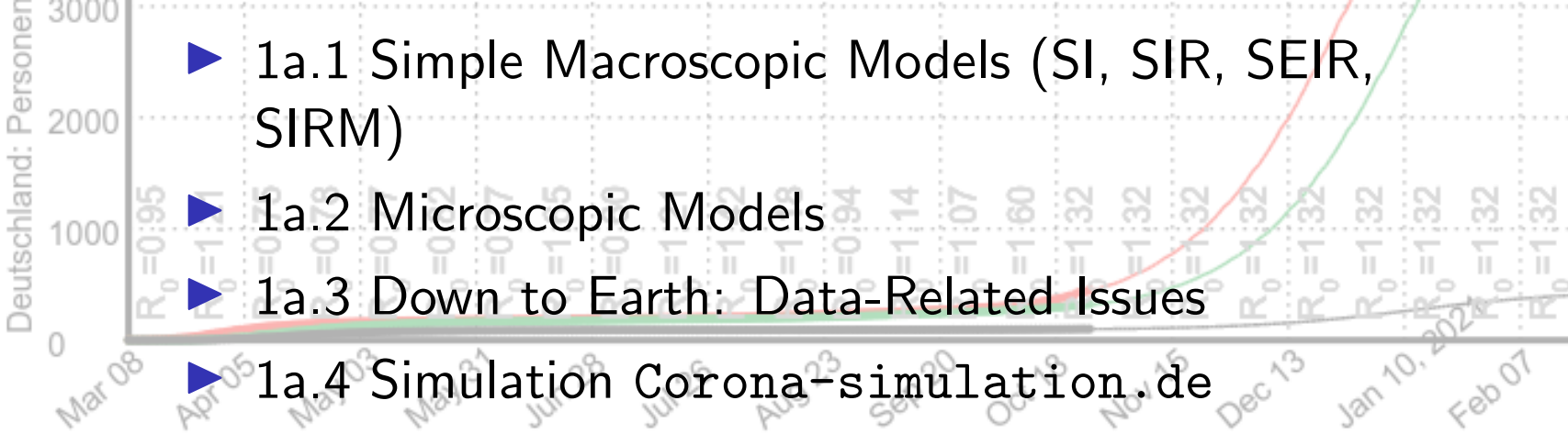


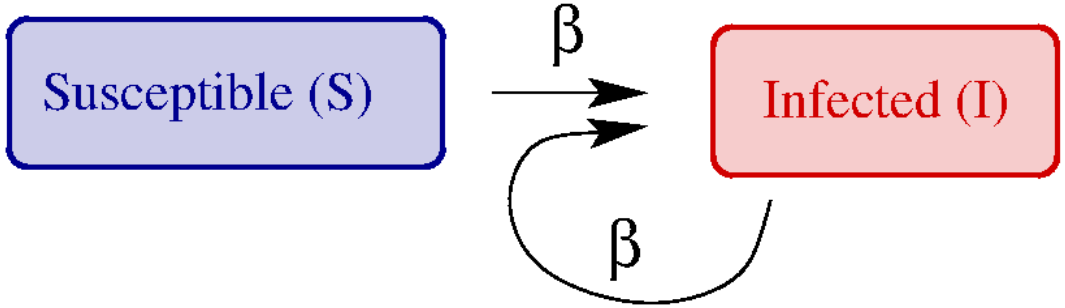
- 1a.1 Simple Macroscopic Models (SI, SIR, SEIR, SIRM)
- 1a.2 Microscopic Models
- 1a.3 Down to Earth: Data-Related Issues
- 1a.4 Simulation `Corona-simulation.de`

Martin Tre

1a.1 Simple macroscopic models I: SI model

Compartemental models: consider different status such as susceptible, infected, or recovered and transitions between them

- As in any macroscopic model on infection dynamics, the basic dynamic quantities are *percentages of the population* (e.g., of a country) rather than individual persons
- Scale separation: The *infection dynamics* is much faster than the rest of the *population dynamics* (births, "normal" deaths, in- and outwards directed migration/moves) $\Rightarrow$ population number $N = \text{const.}$
- Two compartiments: any person can be either *susceptible* to infection (S), or already infected (I) which includes actually ill, recovered, or dead. Particularly, there is no reverse transition I$\rightarrow$S



SI model II

- All infected persons become *contagious instantaneously* and remain so all the time (notice the inconsistency to the point above)
- The *rate of contagion* β (# persons per time unit if everybody else is S) remains constant

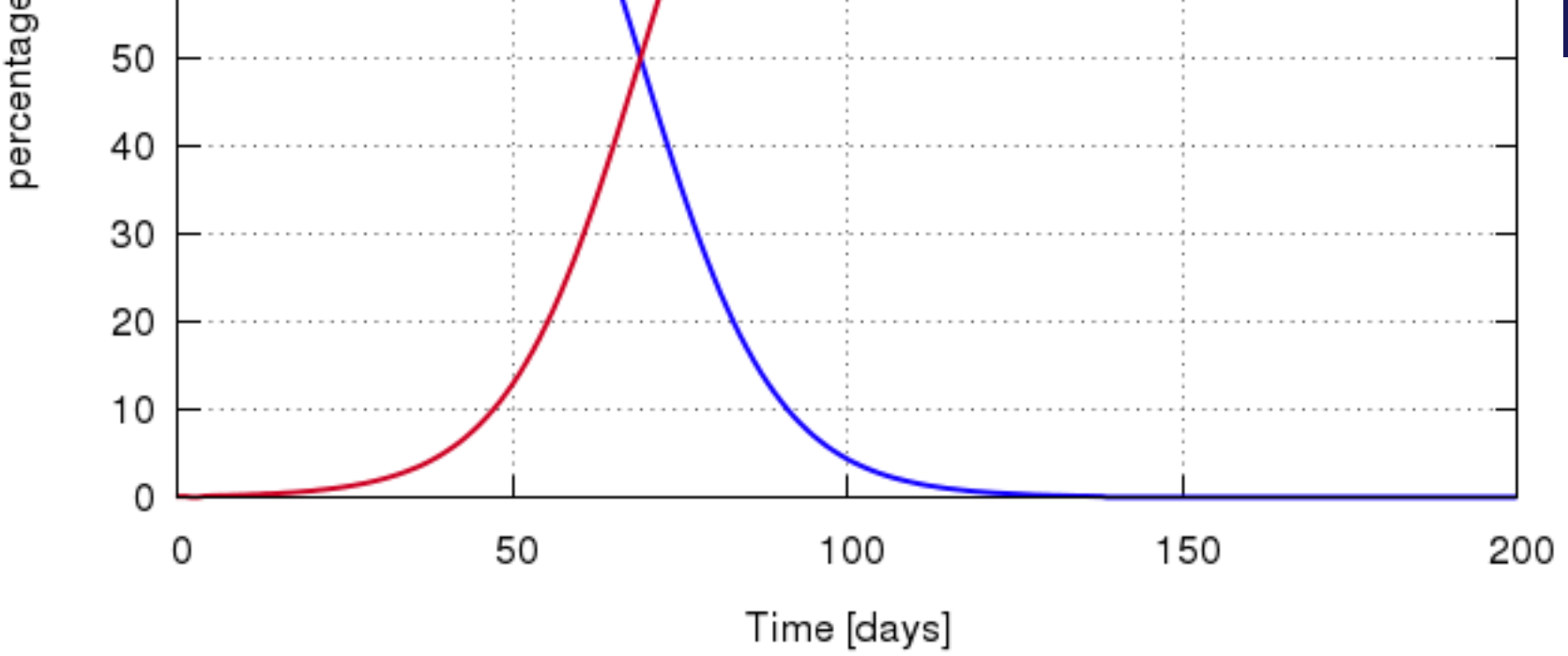
$$\Rightarrow \quad \begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= -\beta I S, \\ \frac{\mathrm{d}I}{\mathrm{d}t} &= +\beta I S \end{aligned} \qquad \text{SI model}$$

- $S = N_S/N$: fraction of susceptible
- $I = N_I/N$: fraction of infected
- $\frac{\mathrm{d}}{\mathrm{d}t}(S+I) = 0 \Leftrightarrow$ conservation of population number $N = \text{const.}$

Rewrite with $S + I = 1$:

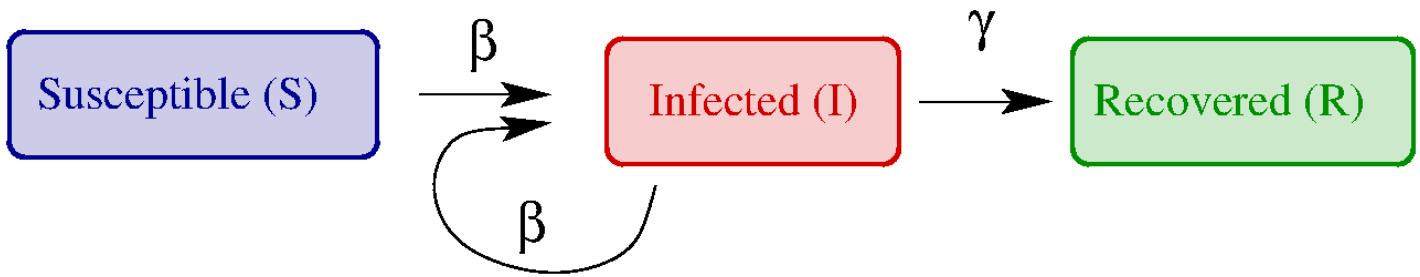
$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta I(1-I)$$

$\Rightarrow$ *classical model for limited growth* with saturation 1


percentage
50
40
30
20
10
0
0
50
100
150
200
Time [days]

SIR model

- Unlike the situation in the SI model, infected people recover/die after an average time $1/\gamma$ thereby becoming *no longer contagious*
- Chained models for the transitions susceptible-infected (SI) and infected-recovered persons(IR), $R =$ fraction of recovered:



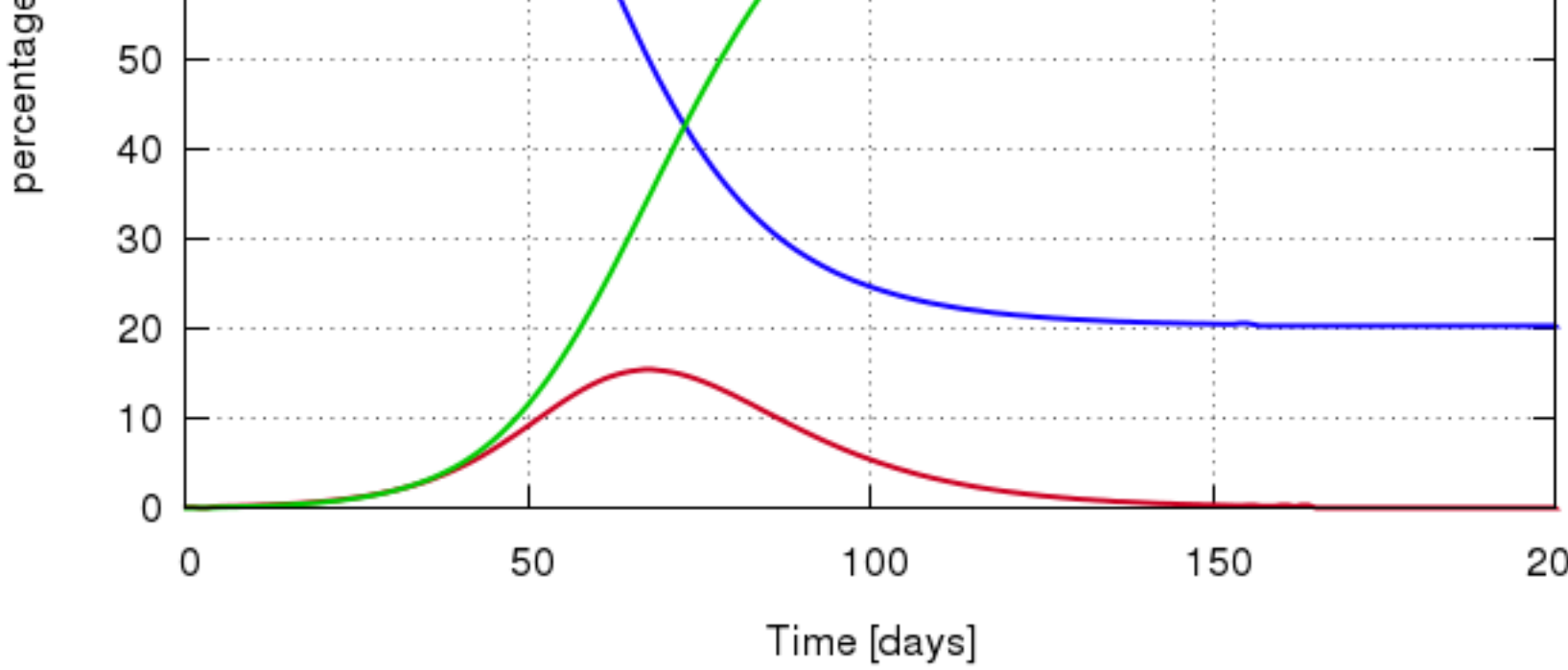
$$\begin{aligned} \frac{\mathrm{d}S}{\mathrm{d}t} &= -\beta I S, \\ \frac{\mathrm{d}I}{\mathrm{d}t} &= +\beta I S - \gamma I, \\ \frac{\mathrm{d}R}{\mathrm{d}t} &= +\gamma I \end{aligned}$$

SIR model

- Conservation of the population number: $S + I + R = 1$

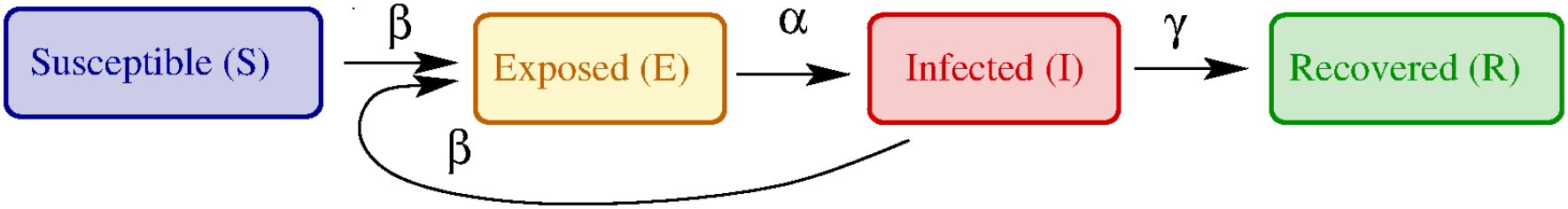
? Show that the initial reproduction number is given by $R_0 = \beta/\gamma$

! Initially ($S = 1$), any infected person infects β other persons per day but recovers after an exponentially distributed time $\tau_R \sim \text{Exp}(\gamma)$, so the average #infected people $= \beta E(\tau_R) = \beta/\gamma$


percentage
50
40
30
20
10
0
0
50
100
150
20
Time [days]

SEIR model

- Adds to the SIR model a finite *incubation time* $\tau_I \sim \text{Exp}(\alpha)$ where people are infected but not yet contagious ("exposed", E)
- Triple chain with $S + E + I + R = 1$:

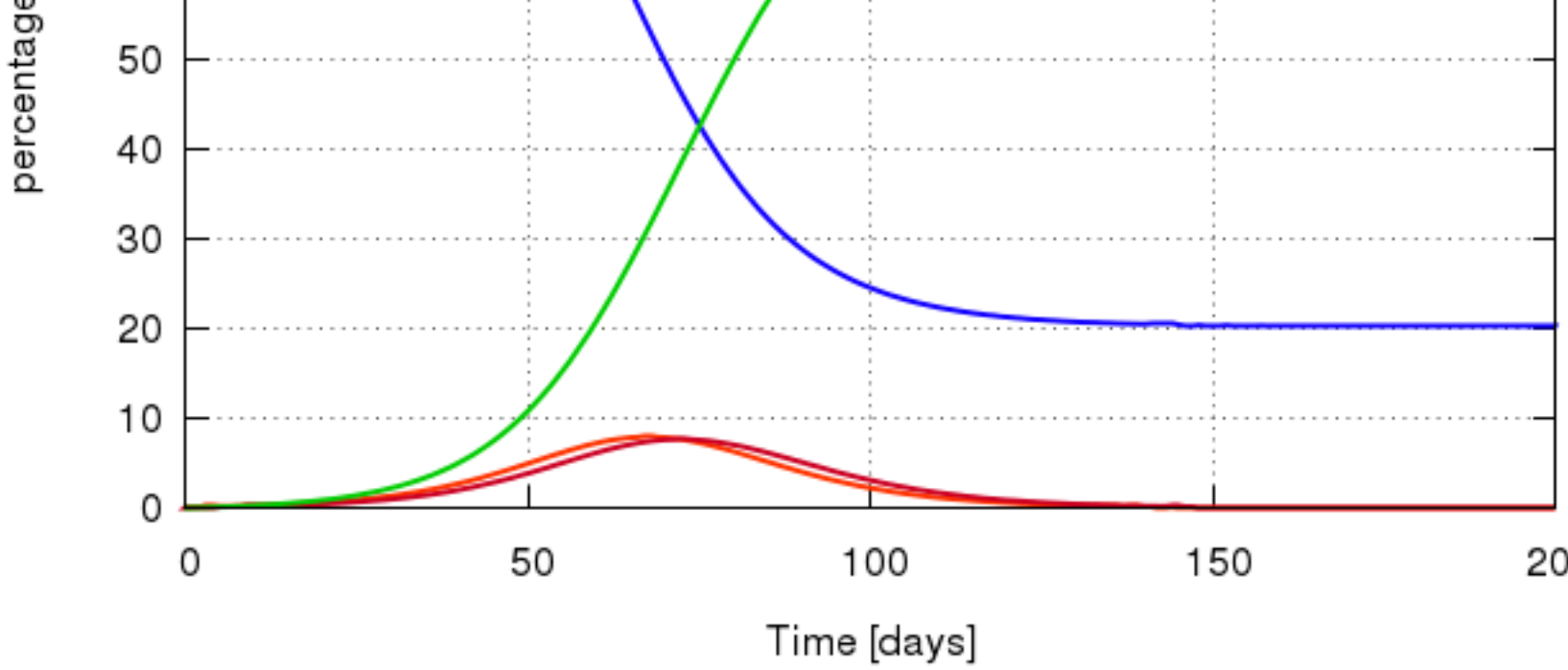


$$\begin{aligned}
\frac{\mathrm{d}S}{\mathrm{d}t} &= -\beta I S, \\
\frac{\mathrm{d}E}{\mathrm{d}t} &= +\beta I S - \alpha E, \\
\frac{\mathrm{d}I}{\mathrm{d}t} &= +\alpha E - \gamma I, \\
\frac{\mathrm{d}R}{\mathrm{d}t} &= +\gamma I
\end{aligned}$$

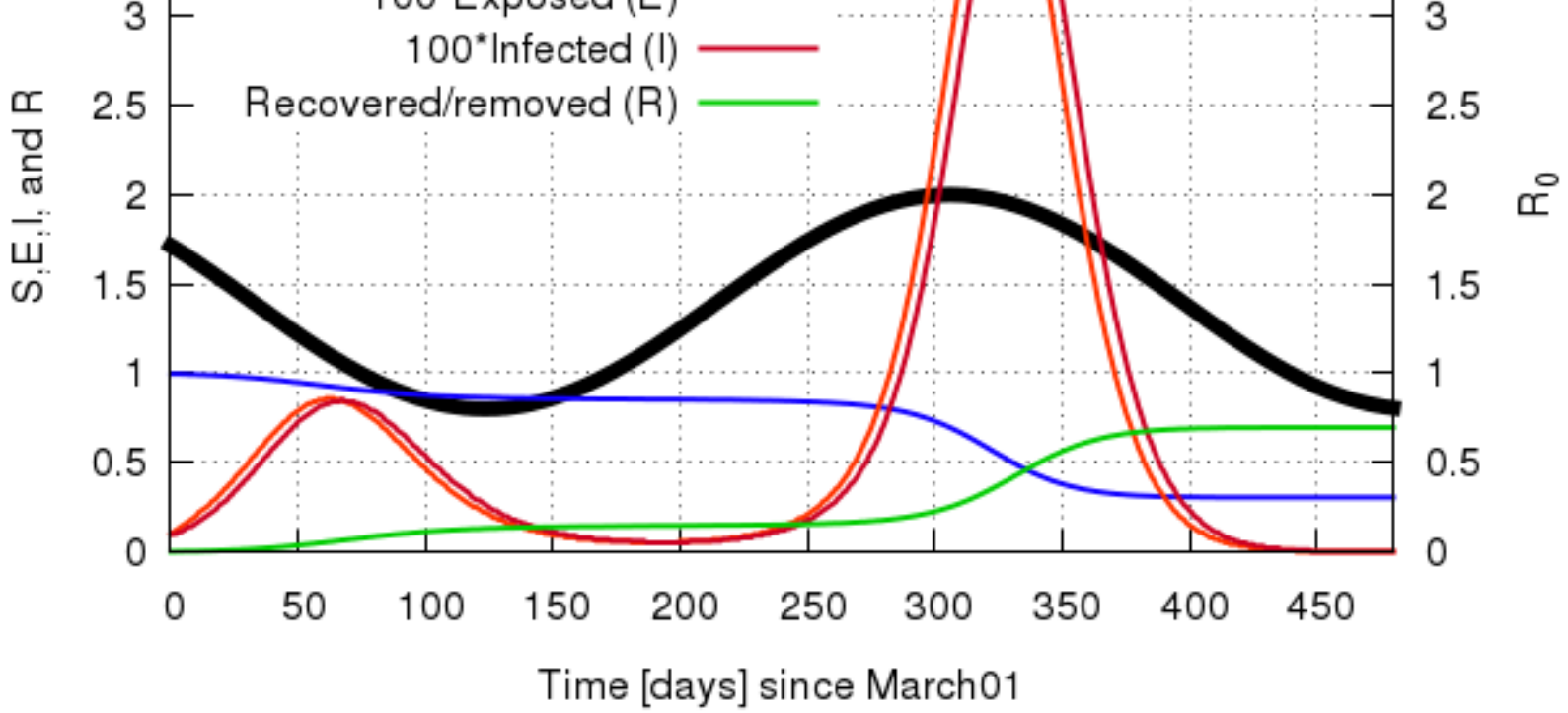
SEIR model

? Show that $R_0 = \beta/\gamma$ and that the initial time for doubling of the infected is given by $\tau = (1/\gamma + 1/\alpha)/\log_2(R_0)$

! R_0 as in the SIR model. The average time for passing an infection is the sum $1/\gamma + 1/\alpha$ of the incubation and infection times. In this timescale, there are $\log_2(R_0)$ doublings.


percentage
50
40
30
20
10
0
0
50
100
150
20
Time [days]

S


100*Exposed (E)
100*Infected (I)
Recovered/removed (R)
S,E,I, and R
R_0
Time [days] since March01
0
50
100
150
200
250
300
350
400
450
0
0.5
1
1.5
2
2.5
3

Iterated map models

- The SI, SIR, SEIR models were **ordinary differential equations** (ODEs)
- Another more direct approach are **iterated maps**: models for time evolution by classical model chaining
- can be interpreted as numerical solutions of ODEs but they are more flexible allowing "real" memory, e.g., truly nonzero incubation time instead of an exponential distributed one
- Of course, this also means we need initialize all past values within the memory time

Iterated SIR model with memory (SIRM)

- An infected person contacts R_0 persons and infects $R_0 S$ persons *exactly* τ_I days after his/her own infection

$\Rightarrow$ need history of all fractions $I_{t'}$ of persons infected *exactly* at day $t' \leq t$

- The person recovers exactly τ_R days after infection

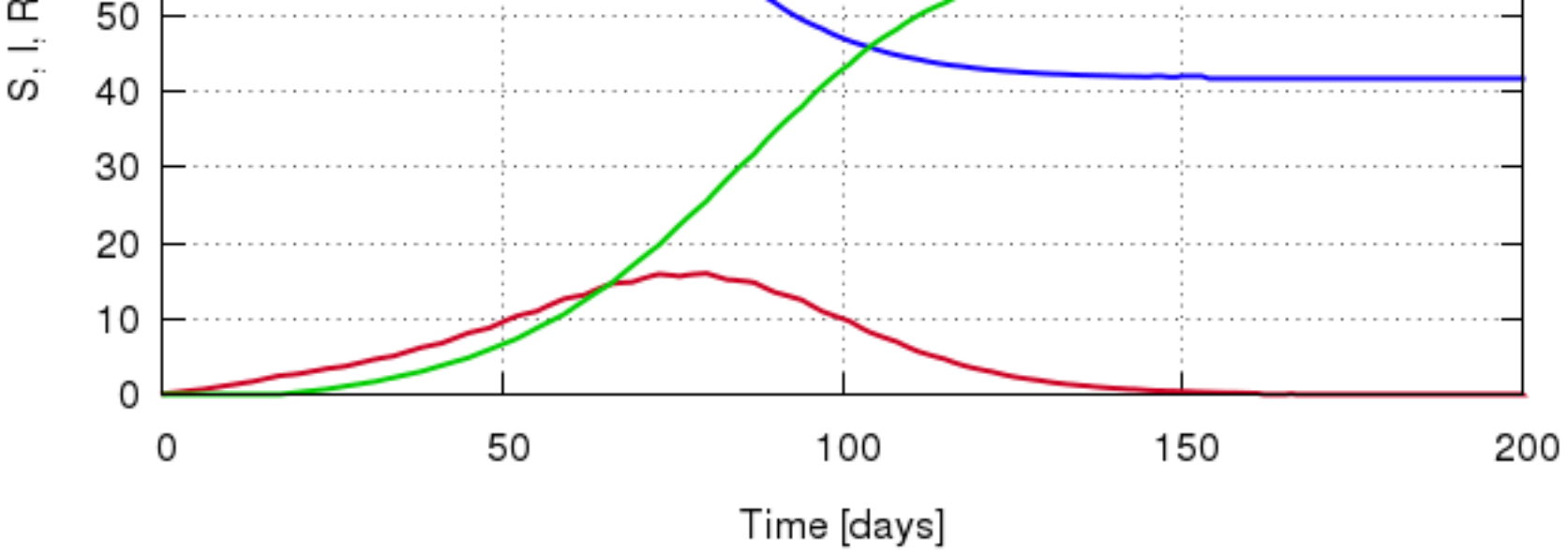
$\Rightarrow$ The total fraction of ill persons (*active cases*) at day t is given by

$$I(t) = \sum_{j=i-\tau_I+1}^{i} I_j$$

$$\begin{aligned} I_t &= R_0 S(t-\tau_I) I_{t-\tau_I}, \\ S(t) &= S(t-1) - I_t, \\ R(t) &= R(t-1) + I_{t-\tau_R}, \\ I(t) &= 1 - S(t) - R(t) \end{aligned}$$

SIR model with memory

Notice that the recovery does not influence the infection process since only infection day τ_I is contagious


S, I, R
50
40
30
20
10
0
0
50
100
150
200
Time [days]

1a.2 Microscopic Models

The principle is straightforward: Just break down the compartemental models to single persons (remember the definition of a microscopic model!)

- The health status of each person i is exactly one out of a set, e.g. status $\in \{$ S, E, I, R $\}$
- Transition $S_i \to E_i$ if an S person i is sufficiently close to an I person j sufficiently long, e.g.

$$S_i(t) \to E_i(t) \quad \text{if} \quad d_{ij}(t') \leq 1.5\,\mathrm{m} \;\forall\; t' : t - \tau_E \leq t' \leq t$$

- Transition to an I person after an incubation time τ_I
- Transition to an R person after a time period $\tau_R > \tau_I$

So the pandemic micromodel is easy: It gets interesting when adding a **particle dynamics model** for the motion of the people to model, e.g., *superspreading events*

Microscopic example

- Time t: superspreading event
- Time $t + \tau$: three people infected in the middle group
- Time $t + 2\tau$: one of the newly infected moves to the other group
- Time $t + 3\tau$: incubation time over (also at the left group)
- Time $t + 4\tau$: two infections in two groups

1a.3 Down to reality/econometrics: what can be observed?

We want to know: **#Infections** $N_I(t) = N\,I(t)$,
ideally its "age structure" $I_0, I_1, ..., I_t$

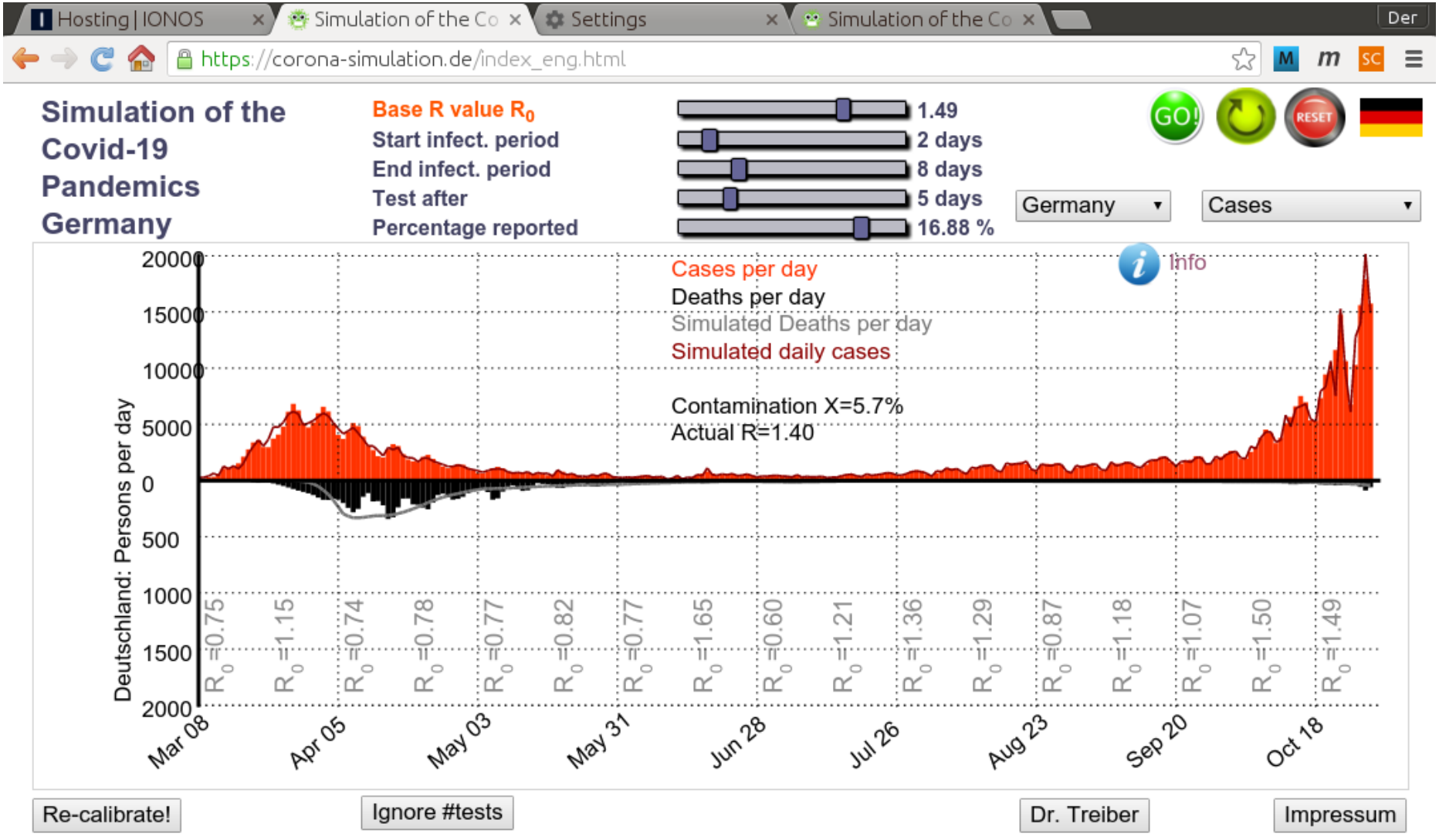
We do know: **#positive tests** $N_T(t)$ ("cases") and
#Covid-19 deaths $N_D(t)$ including the history $t' \leq t$

Many uncertainties:

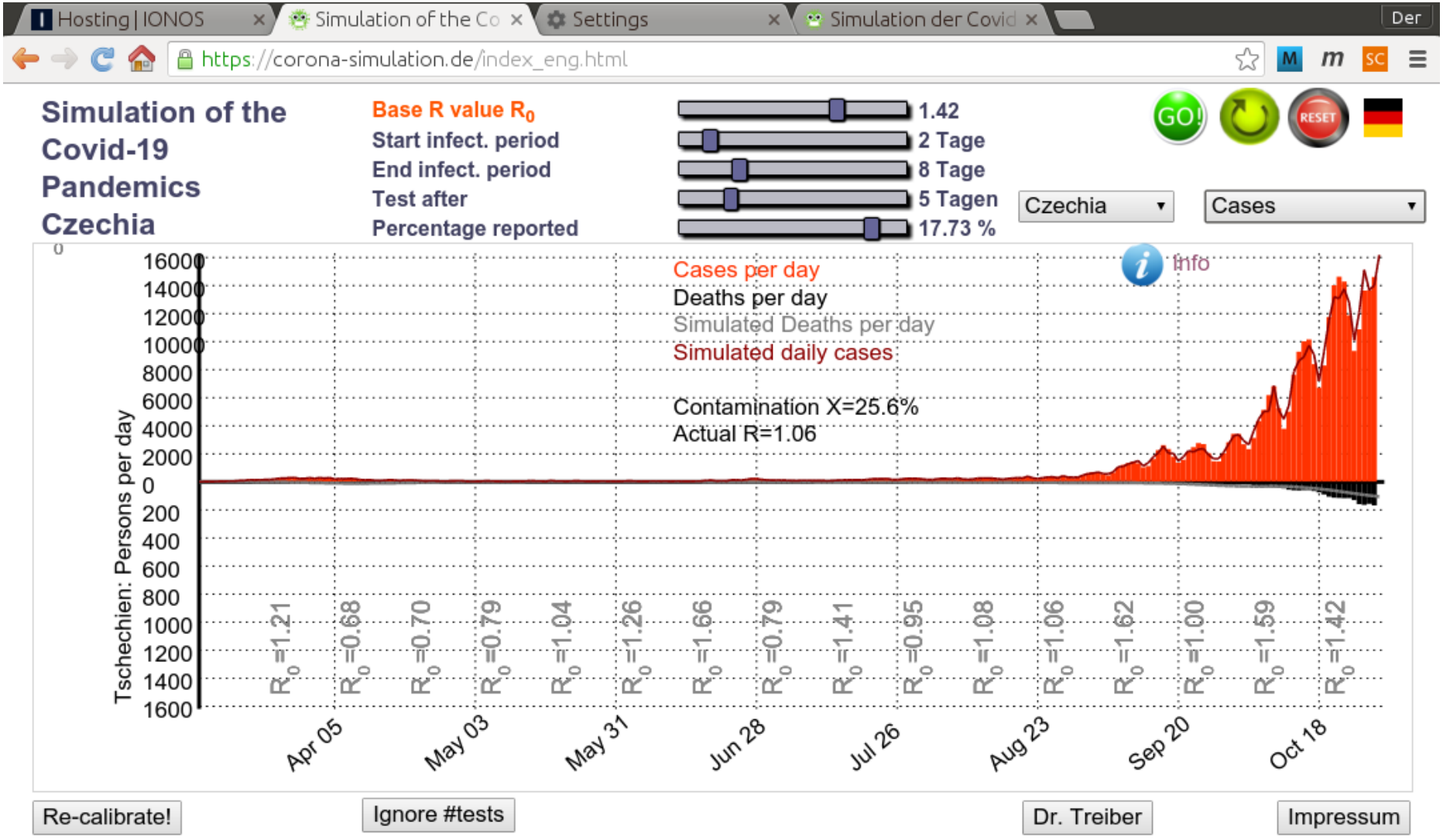
- The tests have an imperfect **sensitivity** $P(\text{positive}|\text{infected}) \approx 99\,\%$
- ... and an imperfect **specifity** $P(\text{negative}|\text{not infected}) \approx 99\,\%$
- Different/inconsistent definitions of a "Covid-19 death" event
- There is a high number of untested and potentially ill people $\Rightarrow$ high number of unreported cases, probably $\gg N_T$
- The fraction of reported cases depends on the number of tests via a monotonously increasing but otherwise unknown function

Corona-simulation.de (as of Oct 30, 2020)

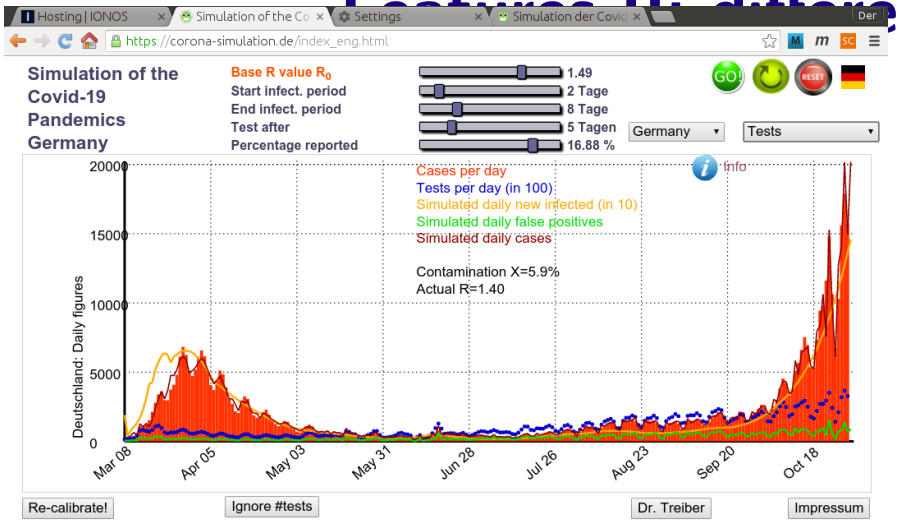
Interactive *data-driven* simulator based on an extended SIRM model

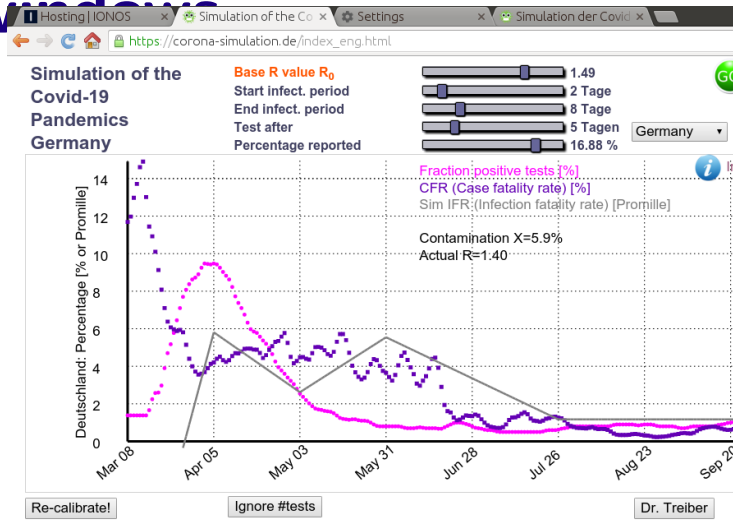


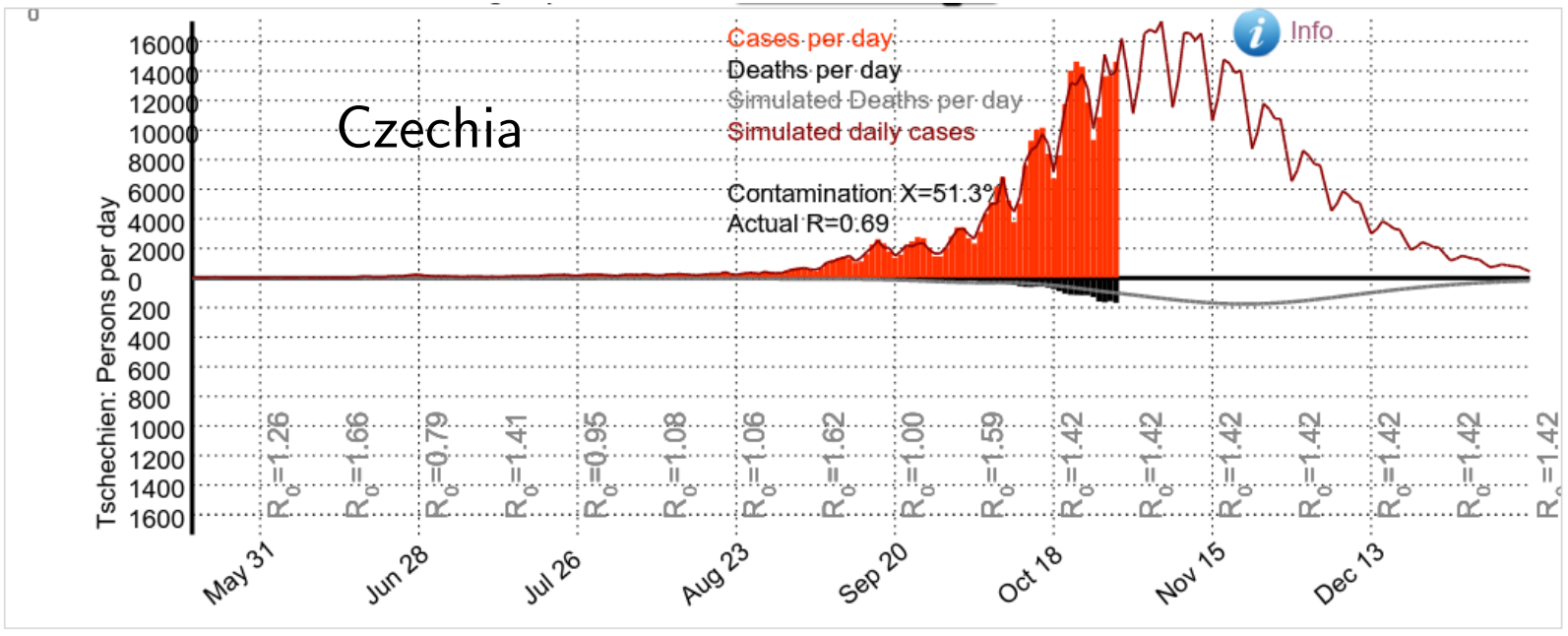
Features I: different countries



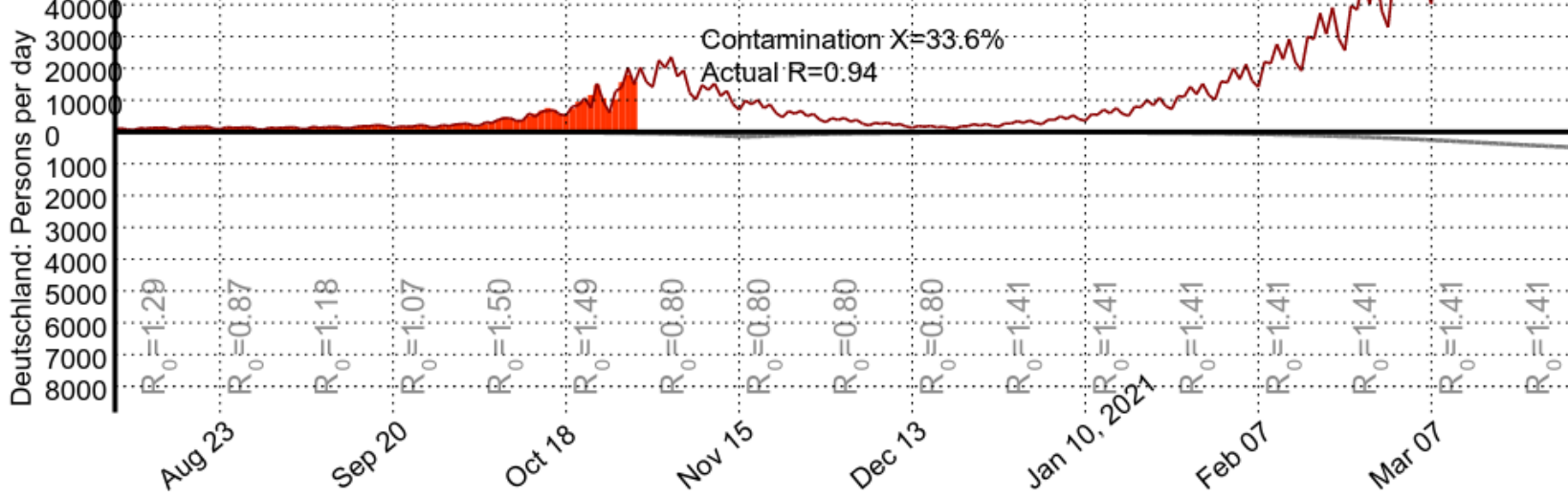
Features II: different windows





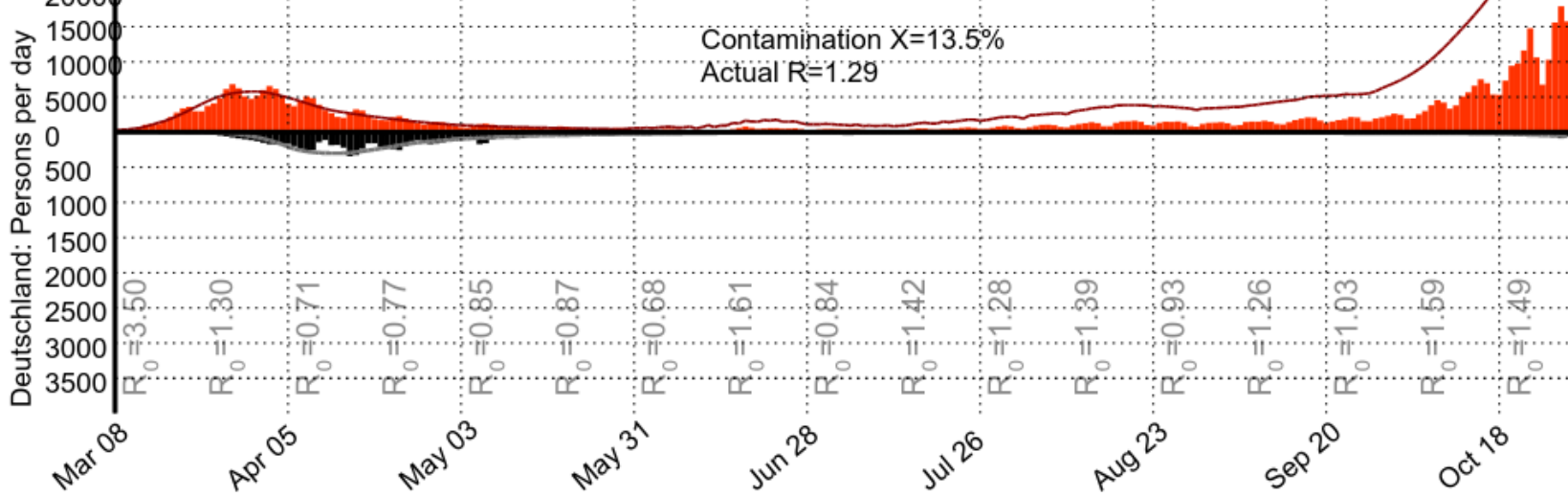

Czechia
Cases per day
Deaths per day
Simulated Deaths per day
Simulated daily cases
Contamination X=51.3%
Actual R=0.69
Info
Tschechien: Persons per day
16000
14000
12000
10000
8000
6000
4000
2000
0
200
400
600
800
1000
1200
1400
1600
R0=1.26
R0=1.66
R0=0.79
R0=1.41
R0=0.95
R0=1.08
R0=1.06
R0=1.62
R0=1.00
R0=1.59
R0=1.42
R0=1.42
R0=1.42
R0=1.42
R0=1.42
R0=1.42
R0=1.42
May 31
Jun 28
Jul 26
Aug 23
Sep 20
Oct 18
Nov 15
Dec 13

TECHNISCHE UNIVERSITÄT DRESDEN



Re-calibrate! Ignore #tests Dr. Treiber Impressu

TECHNISCHE UNIVERSITÄT DRESDEN



Re-calibrate! Include #tests Dr. Treiber Impressu

Summary/take-home messages

- Only **data brings us "down to Earth"** allowing for
  - tests of the model quality
  - doing useful things such as projection scenarios (do not forget Mark Twains quote about predictions!)
- Always **check definitions of events**, e.g., "Covid-19 infection" (including all symptom free people?) or "Covid-19 death" (including fatal traffic accidents of a test-positive persons?)
- **Do not confuse/mix proxies with the real quantities**, e.g., positive tests *vs.* infection events. Also check how well the proxy *represents* the interesting quantities (#positive tests is a poor proxy for the #infections, #*recorded* Covid-19 death is a much better proxy for all the Covid-19 deaths)
- **Check your sample.** Is it essentially the population or only a small and unknown fraction thereof?
- **Be careful with exponentially growing things** since small changes in the scenario setting can greatly influence the result