



Mathematical Epidemiology for Risk Analysts

Modelling of Security and Security of Modelling

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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

Tomas Rosa



Tomáš is a head of the Competence Centre for Cryptology and Biometrics of Raiffeisen Bank International in Prague. In these days, he is also a member of the expert team KoroNERV-20 for mitigating the impact of the COVID-19 pandemic in his country.

He researches mathematical modelling as a platform to both gain and protect the information spread among data records of observable variables of many kinds.

Tomáš holds Ph.D. in mathematical cryptology with the Best Doctoral Work Award in a combined study at the Faculty of Mathematics and Physics of Charles University in Prague, and the Faculty of Electrical Engineering of Czech Technical University in Prague.

Agenda

- ▶ 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
 - ▶ Anti-epidemic interventions design and validation
 - ▶ Model invertibility and reversibility

Mathematical Epidemiology Primer

Modelling of Security

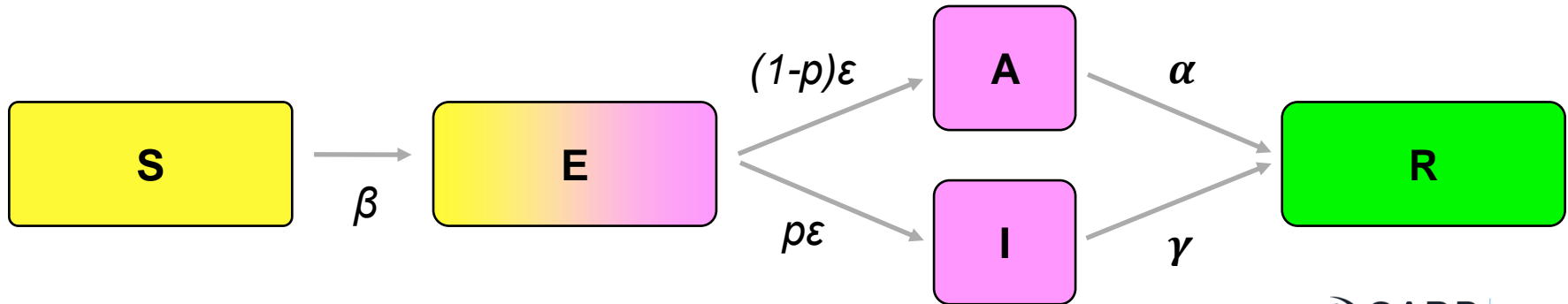
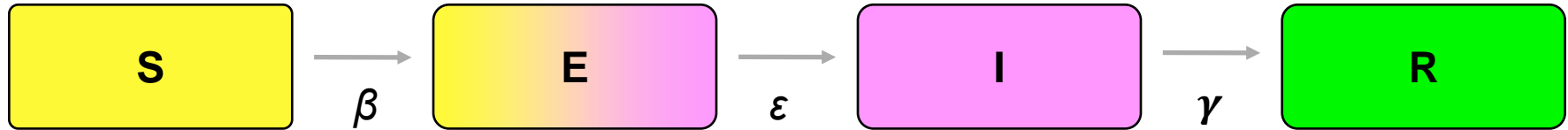


SIR Compartmental Epidemic Model

- based on Kermack-McKendrick theory since 1927

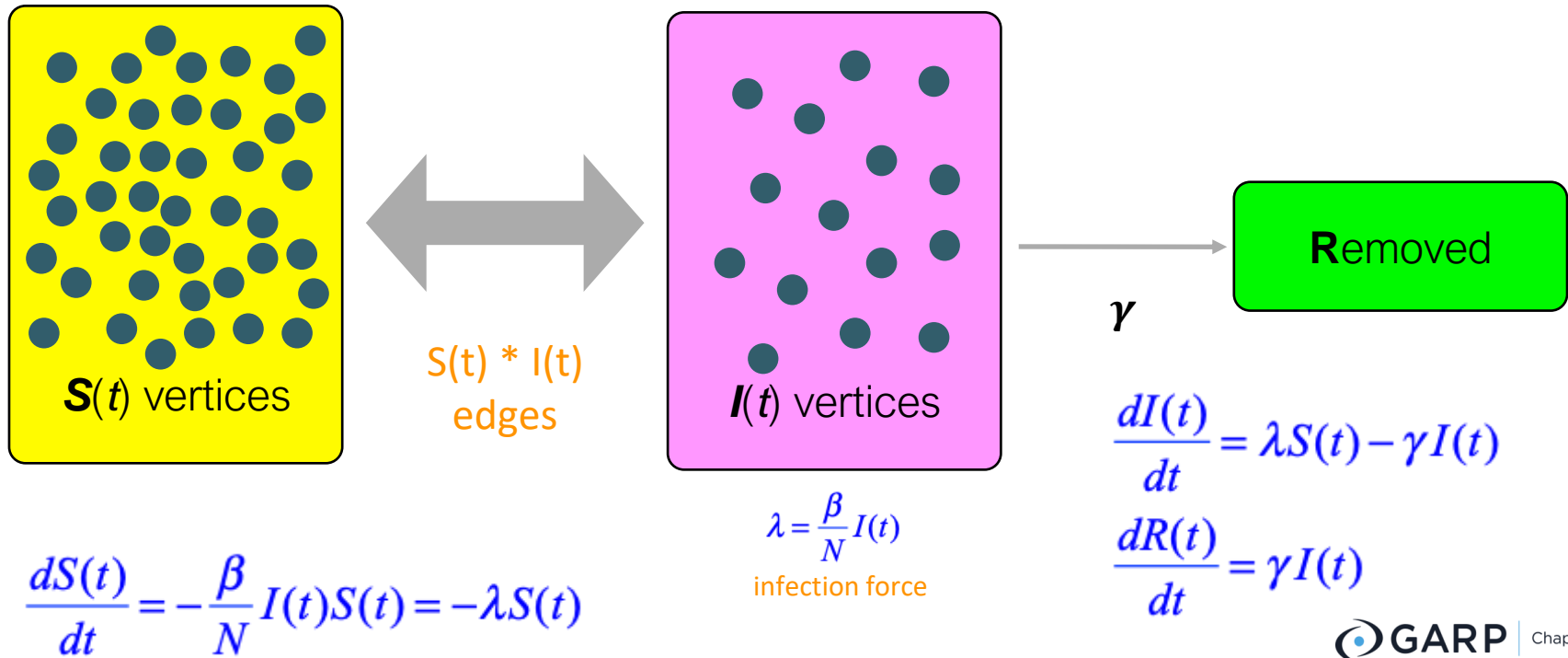


Towards COVID-19 Quantitative Realities - SEIR and SEAIR



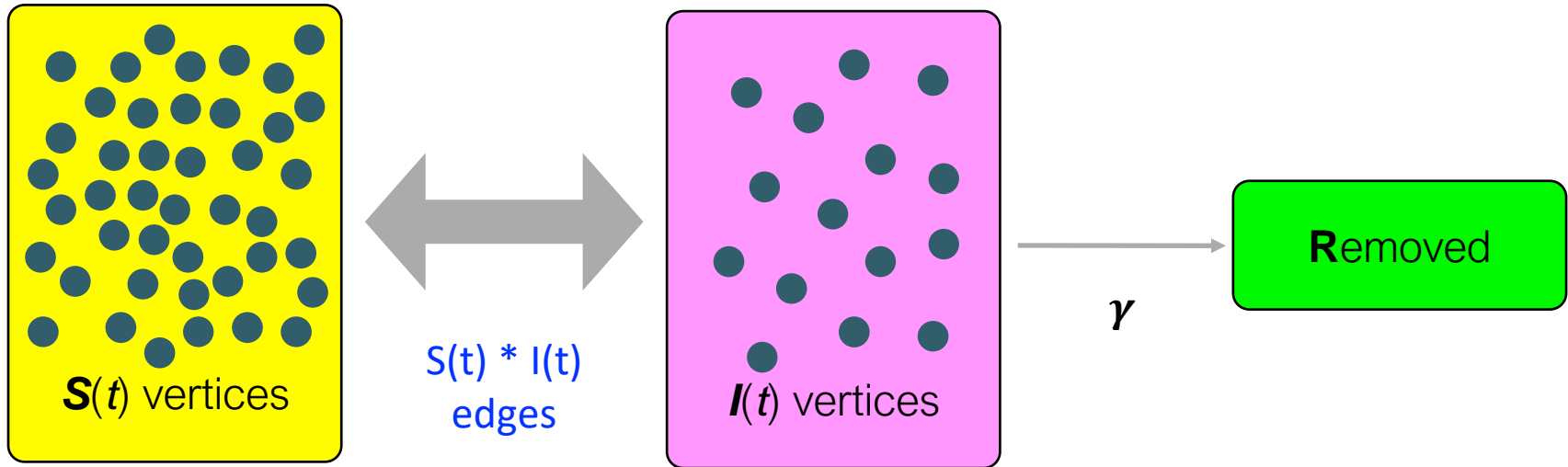
SIR Compartmental Epidemic Model

- 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

OurWorldInData Engine for “Reproduction Rate”

PLOS ONE

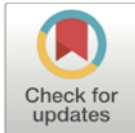
RESEARCH ARTICLE

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

Francisco Arroyo-Marioli¹, Francisco Bullano¹, Simas Kucinkas^{2*}, Carlos Rondón-Moreno¹

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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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Practice of Epidemiology

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

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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?

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Abstract

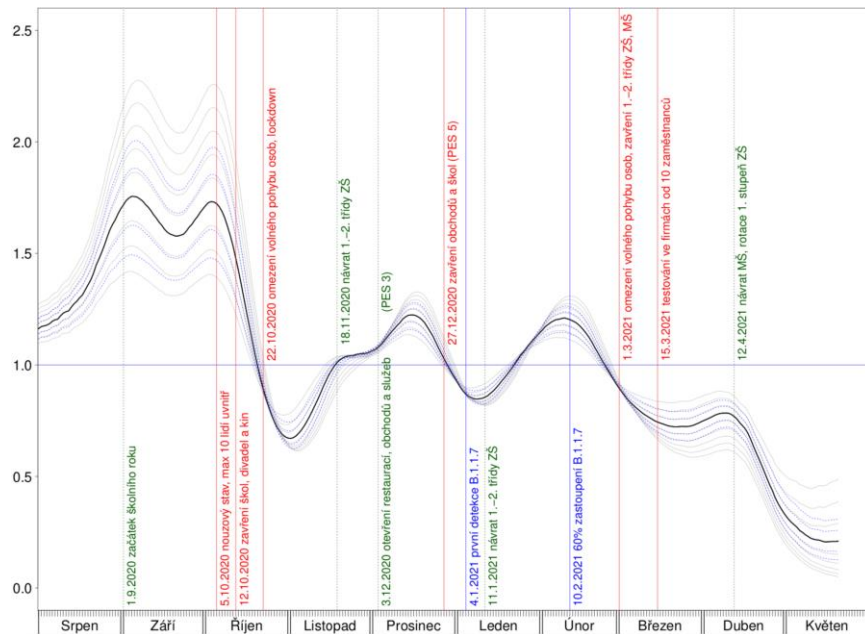
The number of new infections per day is a key quantity for effective epidemic management. It can be estimated relatively directly by testing of random population samples. Without such direct epidemiological measurement, other approaches are required to infer whether the number of new cases is likely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

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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



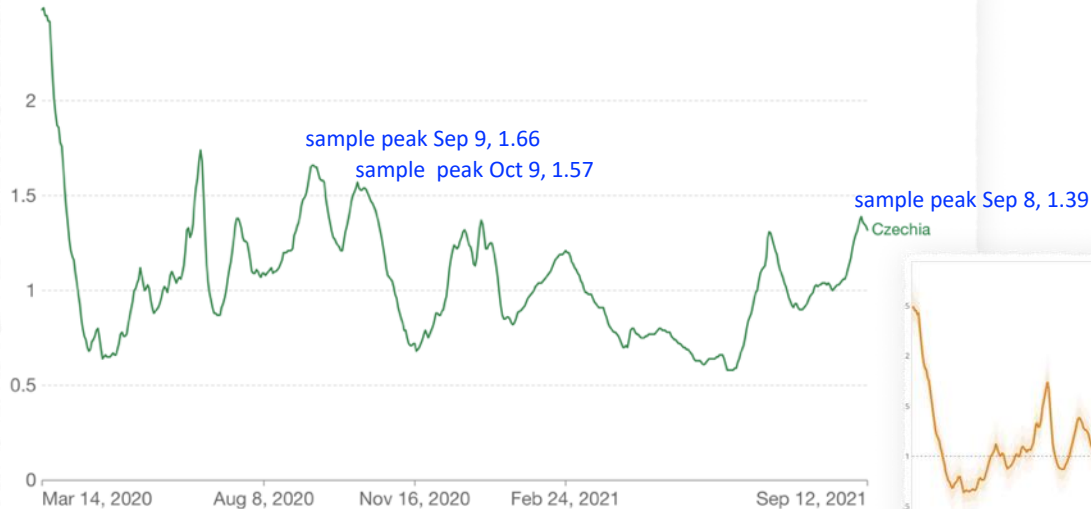
Source: Arroyo-Marioli F, Bullano F, Kucinskas S, Rondón-Moreno C (2021) Tracking R of COVID-19: A new real-time estimation using tBIC BY Kalman filter.

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.

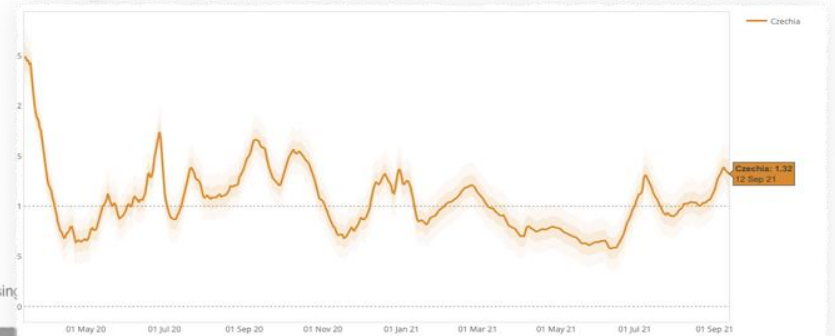


Source: Arroyo-Marioli F, Bullano F, Kucinskas S, Rondón-Moreno C (2021) Tracking R of COVID-19: A new real-time estimation using Kalman filter.

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>



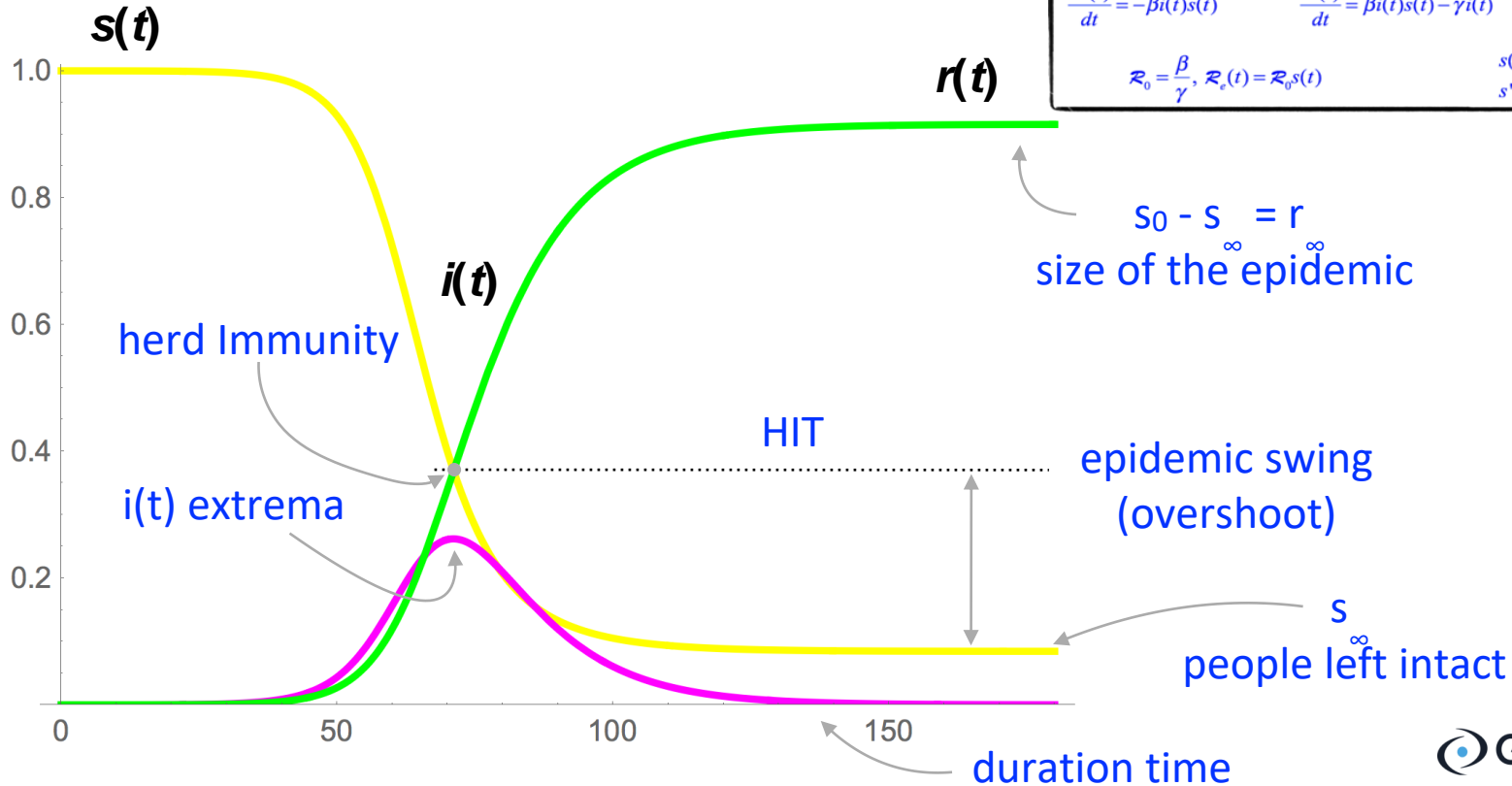
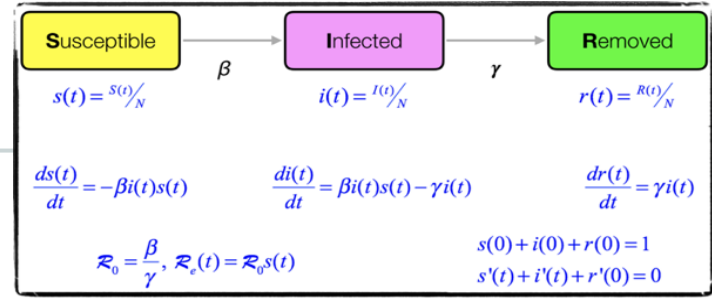
Last updated on 14 September 2021

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

Do not mix R_0 and $R(t)$

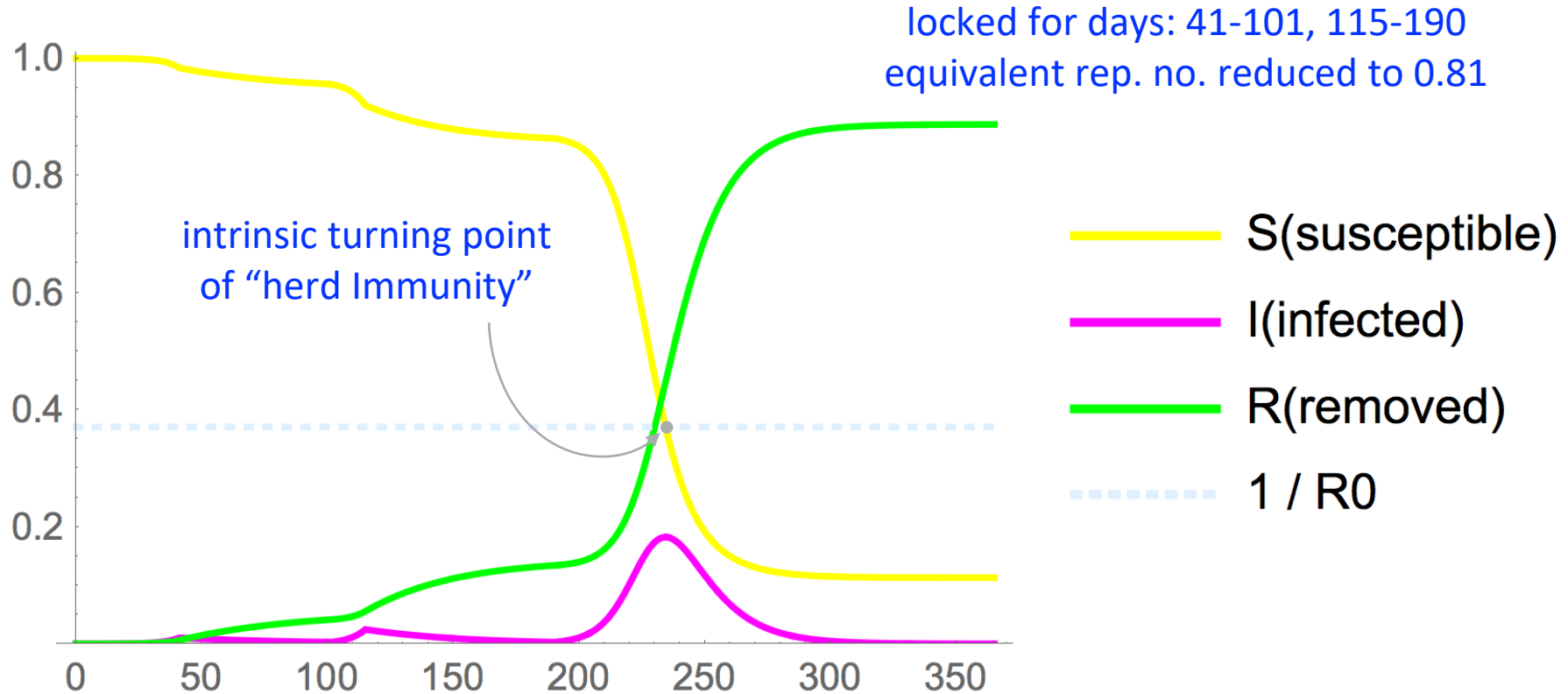
- ▶ Both have something to do with secondary infections, but
 - **R_0 describes qualitative characteristics, $R(t)$ shows local dynamics**
 - **$R(t)$ captures actual countermeasures, seasonality, immunity status, etc.**
 - **their relative influence is hard to distinguish, but the overall picture is 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**

Partial Optimisation Criteria (SIR-based)



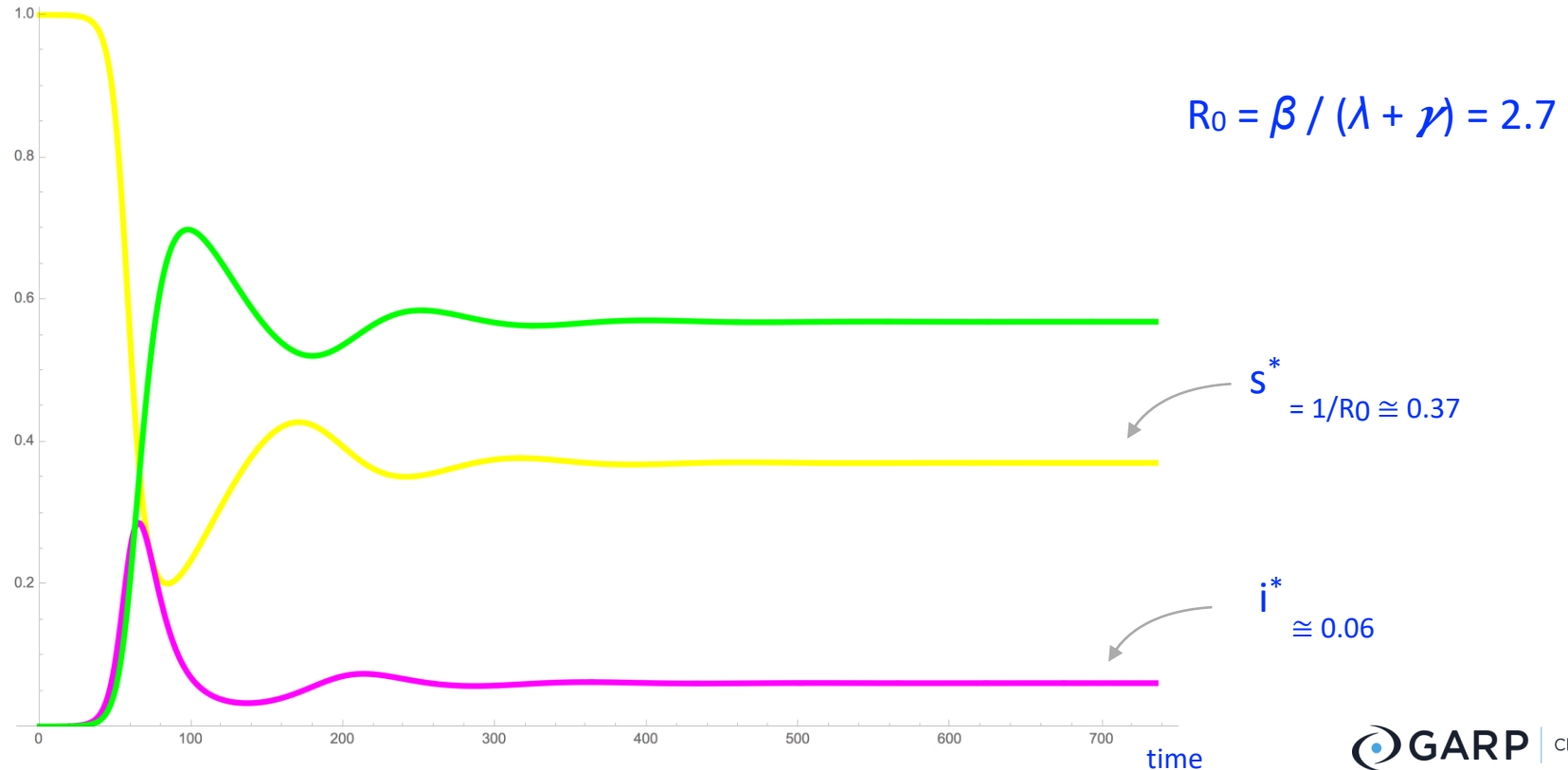
possible endemic size, etc. (not visible in this model)

Example: Qualitative Study of Two Ideal Consecutive Lockdowns

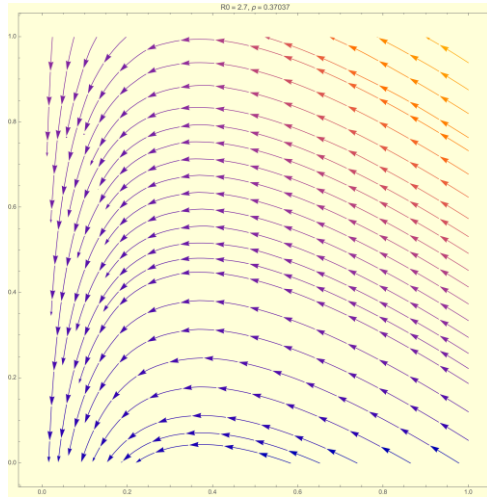


- we set λ very high (with respect to a pure demography) here to illustrate endemic equilibrium in general
- on the other hand, in reality, demography is not the only reason for endemic states anyway

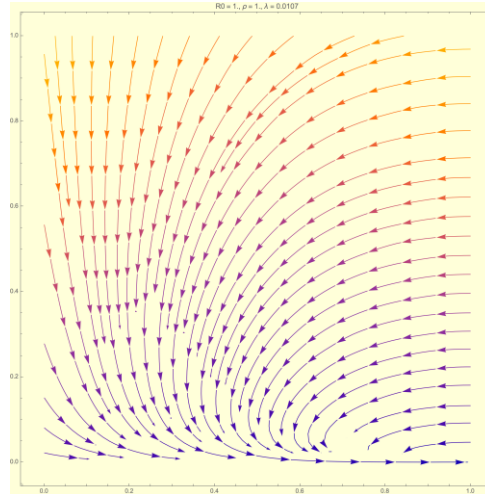
Long-Term Endemic Equilibrium for $R_0 > 1$



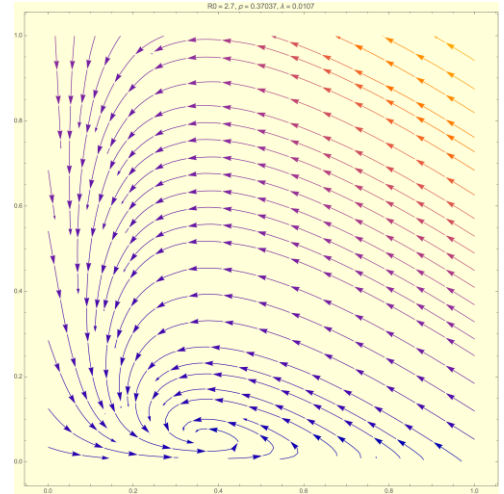
Direction field of the model* equations brings yet-another viewpoint



short-term closed
epidemic outbreak



long-term equilibrium
disease-free



long-term equilibrium
endemic

$i(t)$

$s(t)$

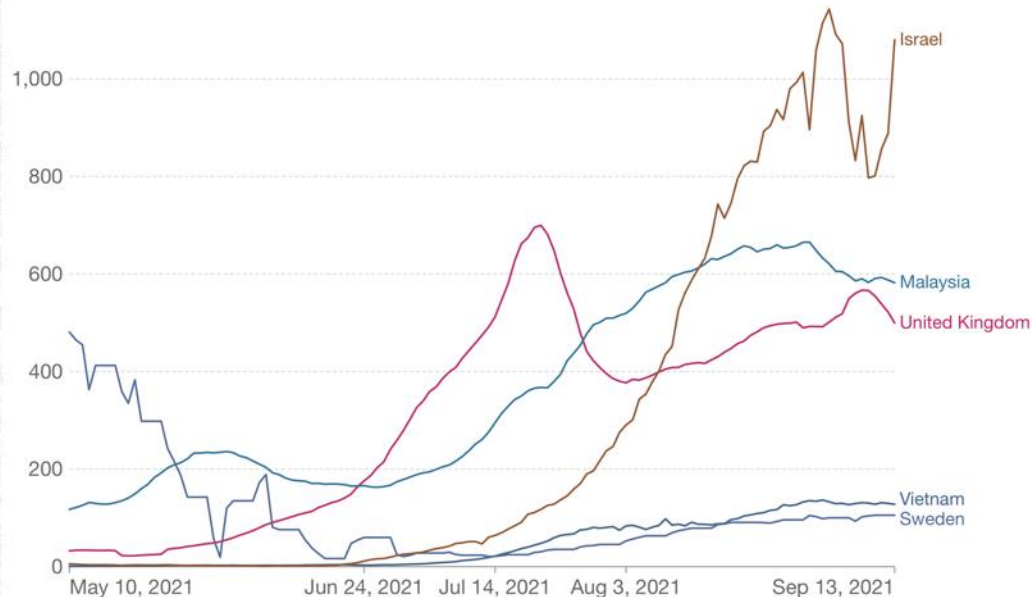
*) SIR and SIR with demography

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

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

ε	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 %	—	—	—	—

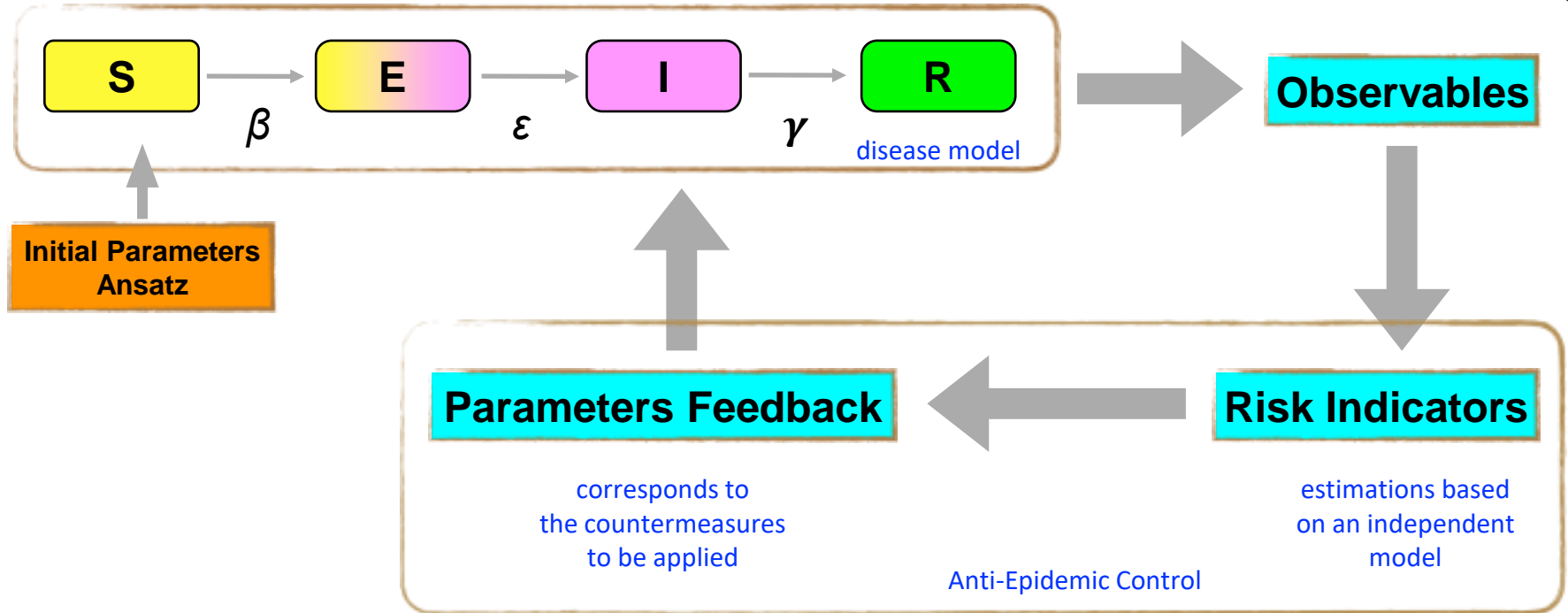
- ▶ Assumptions:
 - vaccine distributed uniformly among yet-susceptible people
 - vaccine efficacy ε - **for spreading**
 - immunity does not vanish in near time (circa one year, at least - does it?)
- ▶ Recovered people fraction bearing natural immunity then sums up with the vaccinated fraction
 - not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

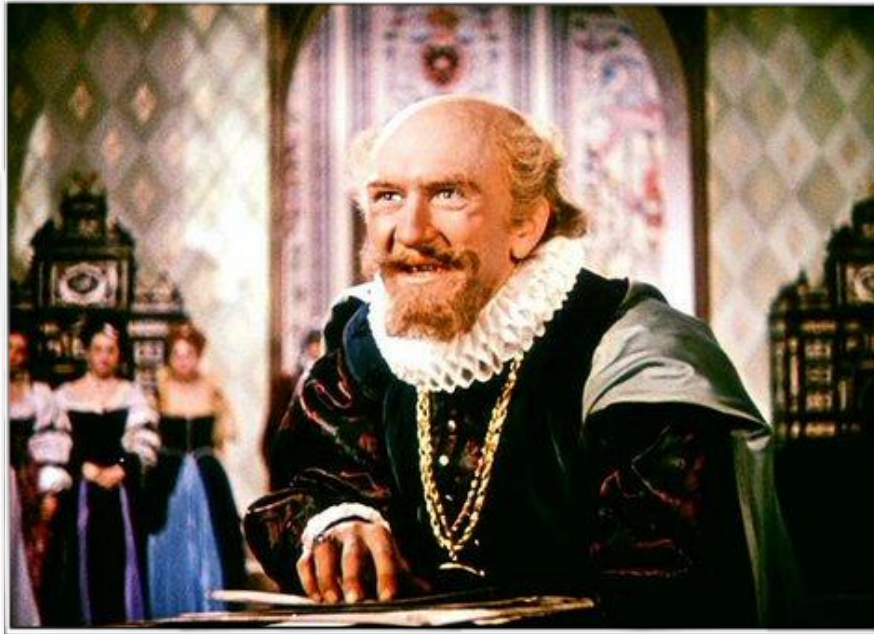
How much can we trust the models?

- ▶ 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

Consider This Control Chain

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

Long Story Short



Trust the mathematics,
not so the mathematicians.

Conclusion

- ▶ 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**