Mathematical Epidemiology for KoroNERV-20
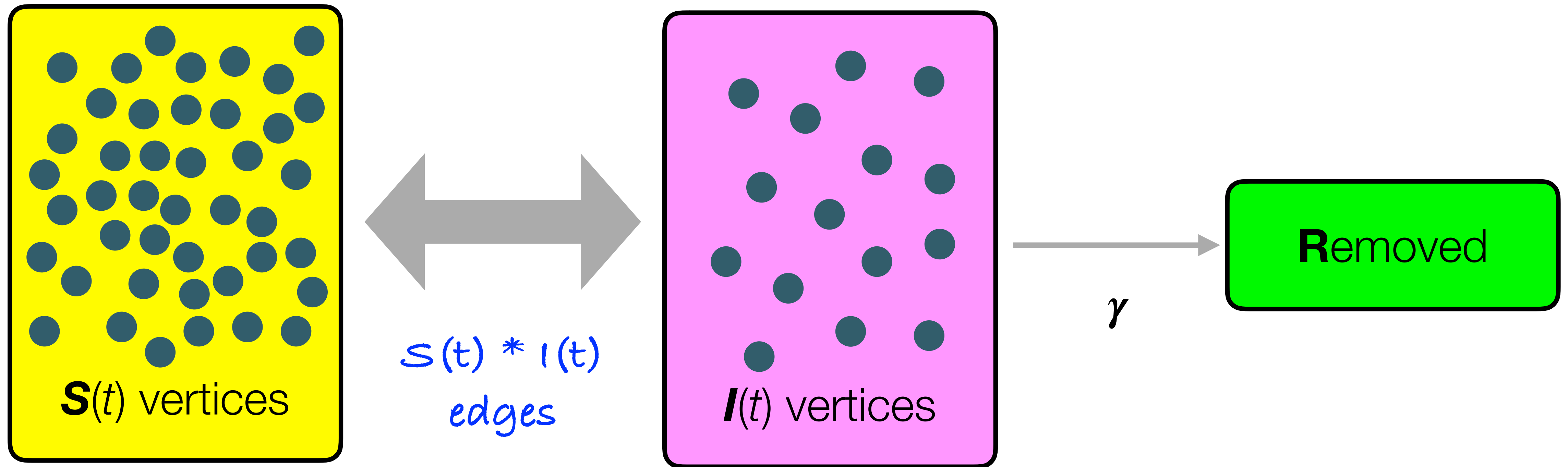## - notes at Sep 14th regular meeting

Tomáš Rosa, Ph.D.
Cryptology and Biometrics Competence Centre of Raiffeisen BANK International in Prague

SIR Compartmental Epidemic Model
- zooming on the mass action mechanism

$S(t)$ vertices

$S(t) * I(t)$ edges

$I(t)$ vertices

Removed

γ

$$\frac{dS(t)}{dt} = -\frac{\gamma \cdot \mathcal{R}_0 \cdot season(t) \cdot control(t)}{N} S(t)I(t) = -\gamma R(t)I(t)$$

$$\frac{dI(t)}{dt} = \gamma \left(\frac{\mathcal{R}_0 \cdot season(t) \cdot control(t)}{N} S(t) - 1 \right) I(t) = \gamma(R(t)-1)I(t)$$

R(t) stands for the effective reproduction number

All Those "*R*"s

$$\mathcal{R}_0 = \frac{\beta}{\gamma}$$

$$\mathcal{R}(t) = \mathcal{R}_0 \frac{S(t)}{N} = \mathcal{R}_0 s(t)$$

$$controlled - \mathcal{R}_0 = \frac{\beta_t}{\gamma_t}$$

*) In this particular model

- *In general, the average number of people one infectious individual infects under particular circumstances.*

- Basic reproduction number R_0

  - inherent model constant, describes important qualitative aspects, e.g. equilibria and their stability

- Effective reproduction number $R_e(t)$, $R(t)$

  - what we observe in daily experience

- Controlled reproduction number $R_{0,t}$

  - what we aim for with our interventions

# OurWorldInData Engine for "Reproduction Rate"

PLOS ONE

RESEARCH ARTICLE

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

Francisco Arroyo-Marioli[1], Francisco Bullano[1], Simas Kucinskas[2]*, Carlos Rondón-Moreno[1]

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

* simas.kucinskas@hu-berlin.de

Check for updates
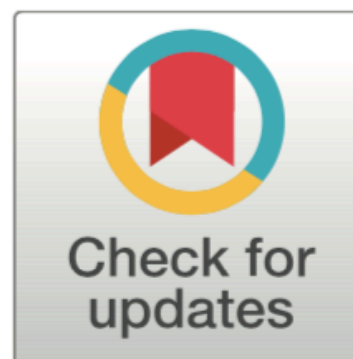
Abstract

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

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.cori@imperial.ac.uk).

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

P.E.S. Simple R Engine

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

Robert Straka[1,2], Arnošt Komárek[3]

7. června 2021

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

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 [iD]

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-

GAM Fatality Incidence vs Kalman-Filtered General Incidence *R(t)* Engines
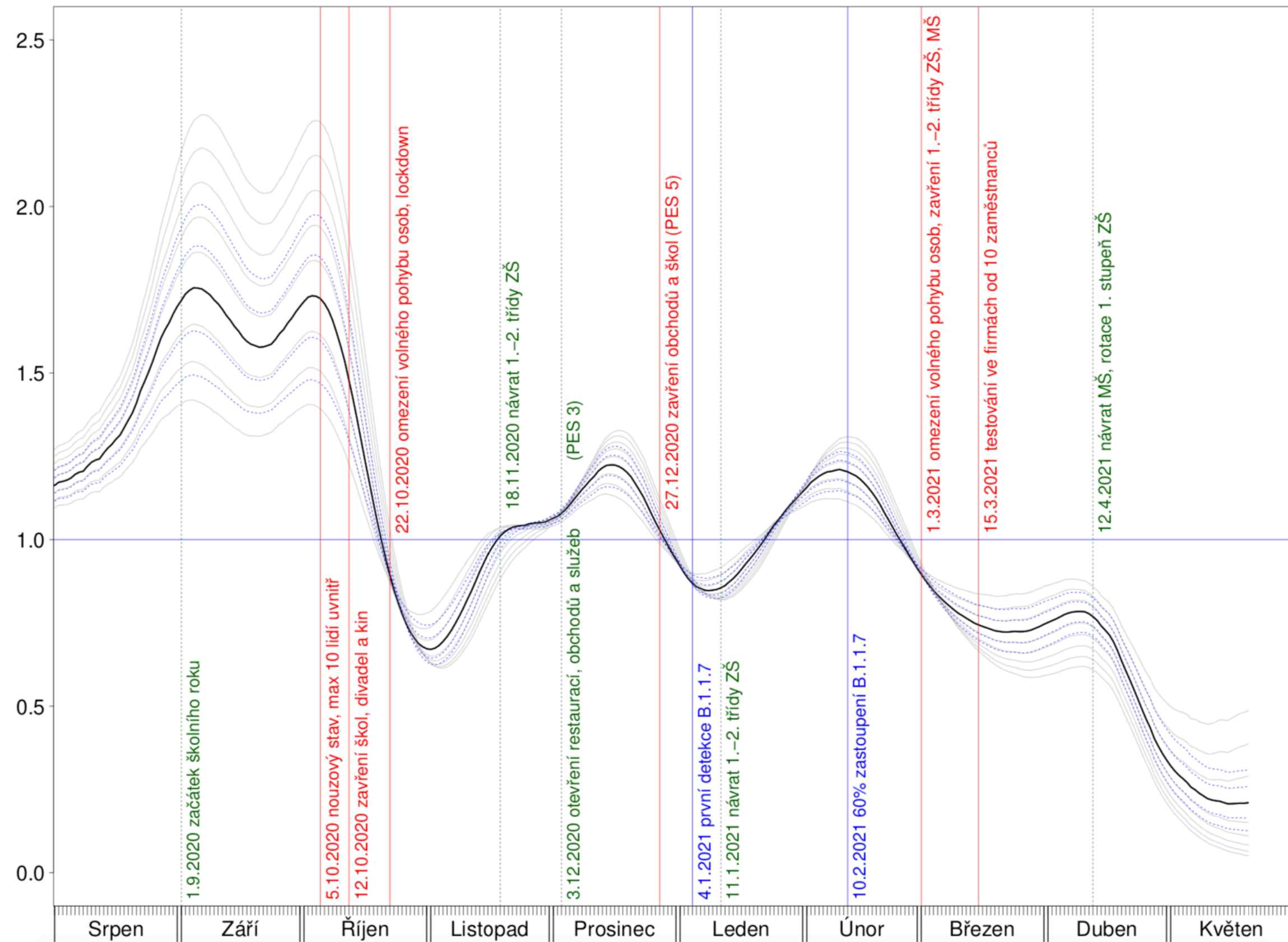
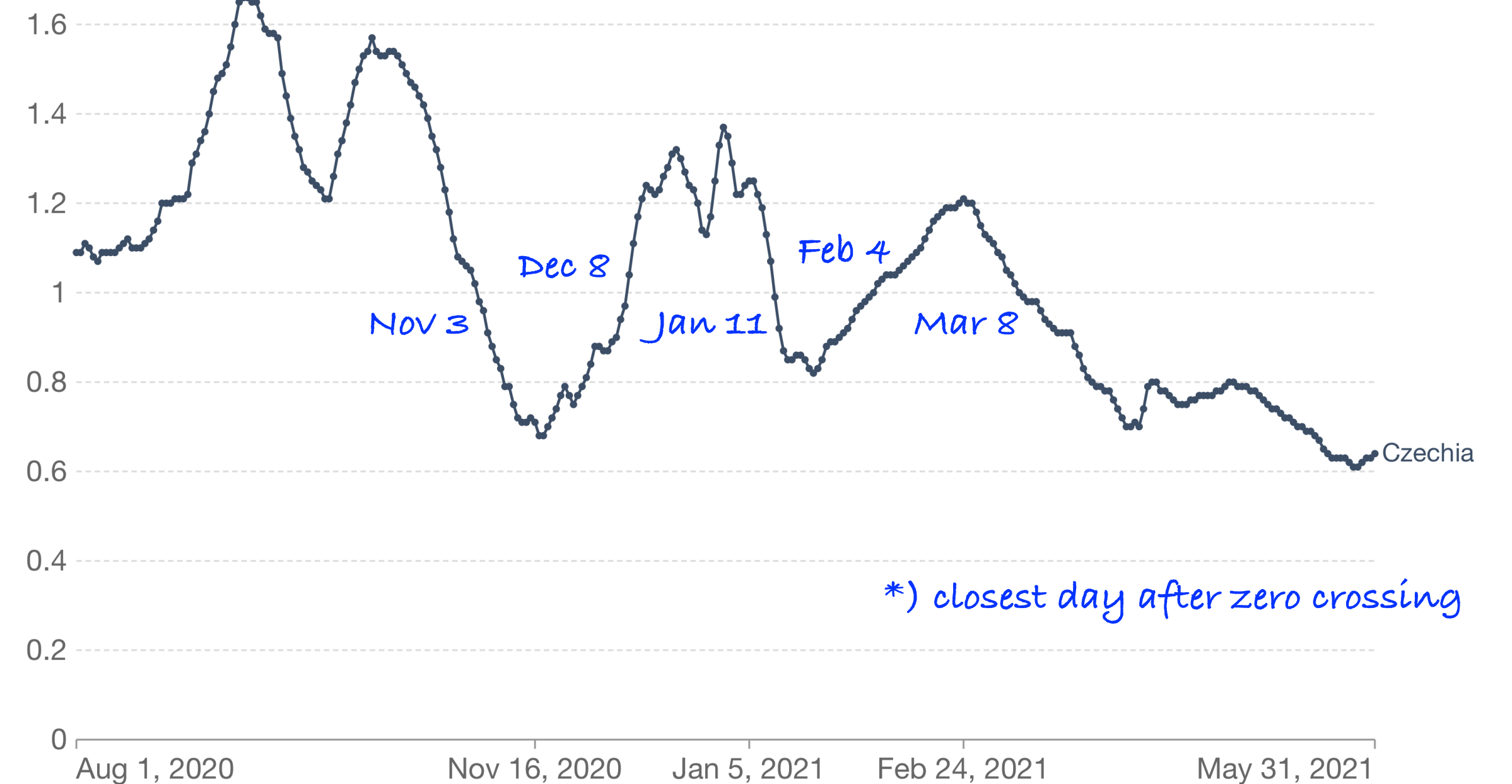[Straka, Komárek] featuring [Wood]

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

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.

*) closest day after zero crossing

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.

CC BY

OurWorldInData featuring [Arroyo-Marioli et al.]

Where are we now?

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

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.
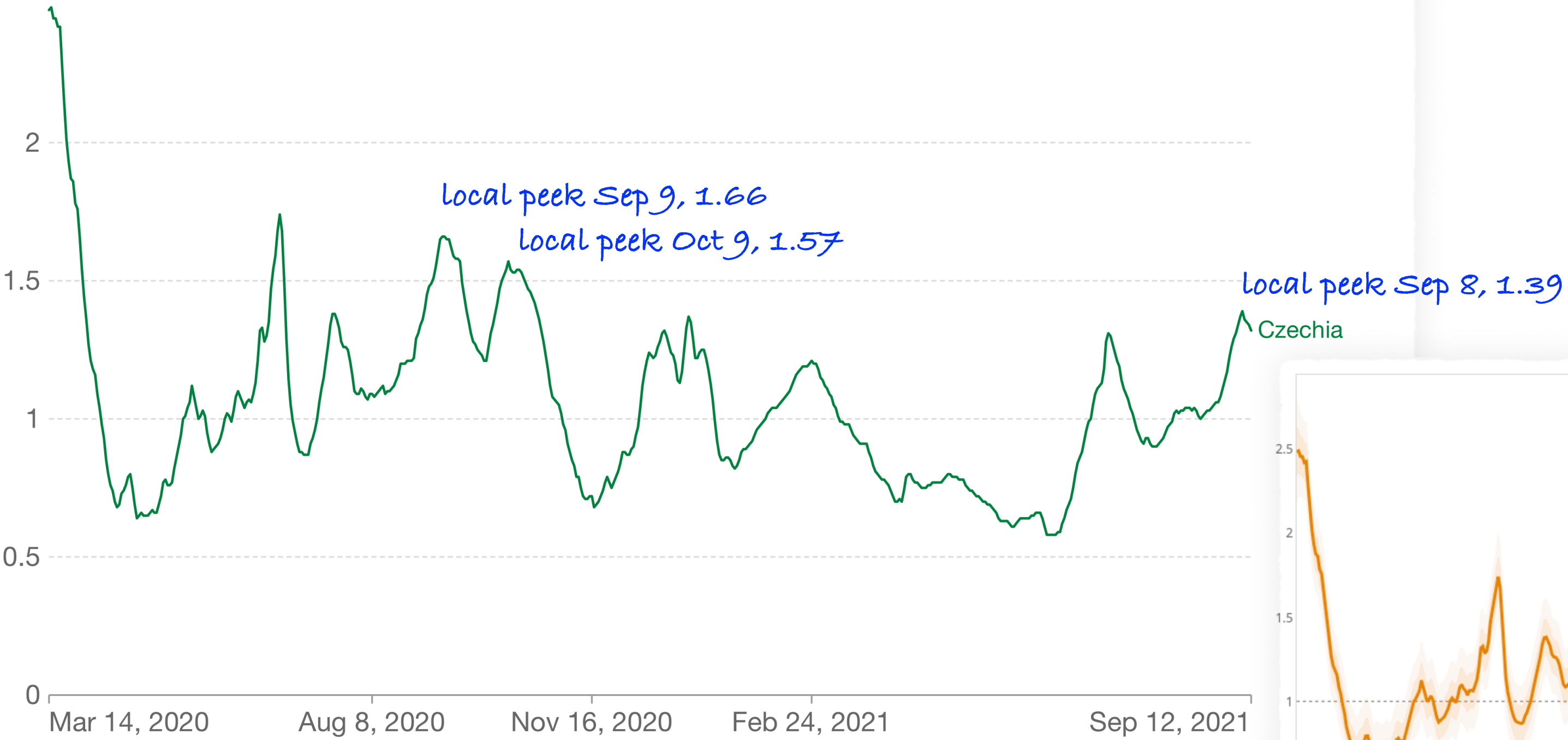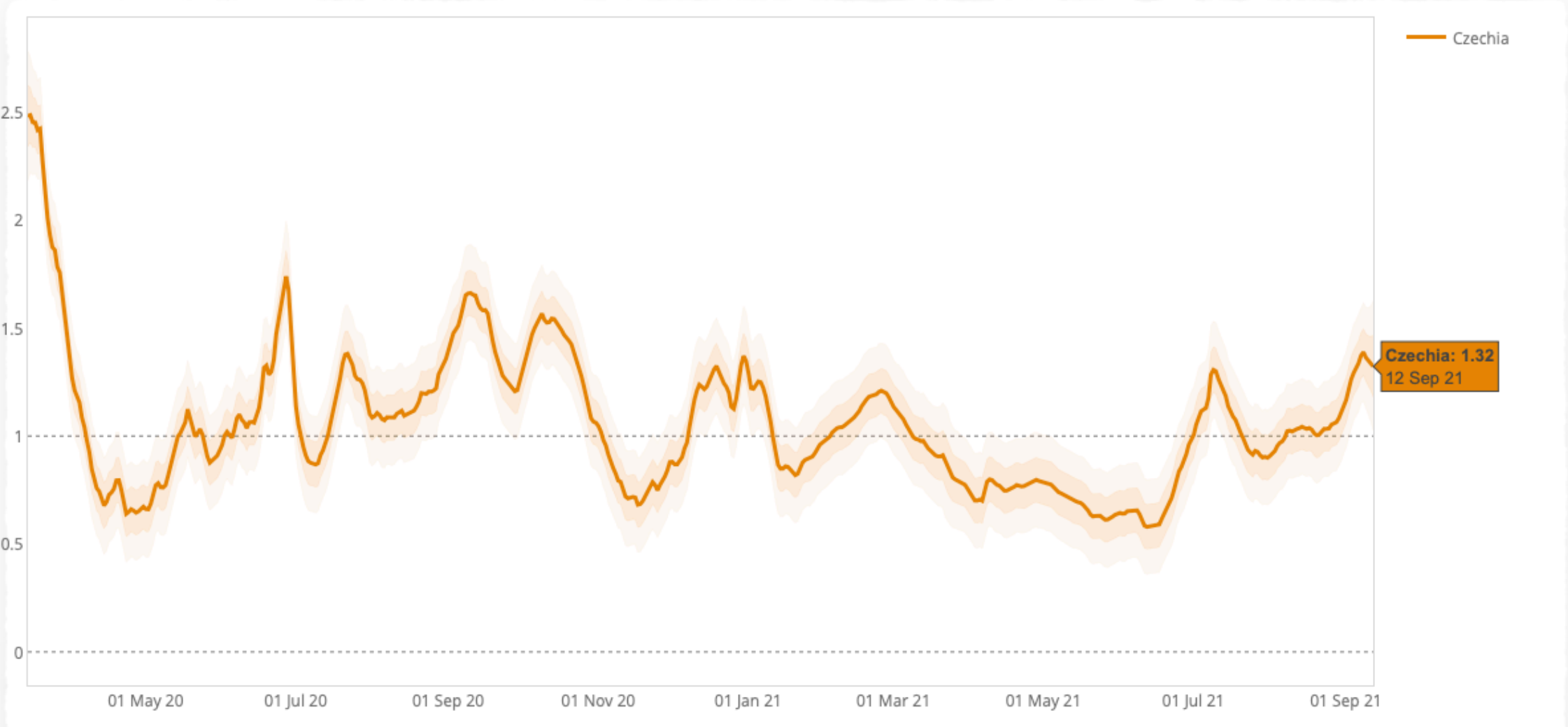
Our World in Data

local peek Sep 9, 1.66
local peek Oct 9, 1.57
local peek Sep 8, 1.39

Czechia

Mar 14, 2020   Aug 8, 2020   Nov 16, 2020   Feb 24, 2021   Sep 12, 2021

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

Date	Value
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,
https://onemocneni-aktualne.mzcr.cz/api/v2/covid-19

Czechia

Czechia: 1.32
12 Sep 21

01 May 20   01 Jul 20   01 Sep 20   01 Nov 20   01 Jan 21   01 Mar 21   01 May 21   01 Jul 21   01 Sep 21

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

Last updated on 14 September 2021

Conclusion

* **Do not mix R0 and $R(t)$**

  - R0 describes qualitative characteristics, $R(t)$ shows local dynamics

  - $R(t)$ 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 $R(t) = 1$

  - $R(t)$ 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 $R(t)$, however; do not forget on confidence intervals

  - many different methods, all of them having certain assumptions - this has to be considered

Attachments - presented and discussed together with this note

‣ All the papers explicitly noted in this presentation

Revision History

- 2021/09/14: release version 1

- 2021/09/14: release version 1.1 - graphs updated, typos corrected