

# Mathematical Epidemiology for Risk Analysts

Modelling of Security and Security of Modelling

Tomas Rosa, Ph.D.  
Cryptology and Biometrics Competence Centre  
Raiffeisen Bank International

## Tech Tips

- Make sure your speakers are on – there is no dial in #
- Hit F5 any time your console freezes
- For a LIVE event you should be hearing music now
- Use the “Ask a Question” feature to report issues
- Webcast starts at the top of the hour

# Agenda

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- ▶ Modelling of health security - mathematical epidemiology
  - ▶ Compartmental models
  - ▶ Reproduction number(s)
  - ▶ Epidemic and endemic states
  - ▶ Vaccination
- ▶ Security of modelling - on the risk of relying on epidemiological models
  - ▶ Countermeasures design and validation
  - ▶ Model invertibility and reversibility
- ▶ Quo vadis?

# Mathematical Epidemiology Primer

Modelling of Security



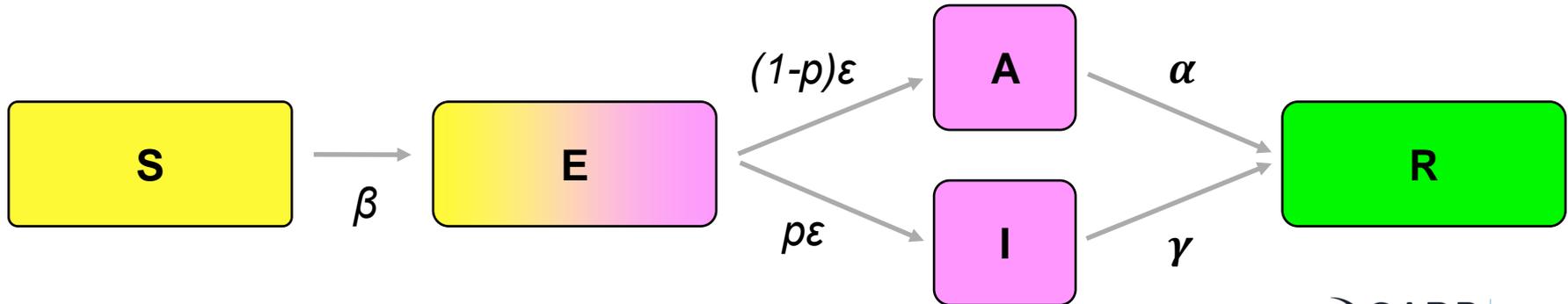
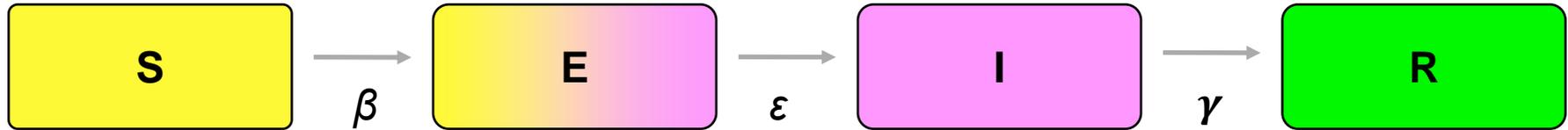
# SIR Compartmental Epidemic Model

- based on Kermack-McKendrick theory since 1927

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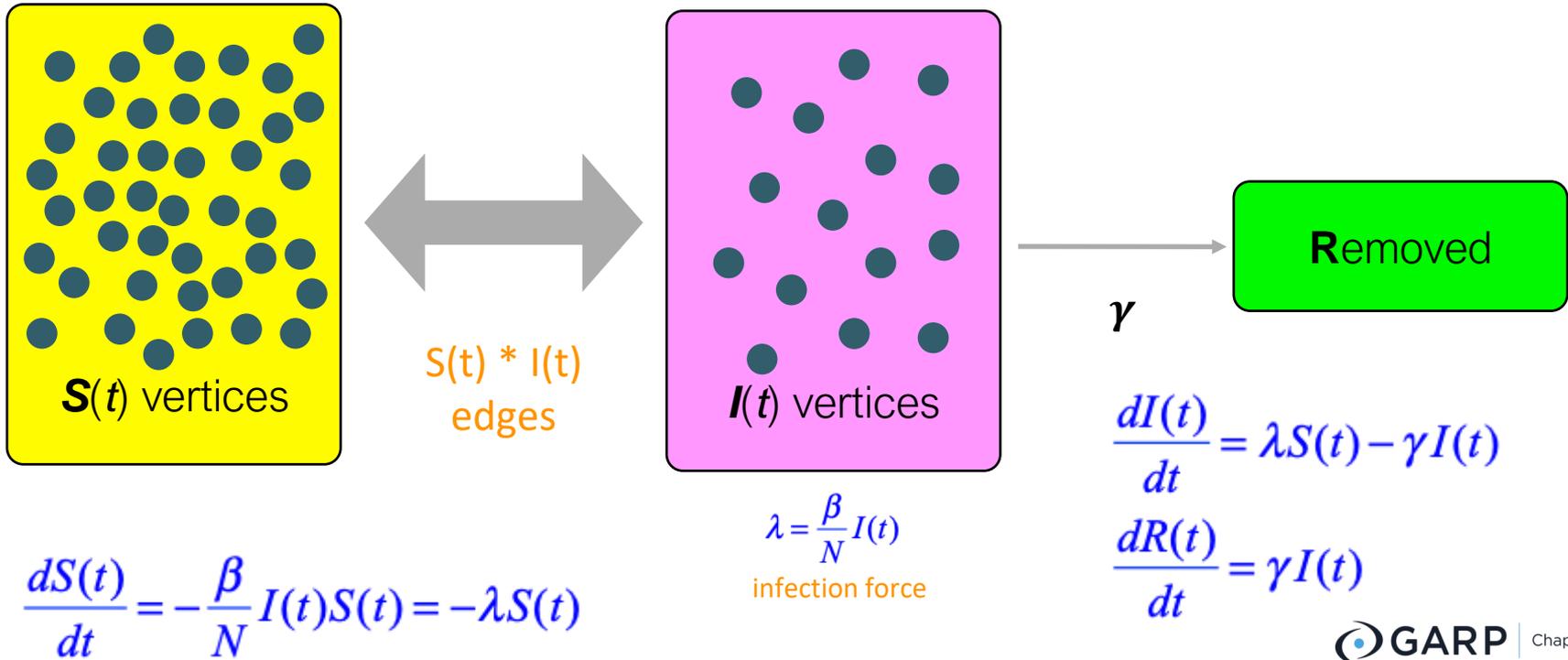


# Towards COVID-19 Quantitative Realities - SEIR and SEAIR



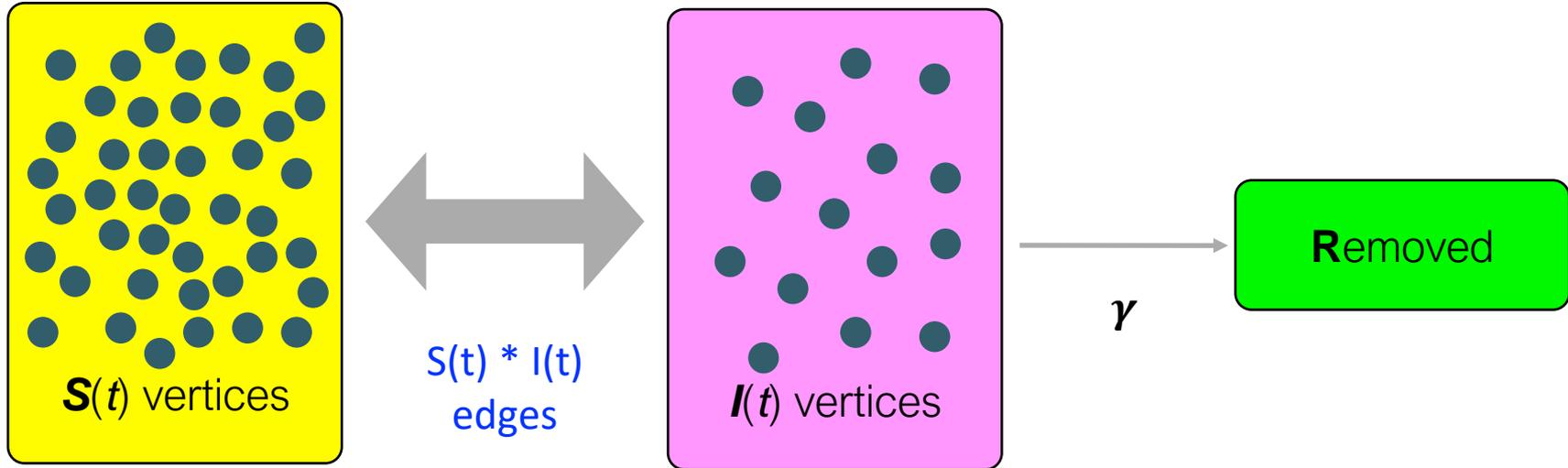
# SIR Compartmental Epidemic Model

- zooming on the mass action mechanism



# SIR Compartmental Epidemic Model

- zooming on the mass action mechanism & **noting the effective R(t)**



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

$R(t)$  stands for the effective reproduction number

# All Those "R"s

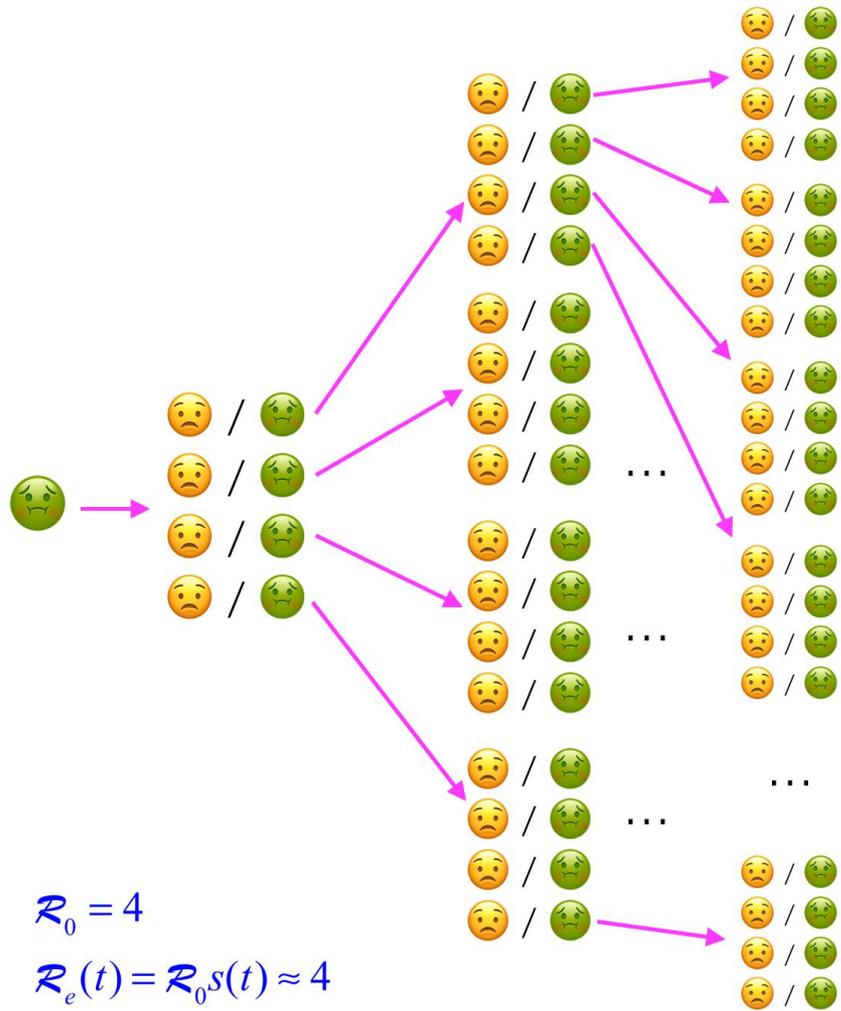
$$\mathcal{R}_0 = \frac{\beta}{\gamma}$$

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

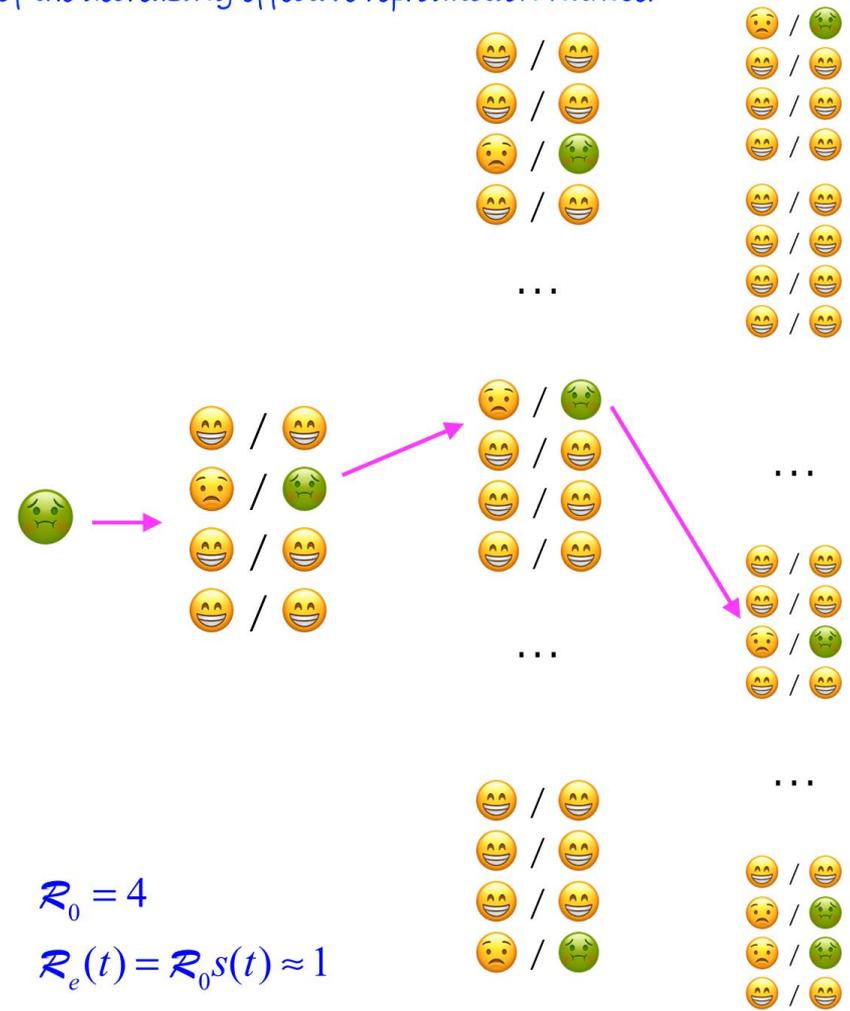
$$\text{controlled} - \mathcal{R}_0 = \frac{\beta_t}{\gamma_t}$$

- ▶ In general, it is the average number of people one infectious individual infects under particular circumstances
- ▶ **Basic** reproduction number  $\mathcal{R}_0$ 
  - inherent model constant, describes important qualitative aspects, e.g. equilibria and their stability
- ▶ **Effective** reproduction number  $\mathcal{R}_e(t)$ ,  $\mathcal{R}(t)$ 
  - what we observe in daily experience
- ▶ **Controlled** reproduction number  $\mathcal{R}_{0,t}$ 
  - what we aim for with our interventions

\*) In this particular model



The effect of the decreasing effective reproduction number



# OurWorldInData Engine for “Reproduction Rate”

## PLOS ONE

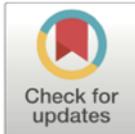
RESEARCH ARTICLE

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

Francisco Arroyo-Marioli<sup>1</sup>, Francisco Bullano<sup>1</sup>, Simas Kucinkas<sup>2\*</sup>, Carlos Rondón-Moreno<sup>1</sup>

<sup>1</sup> Central Bank of Chile, Santiago, Chile, <sup>2</sup> Humboldt University of Berlin, Berlin, Germany

\* [simas.kucinkas@hu-berlin.de](mailto: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



American Journal of Epidemiology

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DOI: 10.1093/aje/kwt133

Advance Access publication:

September 15, 2013

## 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

Epidemiologisches Bulletin | 17 | 2020 | 23. April 2020

< 10 > ☰

## 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](mailto:simon.wood@ed.ac.uk)

### Abstract

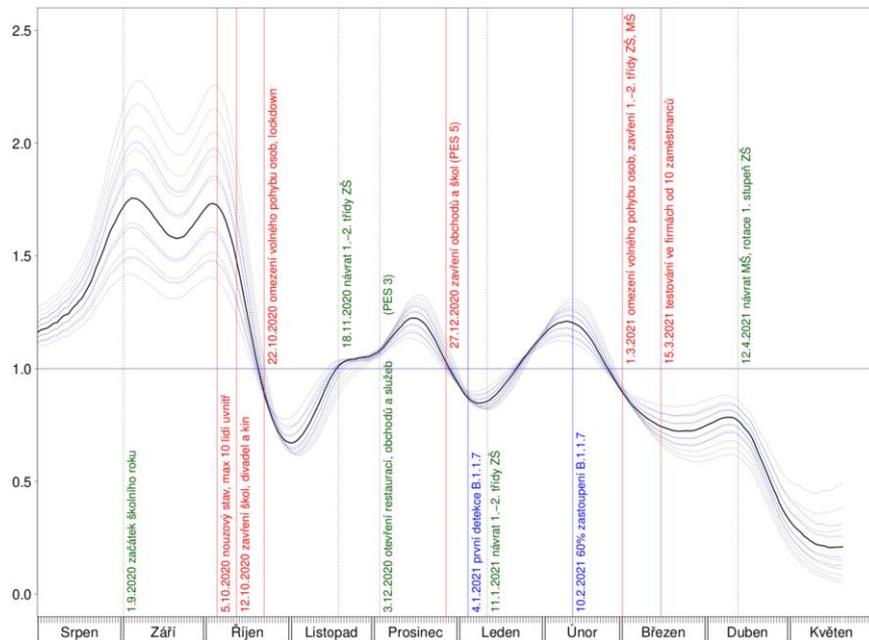
The number of new infections per day is a key quantity for effective epidemic management. It can be estimated relatively directly by testing of random population samples. Without such direct epidemiological measurement, other approaches are required to infer whether the number of new cases is likely 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<sup>1,2</sup>, Arnošt Komárek<sup>3</sup>

7. června 2021

iki Ciepłej i Ochrony Środowiska, Wydział Inżynierii Metali i myślowej, Akademia Górniczo Hutnicza im. Stanisława Staszica w [a@metal.agh.edu.pl](mailto:a@metal.agh.edu.pl)  
matyki, Fakulta jaderná a fyzikálně inženýrská, České vysoké učení  
podobnosti a matematické statistiky, Matematicko-fyzikální fakulta  
[vy.komarek@karlin.mff.cuni.cz](mailto:vy.komarek@karlin.mff.cuni.cz)

# GAM Fatal Cases Incidence vs Kalman-Filtered General Incidence R(t)



[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.

Our World  
in Data



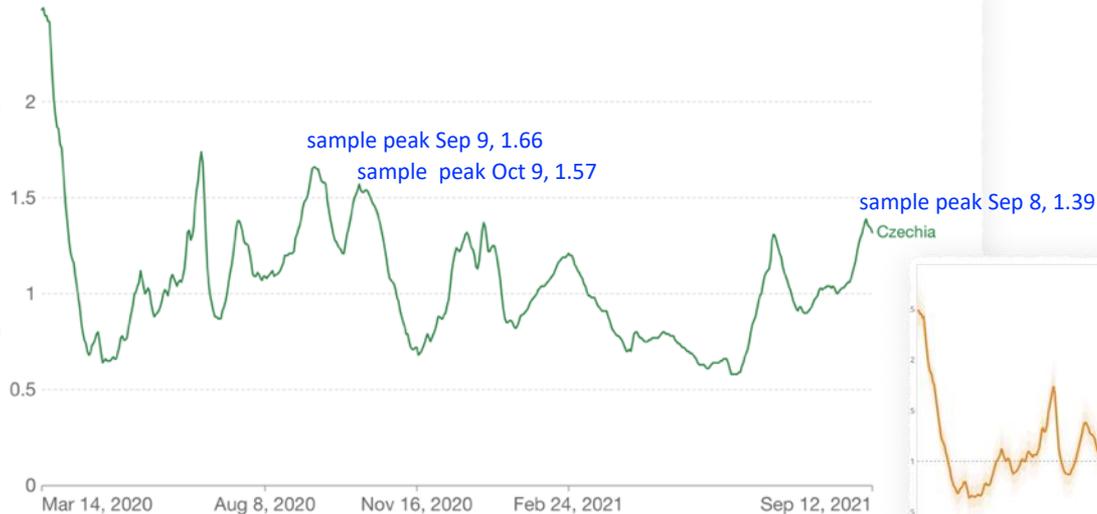
Source: Arroyo-Marioli F, Bullano F, Kucinskas S, Rondón-Moreno C (2021) Tracking R of COVID-19: A new real-time estimation using tBIC BY Kalman filter.

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.

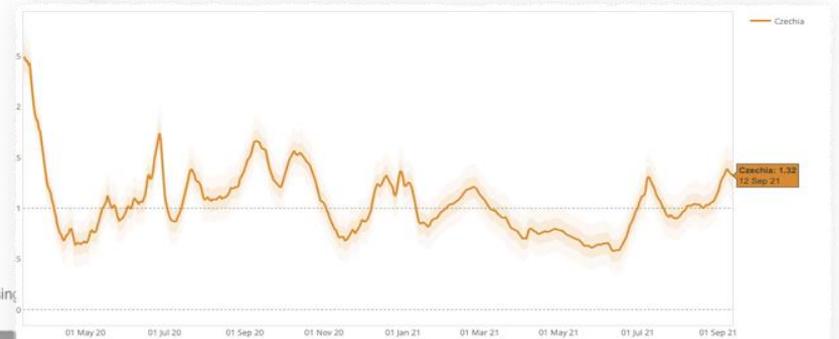


Source: Arroyo-Marioli F, Bullano F, Kucinskas S, Rondón-Moreno C (2021) Tracking R of COVID-19: A new real-time estimation using Kalman filter.

|            |      |
|------------|------|
| 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>



Last updated on 14 September 2021

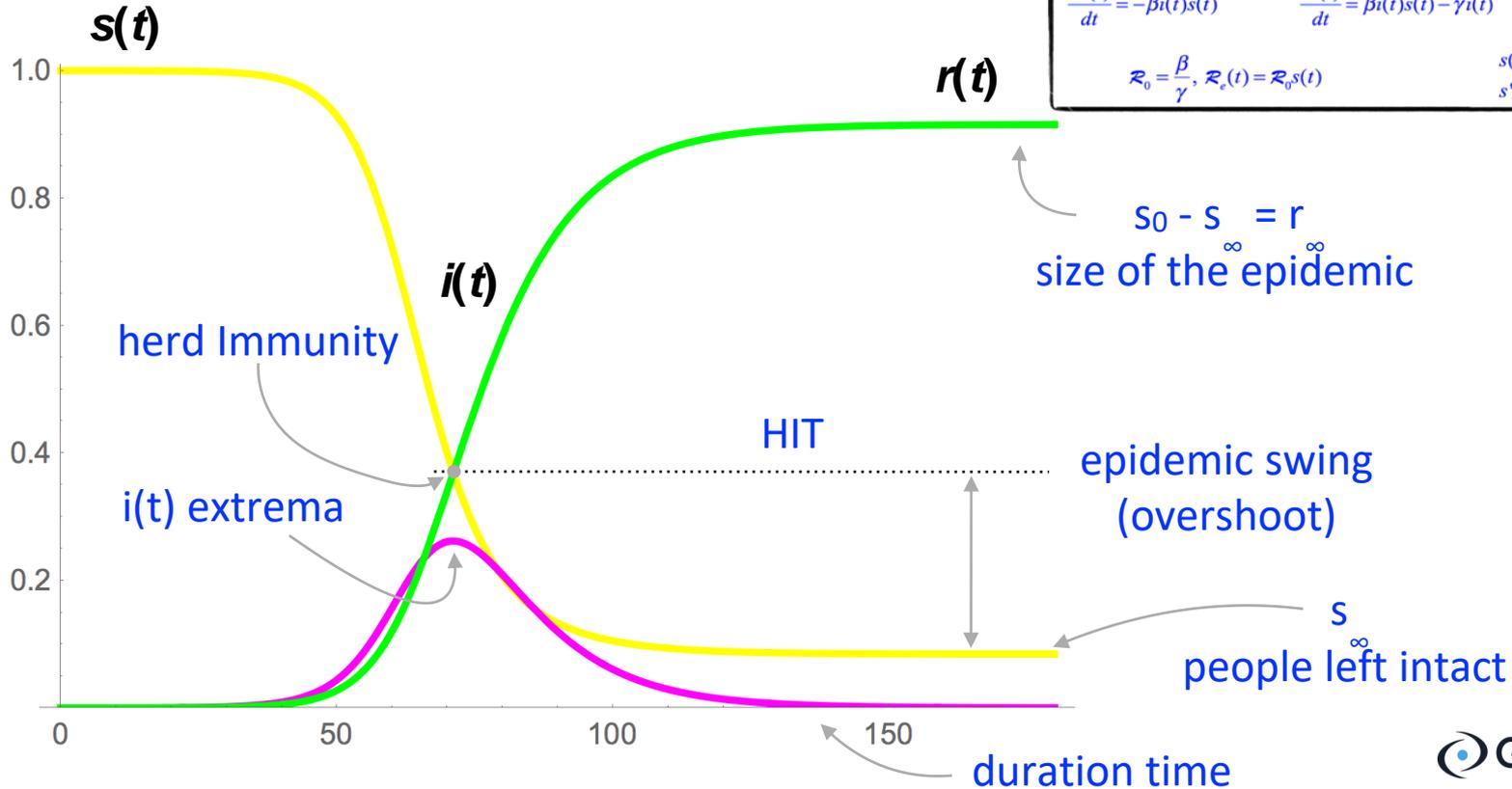
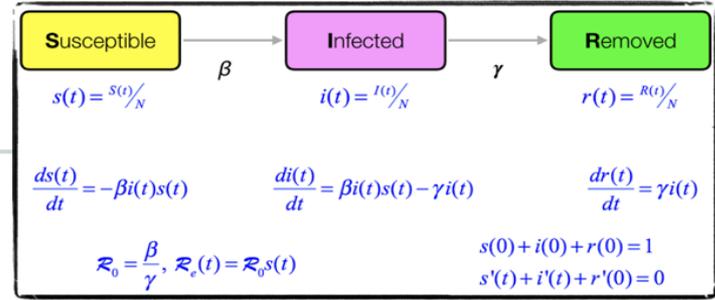
Same engines, confidence intervals marked, cf. <http://www.globalrt.live>.

# 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.

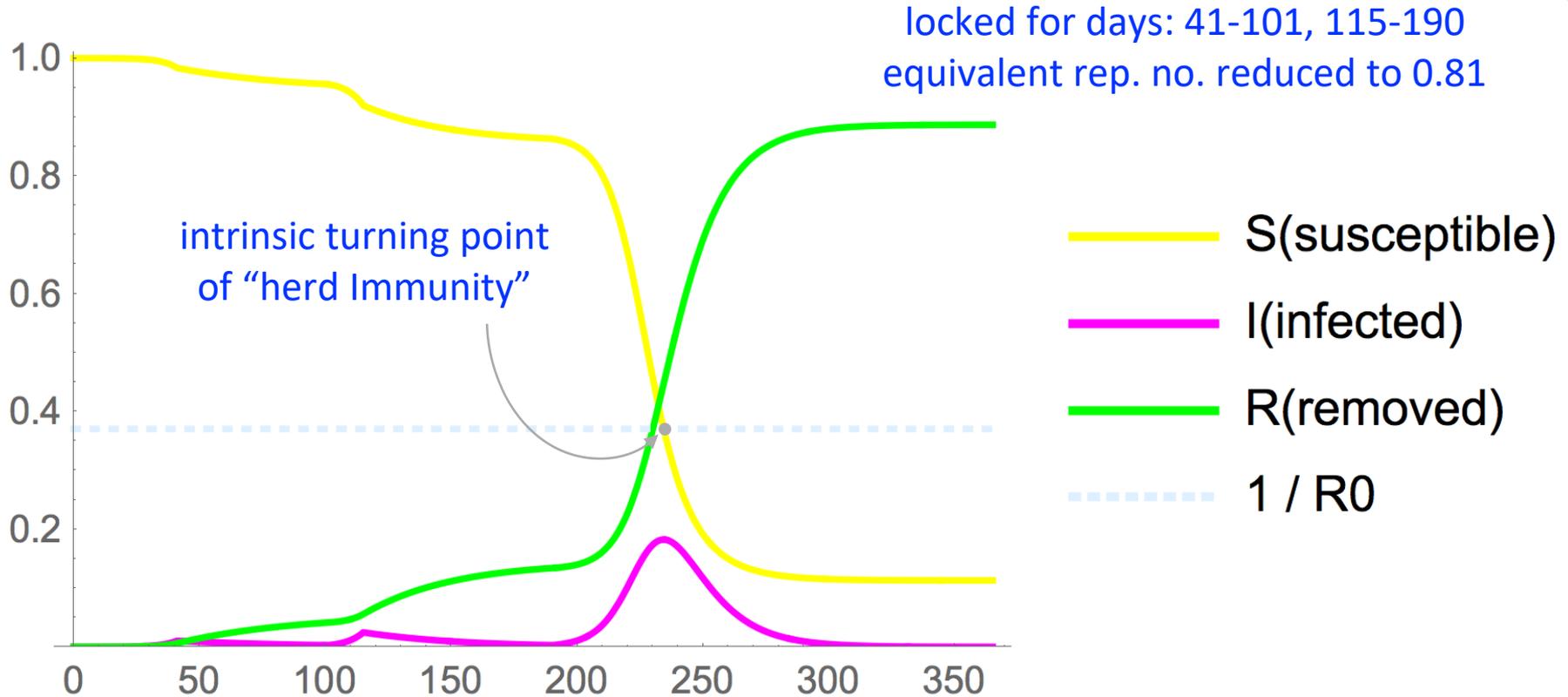


# Partial Optimisation Criteria (SIR-based)



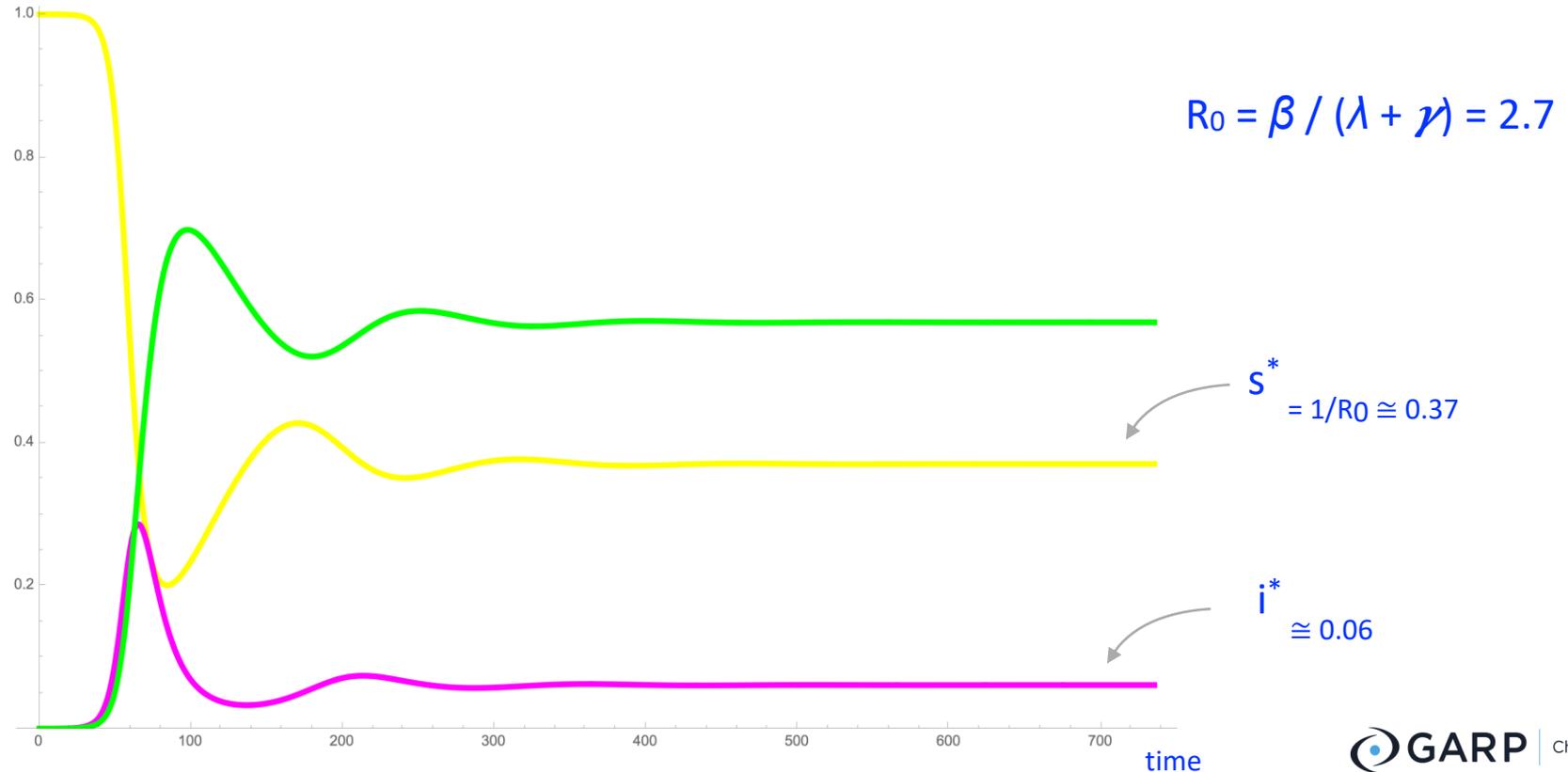
possible endemic size, etc.  
(not visible in this model)

# Example: Qualitative Study of Two Ideal Consecutive Lockdowns

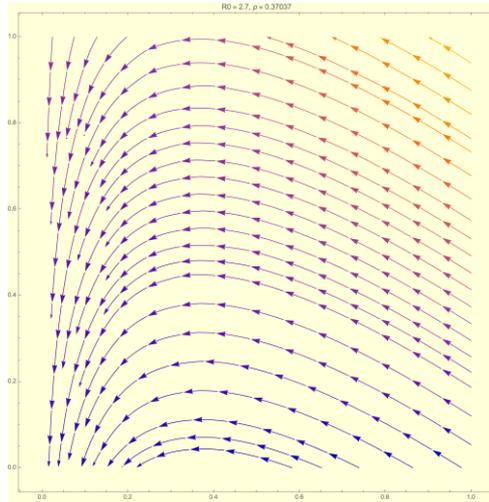


- we set  $\lambda$  very high (with respect to a pure demography) here to illustrate endemic equilibrium in general
- on the other hand, in reality, demography is not the only reason for endemic states anyway

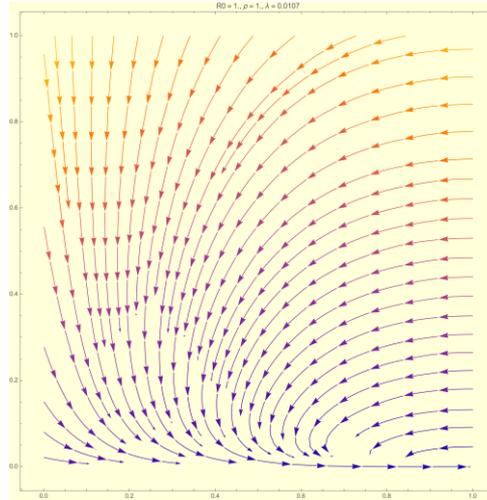
# Long-Term Endemic Equilibrium for $R_0 > 1$



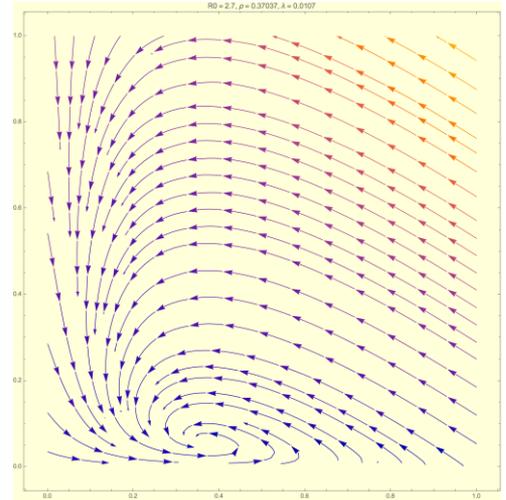
# Direction field of the model\* equations brings yet-another viewpoint



short-term closed  
epidemic outbreak



long-term equilibrium  
disease-free



long-term equilibrium  
endemic

$i(t)$

$s(t)$

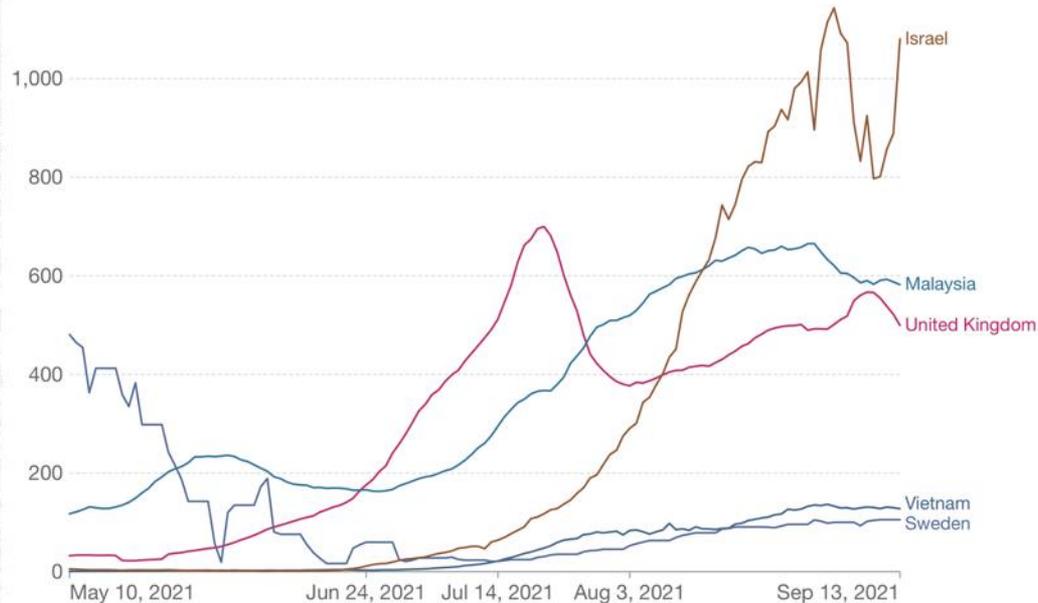
\* ) SIR and SIR with demography

# Well, analyse this...

## Daily new confirmed COVID-19 cases per million people

Shown is the rolling 7-day average. The number of confirmed cases is lower than the number of actual cases; the main reason for that is limited testing.

Our World  
in Data



Source: Johns Hopkins University CSSE COVID-19 Data

CC BY

- ▶ Equilibrium tendencies clearly observable for at least some of those traces
- ▶ Uncomfortably high level of endemic incidence - why?
- ▶ Theory says - there shall be a fast refreshment of susceptible people then
- ▶ Again, ... why?
- ▶ Possible effect of efficient tracing and quarantine
- ▶ It would show the limits of this countermeasure and send a clear warning on yet-another way on how the health service can get exhausted

# Basic Vaccination Equation for the Herd Immunity Threshold

$$\text{threshold}(\mathcal{R}_0, \varepsilon) = \frac{1}{\varepsilon} \left( 1 - \frac{1}{\mathcal{R}_0} \right)$$

| $\varepsilon$ | $R_0$ |      |      |      |      |
|---------------|-------|------|------|------|------|
|               | 2.7   | 3.5  | 4.5  | 5.5  | 6.45 |
| 92 %          | 68 %  | 78 % | 85 % | 89 % | 92 % |
| 86 %          | 73 %  | 83 % | 90 % | 95 % | 98 % |
| 80 %          | 79 %  | 89 % | 97 % | —    | —    |
| 63 %          | 100 % | —    | —    | —    | —    |

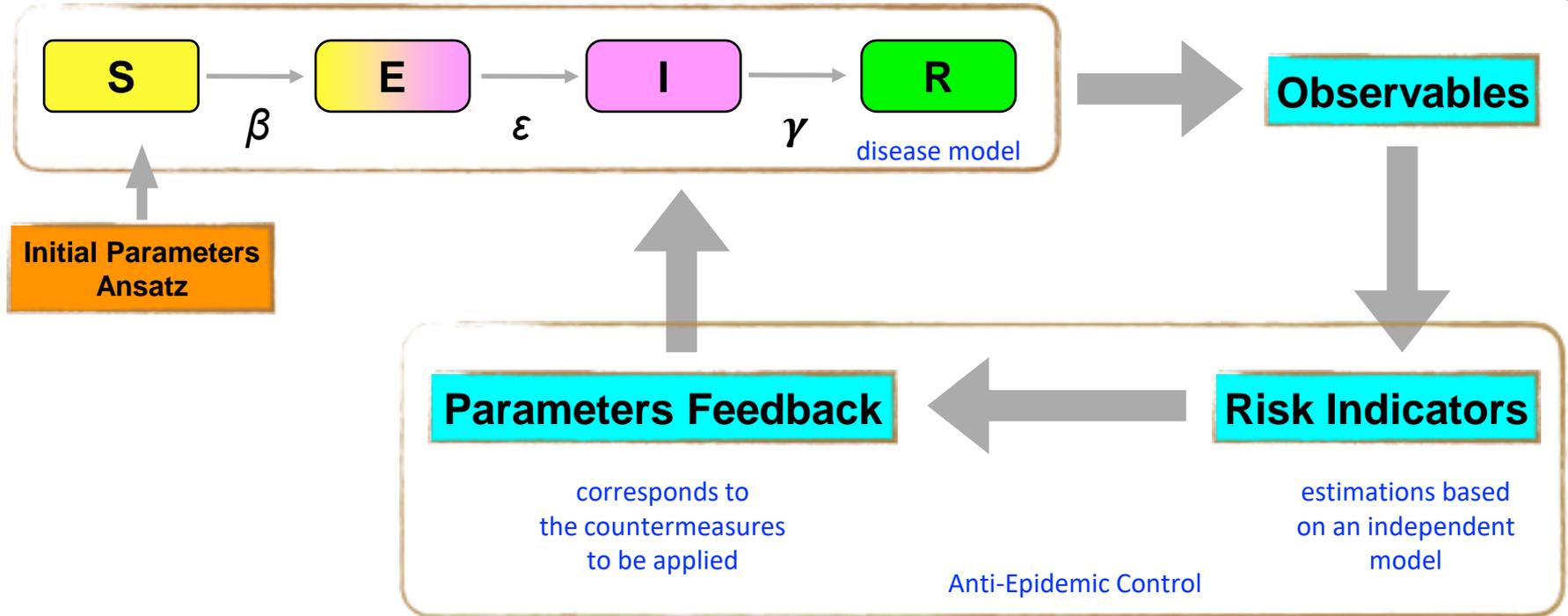
- ▶ Assumptions:
  - vaccine distributed uniformly among yet-susceptible people
  - vaccine efficacy  $\varepsilon$  - **for spreading**
  - immunity does not vanish in near time (circa one year, at least - does it?)
- ▶ Recovered people fraction bearing natural immunity then sums up with the vaccinated fraction
  - not shown here for clarity
  - be careful with overlaps

# The Risk of Relaying on Models

Security of Modelling



# Anti-Epidemic Controls Simulation (for whatever purpose)



\*) Note the SEIR model is just an example

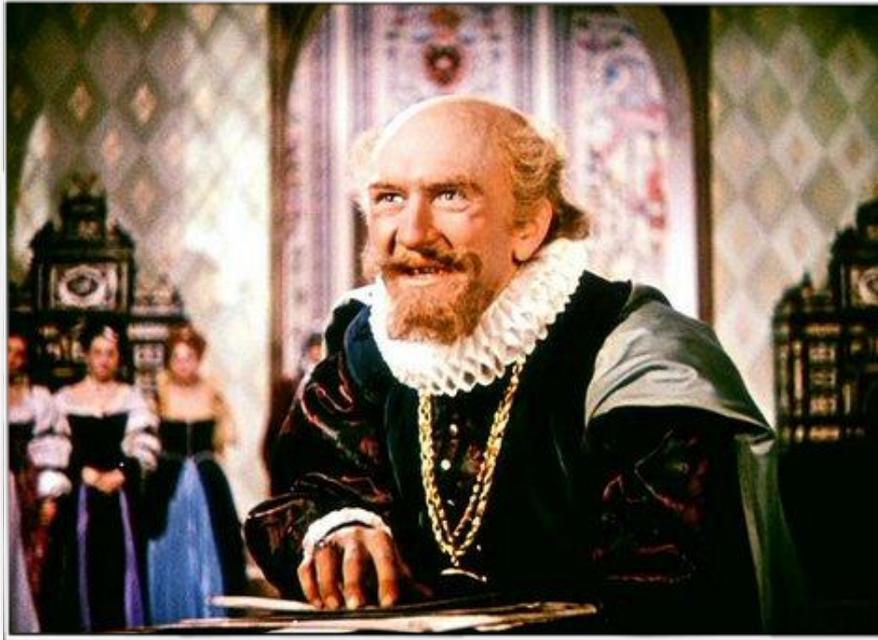
# How much can we trust the models?

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- ▶ Not much, when a deliberate manipulation is under question
  - ▶ There are two principal vulnerabilities allowing for “**anti-epidemic take over**”
    - **invertibility**, we can find a calibration for any physically plausible epidemic forecast
    - **reversibility**, we can track this calibration back in time to see how to manipulate contemporary statistical data to get the desired forecast
- Assuming we can predict the governmental reaction on the forecast, we could control the state this way

# Long Story Short

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Trust the mathematics,  
not so the mathematicians.

# Quo Vadis

Malware Epidemiology



# SCIENTIFIC REPORTS

OPEN

## Web malware spread modelling and optimal control strategies

Wanping Liu<sup>1,2</sup> & Shouming Zhong<sup>1</sup>

Received: 11 October 2016

Accepted: 08 January 2017

Published: 10 February 2017

The popularity of the Web improves the growth of web threats. Formulating mathematical models for accurate prediction of malicious propagation over networks is of great importance. The aim of this paper is to understand the propagation mechanisms of web malware and the impact of human intervention on the spread of malicious hyperlinks. Considering the characteristics of web malware, a new differential epidemic model which extends the traditional SIR model by adding another delitescent compartment is proposed to address the spreading behavior of malicious links over networks. The spreading threshold of the model system is calculated, and the dynamics of the model is theoretically

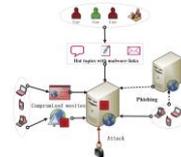


Figure 1. Diagram of web malware spread mechanism. The clients or terminals will get infected once they visit the compromised webpages on the web server which has been attacked.

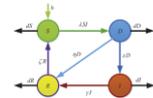


Figure 2. Transition diagram for the SIRD model. The green (susceptible), blue, red, yellow circle represents susceptible, infected, delitescent, attacked, recovered nodes (denoted by S, I, D, R, respectively).

$$\begin{cases} \frac{dS(t)}{dt} = b - \lambda S(t)I(t) + \zeta R(t) - dS(t), \\ \frac{dD(t)}{dt} = \lambda S(t)I(t) - \eta D(t) - \varepsilon D(t) - dD(t), \\ \frac{dI(t)}{dt} = \varepsilon D(t) - \gamma I(t) - dI(t), \\ \frac{dR(t)}{dt} = \eta D(t) + \gamma I(t) - \zeta R(t) - dR(t), \end{cases}$$

# Epidemic Phishing

...or how to incorporate mass action mechanism into phishing spreading



*„This is a really important message concerning the whole banking security. Please share this information with your close contacts to help us protect them, too.“*



# Conclusion

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- ▶ The model description, the ODE system in particular here, can be viewed as an **epidemic code**

**epidemic code** → **the pandemic** → **the government** → **the economics** → **the companies**

- ▶ Recognising the epidemic code and understanding its qualitative meaning, we can sharpen our risk analyses considerably
- ▶ However, the more important decisions are to be made, the more we shall talk about the security and safety of our models
  - simply put **trust, but test**