marioli F, Bullano F, Kucinskas S, Rondón-Moreno C (2021) Tracking R of COVID-19: A new real-time estimation using the Kalman filter.

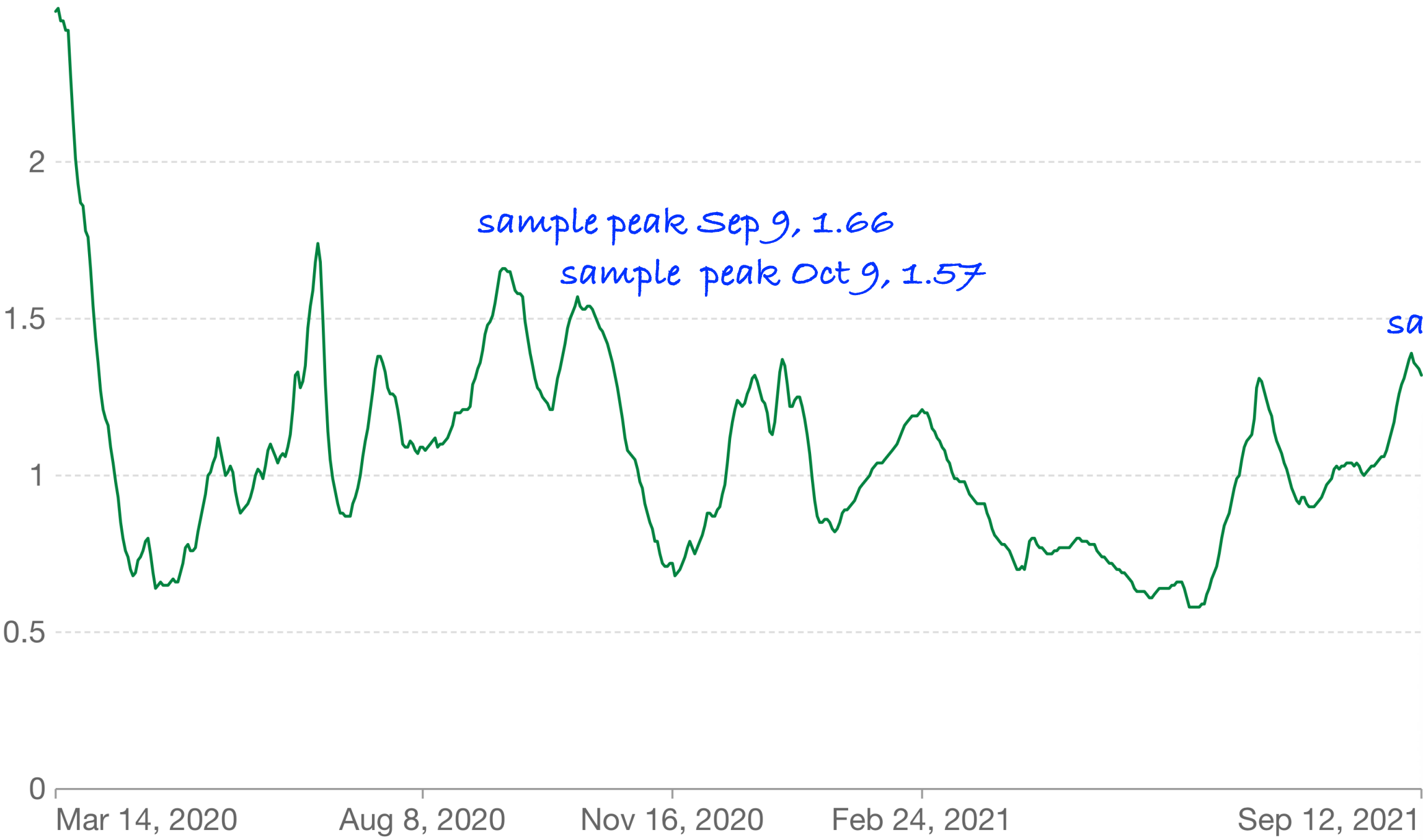
OurWorldInData featuring [Arroyo-Marioli et al.]

Where are we ~~now~~? (It was September 14th)

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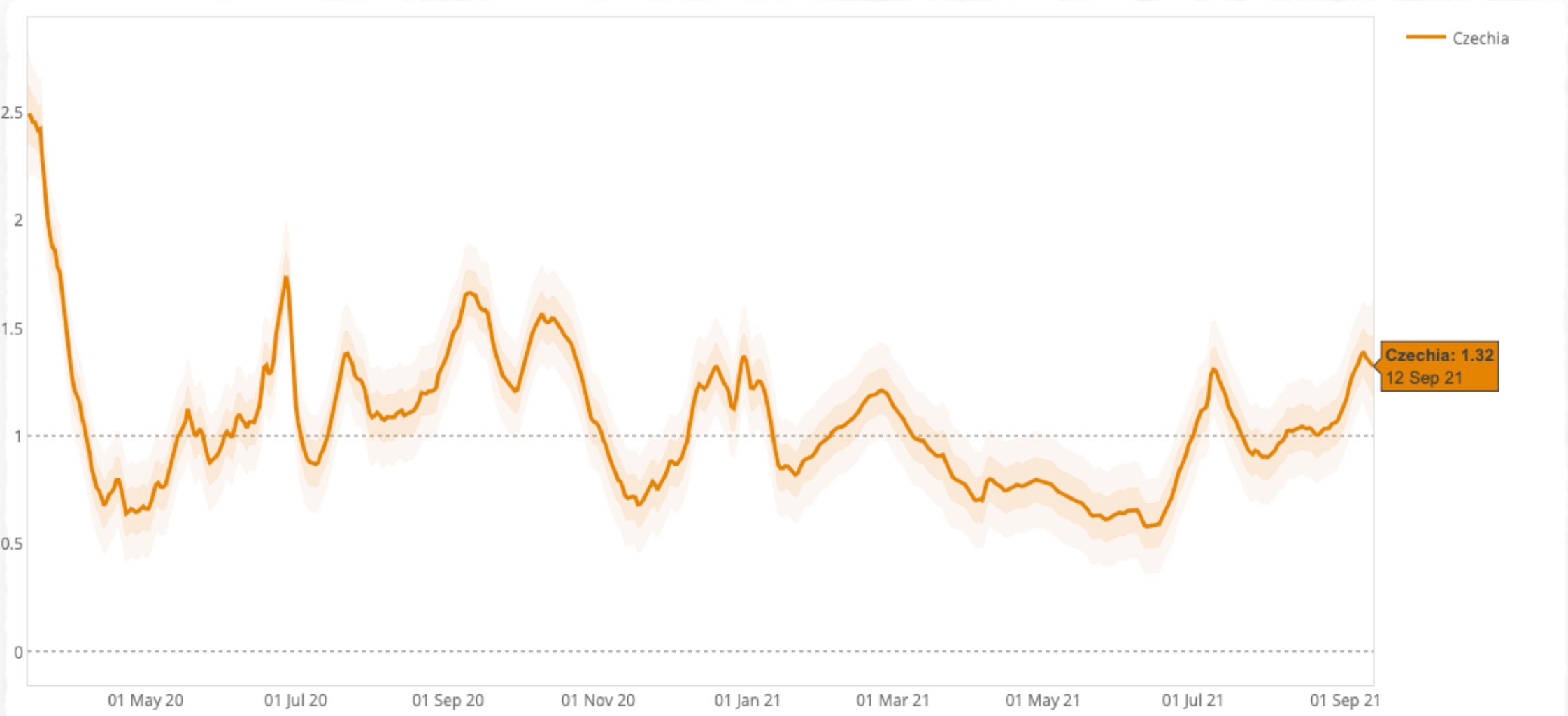
Our World in Data



2021-09-07	1.36
2021-09-08	1.47
2021-09-09	1.43
2021-09-10	1.44
2021-09-11	1.47
2021-09-12	1.38
2021-09-13	1.19
2021-09-14	1.18

P.E.S. engine,

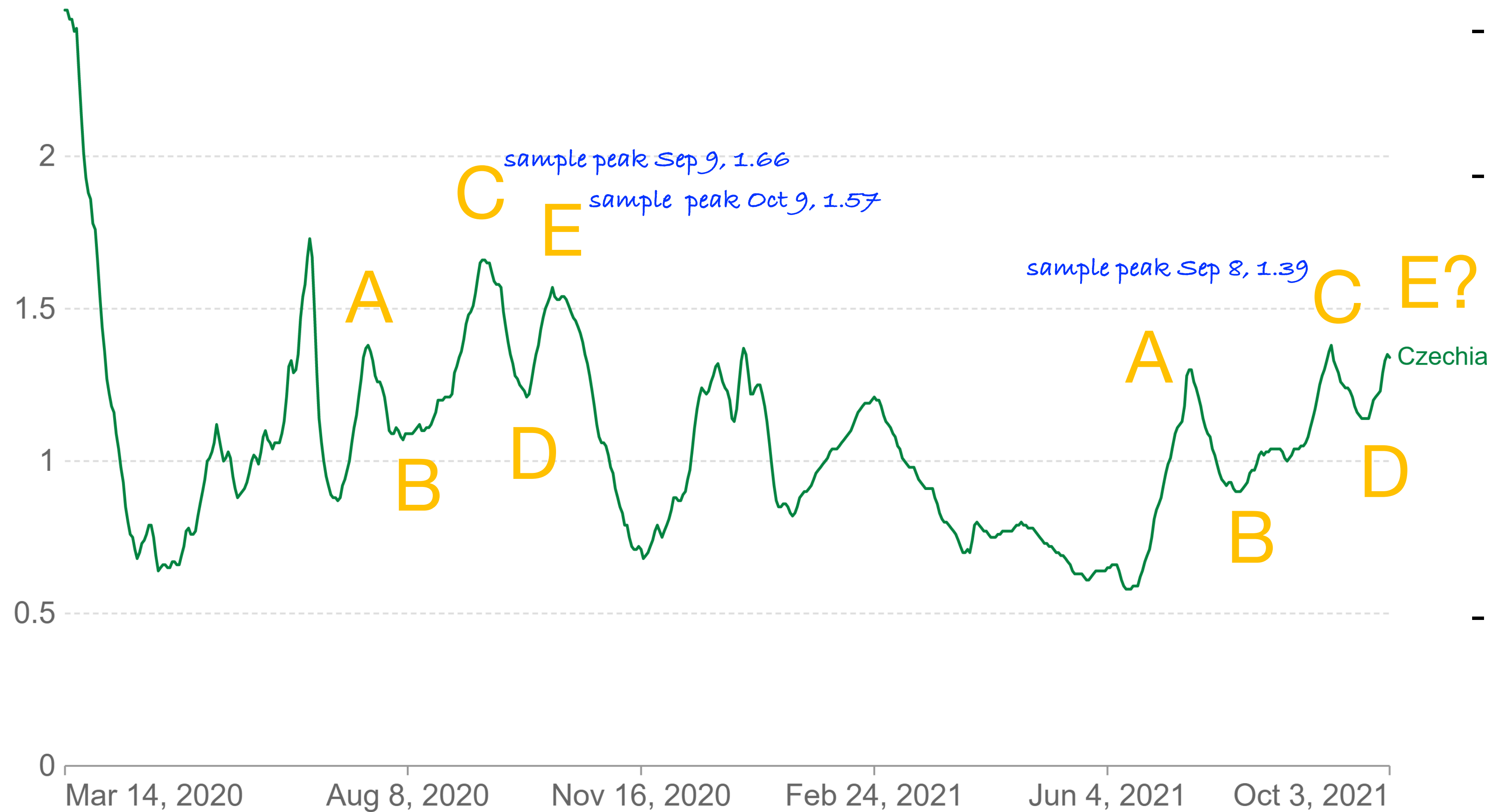
Source: Arroyo-Marioli F, Bullano F, Kucinskas S, Rondón-Moreno C (2021) Tracking R of COVID-19: A new real-time estimation using Kalman filter.



Same engines, confidence intervals marked, cf. <http://www.globalrt.live>.

Estimate of the effective reproduction rate (R) of COVID-19

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- Seasonal oscillations clearly visible
- Amplitude scaling due to:
 - vaccination (↓)
 - natural immunization (↓)
 - countermeasures (↓)
 - different strain, 2.5-times higher R0 (↑)
- Recent data (est.)
 - R(10/03) = 1.34
 - weekly gr. (10/03) = 39.09%
 - weekly gr. (10/05) = 34.48%

Estimate of the effective reproduction rate (R) of COVID-19

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References and Further Reading

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- (2) Brauer, F., Castillo-Chavez, C., and Feng, Z.: *Mathematical Models in Epidemiology*, Texts in Applied Mathematics, Vol. 69, Springer, 2019
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Revision History

- 2021/12/08: release version 1