

# Traffic Econometrics Master's Course

## Lecture 01a: Covid-19 Dynamics

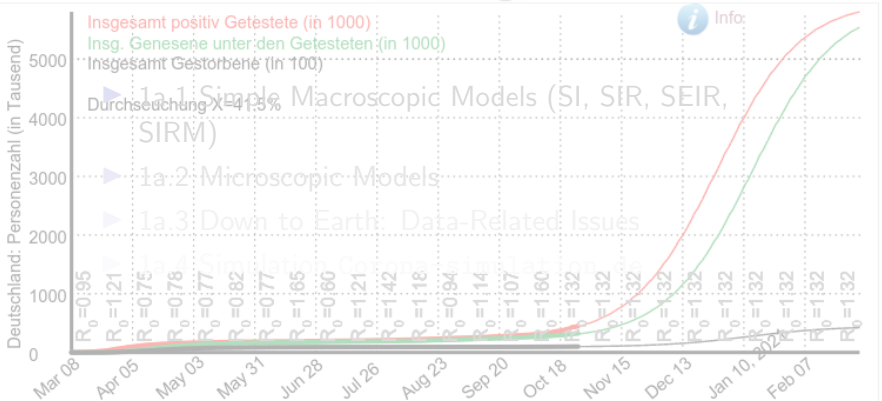
Simulation der  
Covid-19  
Pandemie  
Deutschland

Reproduktionszahl  $R_0$  1.32  
Ansteckungsstart 2 Tage  
Ansteckungsende 8 Tage  
Test nach 5 Tage  
Heilfeld 18.64 %



Deutschland ▾

Simulation (kum) ▾



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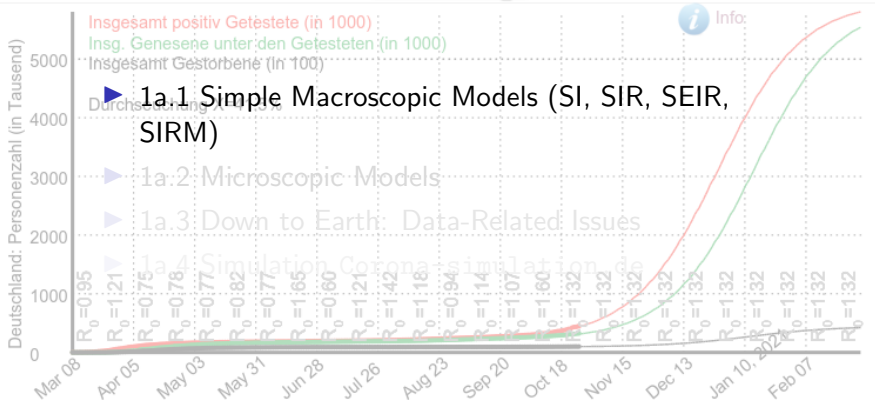
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1a.1 Simple Macroscopic Models (SI, SIR, SEIR, SIRM)

1a.2 Microscopic Models

1a.3 Down to Earth: Data-Related Issues

1a.4 Simulation Corona-simulation.de

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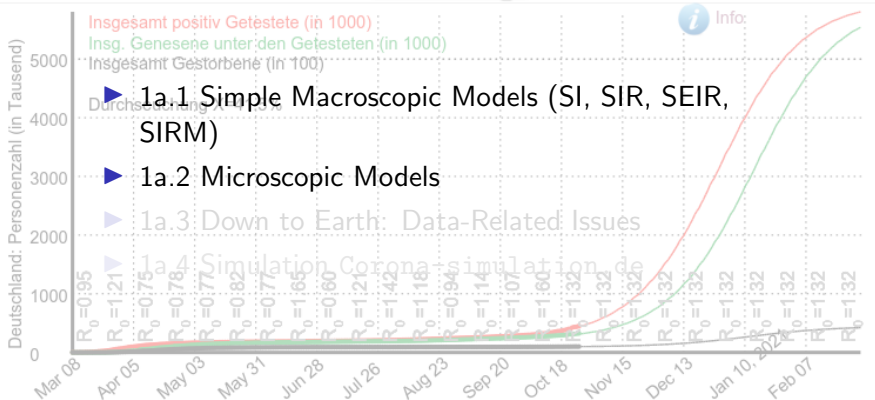
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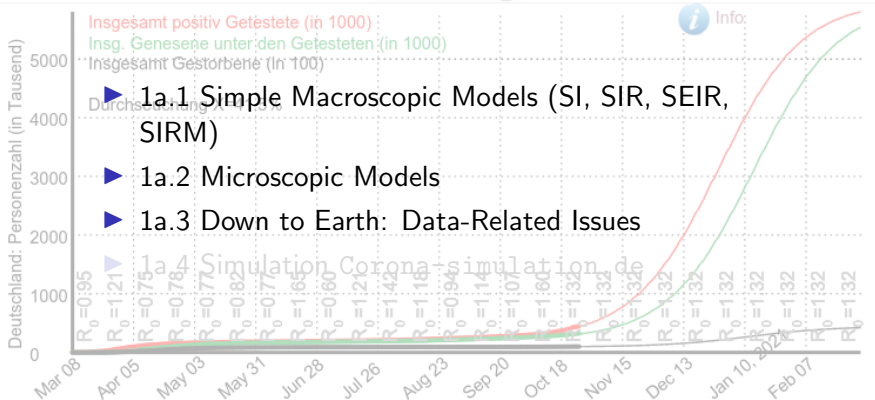
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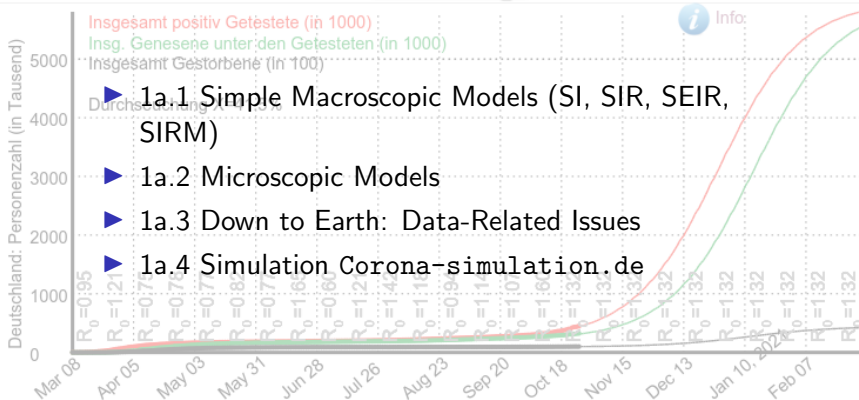
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**Compartmental models:** consider different status such as susceptible, infected, or recovered and transitions between them

- ▶ 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 compartments: 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  $I \rightarrow S$

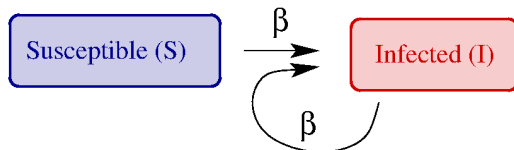
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## 1a.1 Simple macroscopic models I: SI model

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## 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*  $\beta$  (# persons per time unit if everybody else is S) remains constant

$$\Rightarrow \begin{aligned} \frac{dS}{dt} &= -\beta IS, \\ \frac{dI}{dt} &= +\beta IS \end{aligned} \quad \text{SI model}$$

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

Rewrite with  $S + I = 1$ :

$$\frac{dI}{dt} = \beta I(1 - I)$$

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

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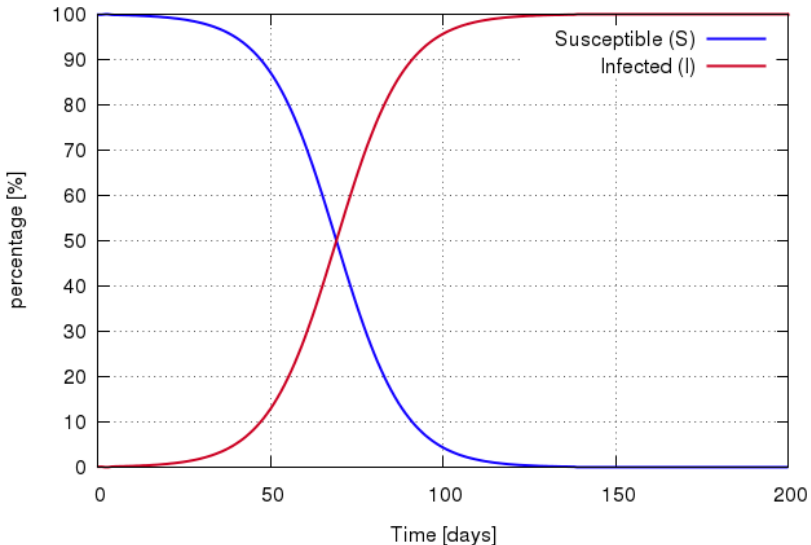
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## SI model III: Simulation

SI model,  $\beta=0.1/\text{day}$ ,  $I(0)=0.1\%$



## 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:

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- ▶ 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  $\beta$  other persons per day but recovers after an exponentially distributed time  $\tau_R \sim \text{Exp}(\gamma)$ , so the average #infected people  $= \beta E(\tau_R) = \beta/\gamma$



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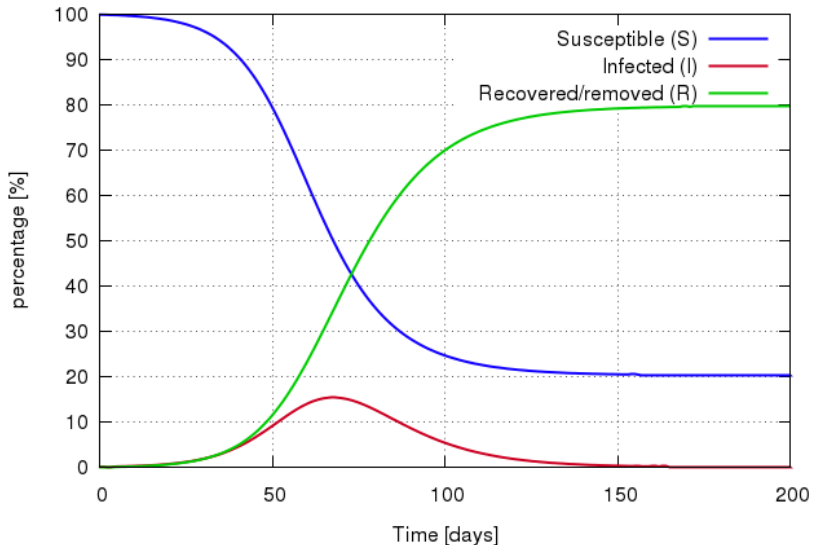
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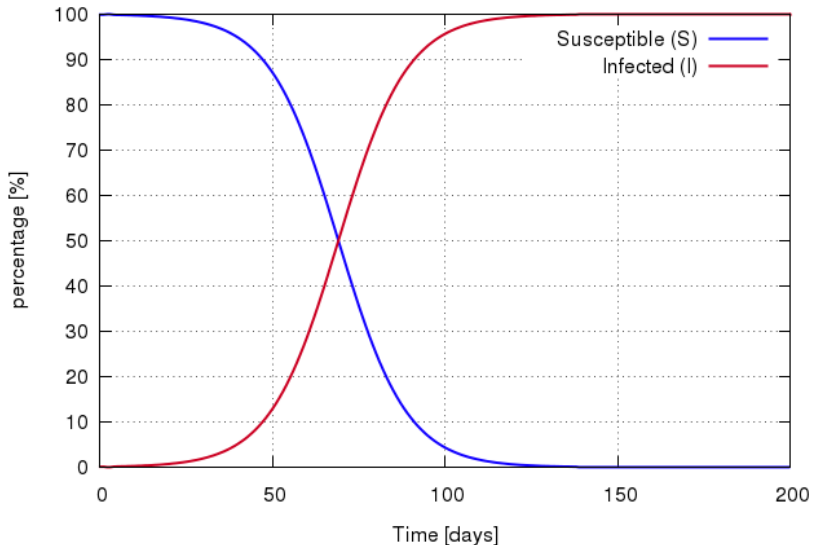
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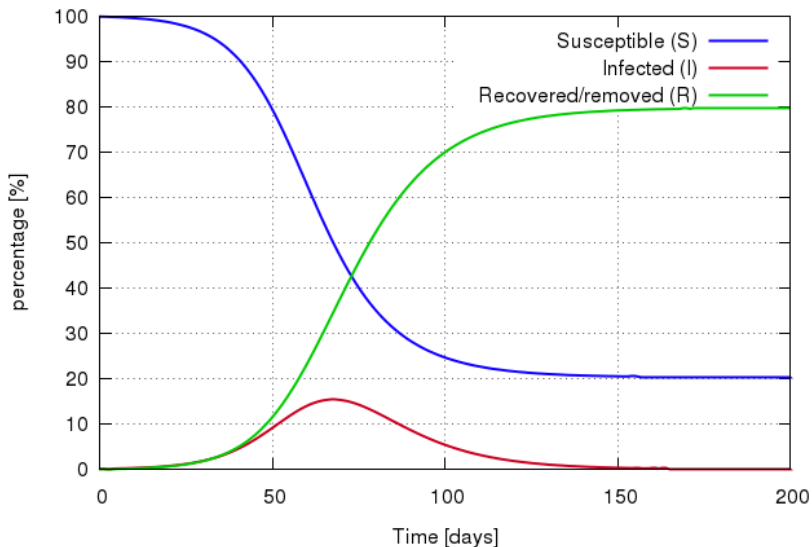
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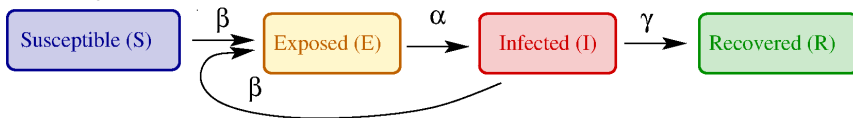




- ▶ Adds to the SIR model a finite *incubation time*  $\tau_I \sim \text{Exp}(\alpha)$  where people are infected but not yet contagious (“exposed”, E)
- ▶ Triple chain with  $S + E + I + R = 1$ :

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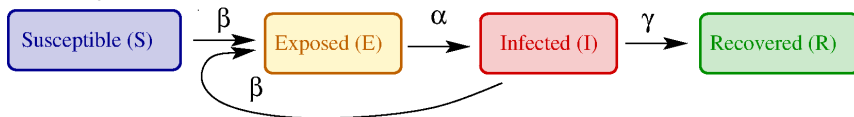
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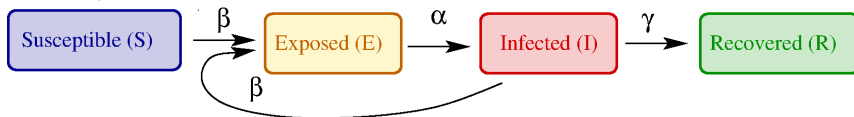
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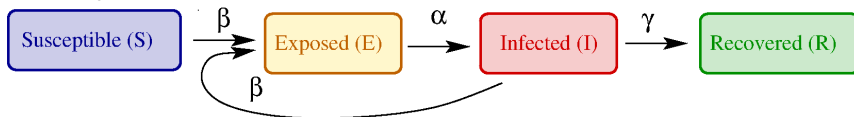
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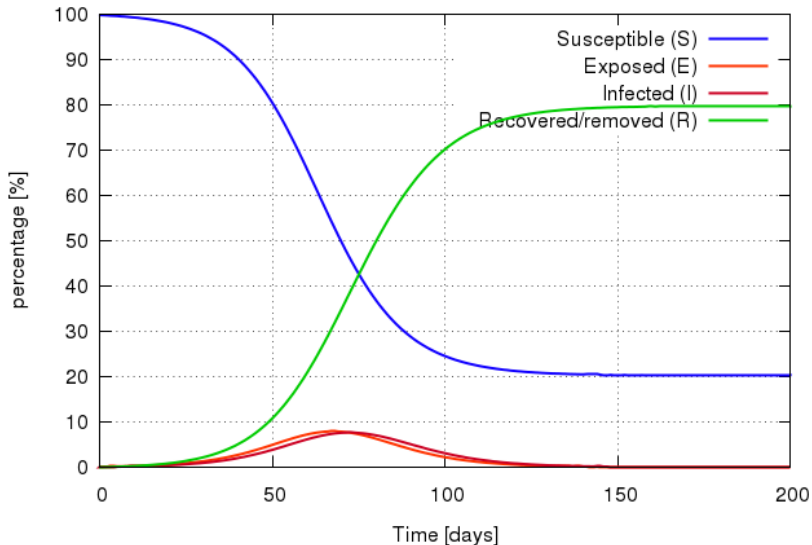
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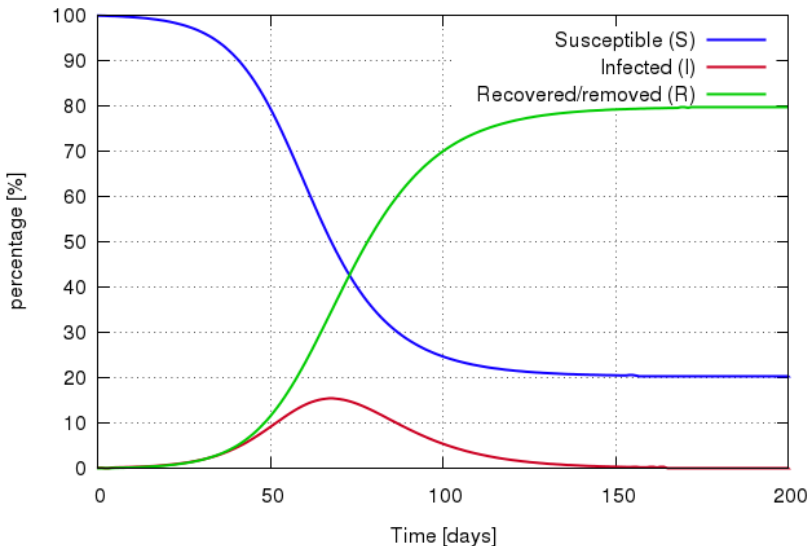
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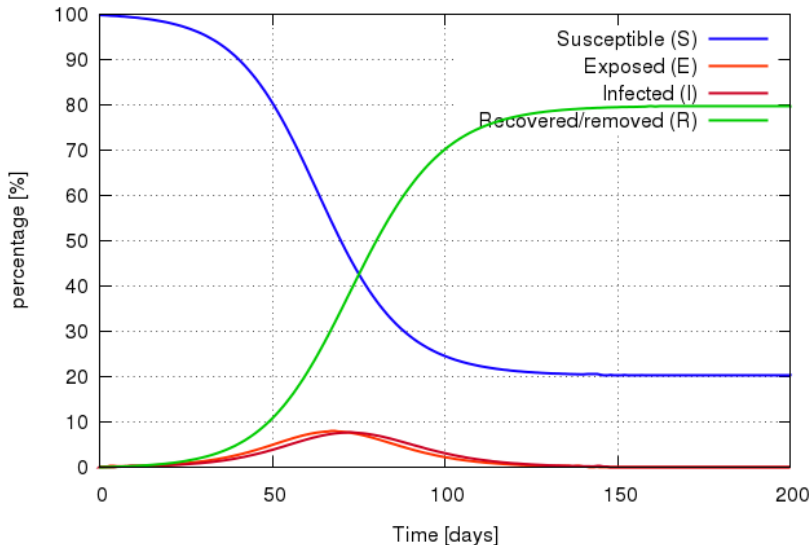
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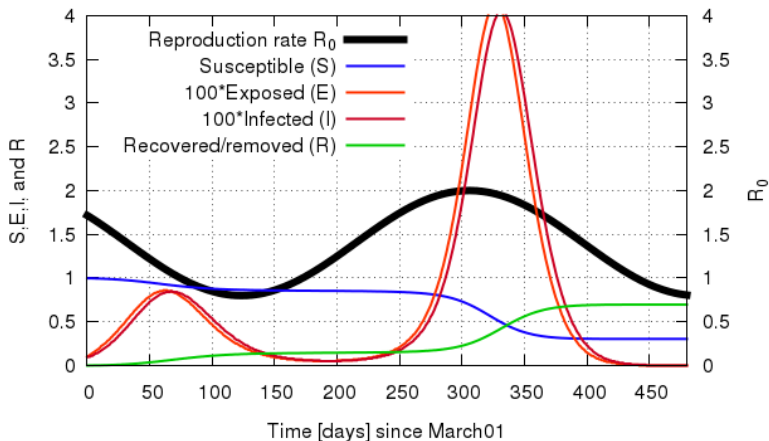
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## Iterated map models

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

## Iterated SIR model with memory (SIRM)

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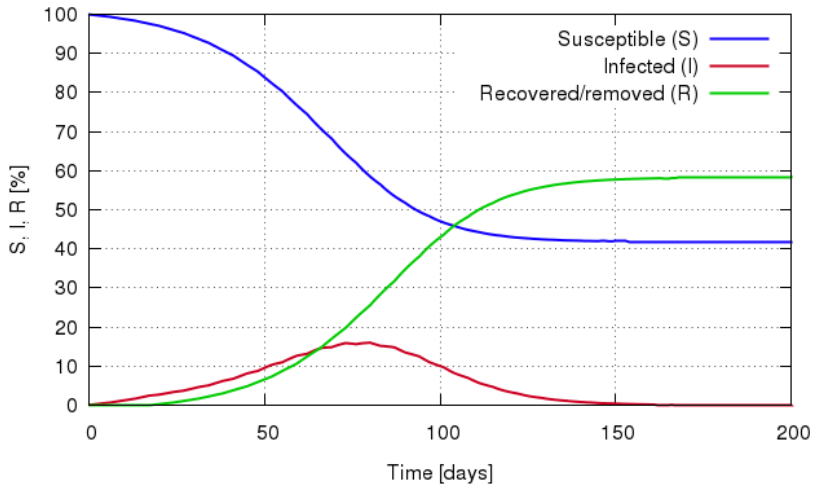
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## Simulation of the SIR model with memory

SIR iterated,  $\tau_I=7$  days,  $\tau_R=18$  days,  $I_t=0.001$  for  $t<\tau_I$



## 1a.2 Microscopic Models

The principle is straightforward: Just break down the compartmental 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  $S_i \rightarrow E_i$  if an S person  $i$  is sufficiently close to an I person  $j$  sufficiently long, e.g.

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

- ▶ Transition to an I person after an incubation time  $\tau_I$
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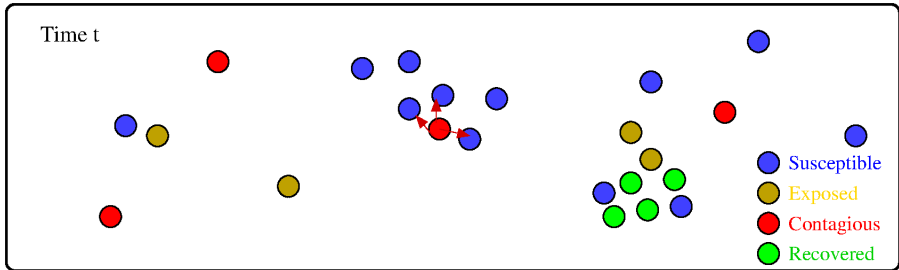
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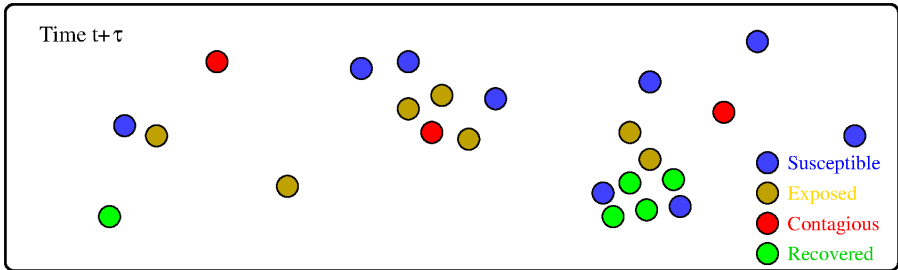
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## Microscopic example



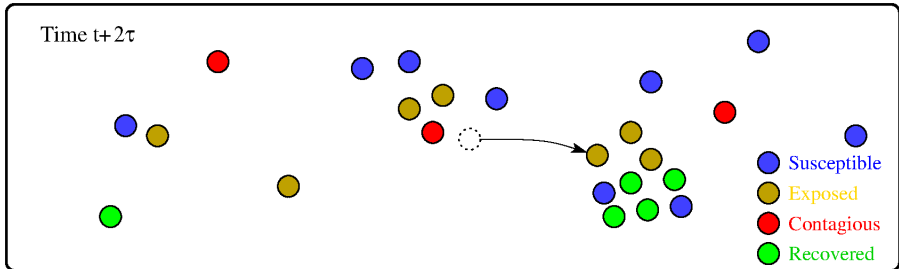
- ▶ Time  $t$ : superspreading event
- ▶ Time  $t + \tau$ : three people infected in the middle group
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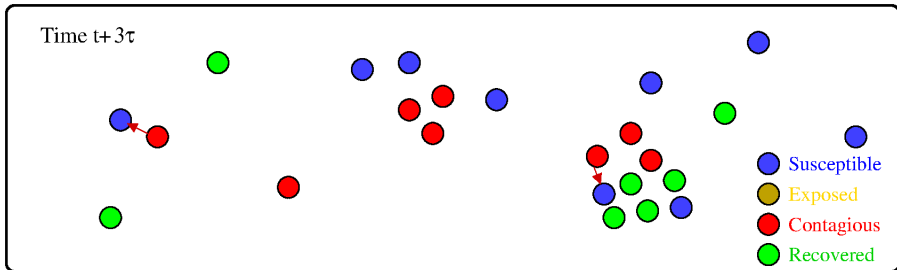
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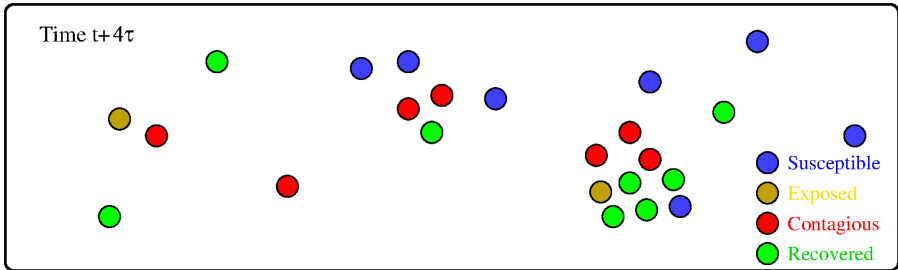
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We want to know: **#Infections**  $N_I(t) = N I(t)$ ,  
ideally its “age structure”  $I_0, I_1, \dots, I_t$

We do know: **#positive tests**  $N_T(t)$  (“cases”) and  
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Many uncertainties:

- ▶ The tests have an imperfect **sensitivity**  $P(\text{positive}|\text{infected}) \approx 99\%$
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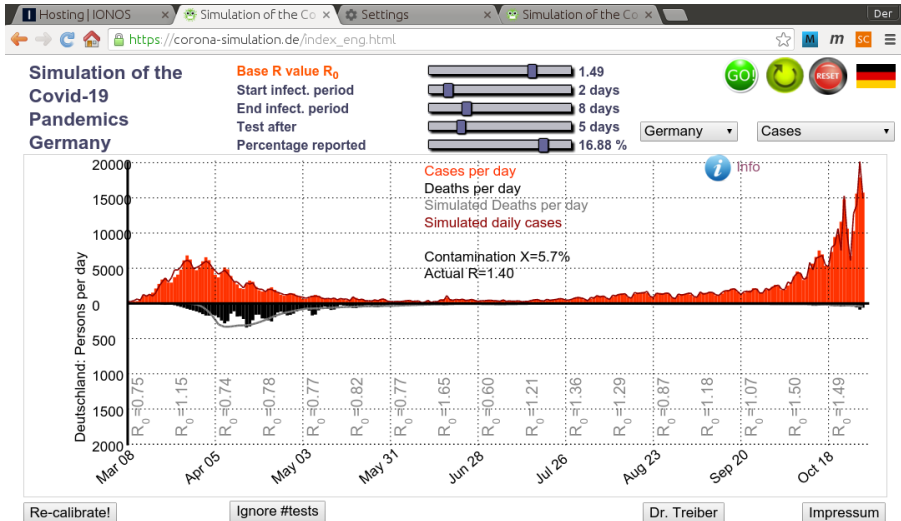
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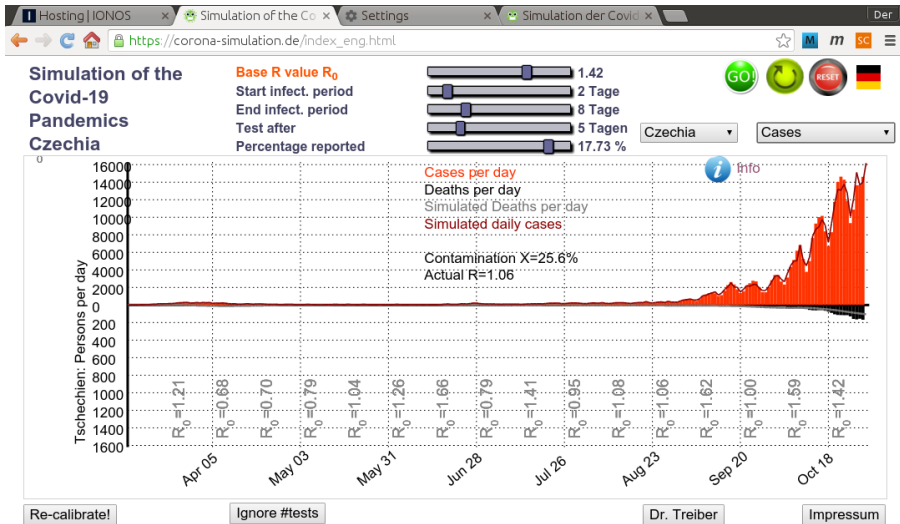


# Corona-simulation.de (as of Oct 30, 2020)

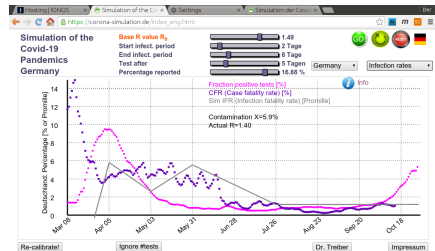
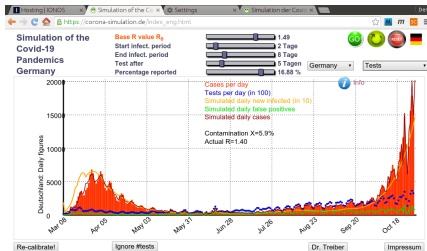
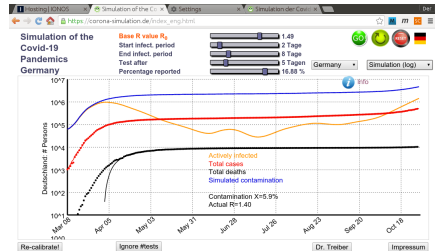
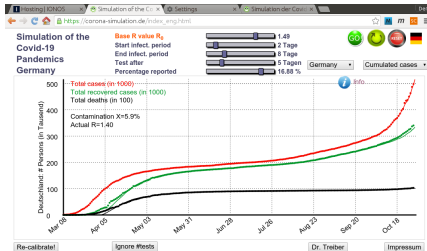
Interactive *data-driven* simulator based on an extended SIRM model



## Features I: different countries

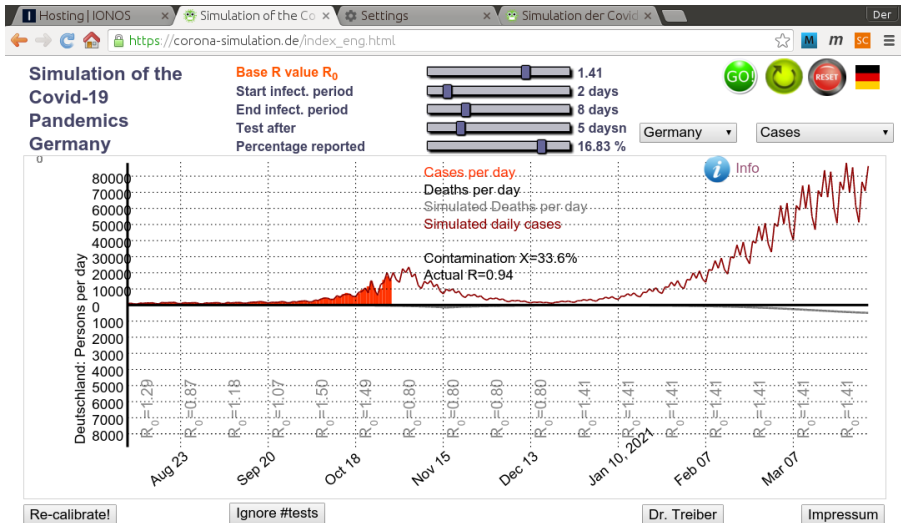


## Features II: different windows

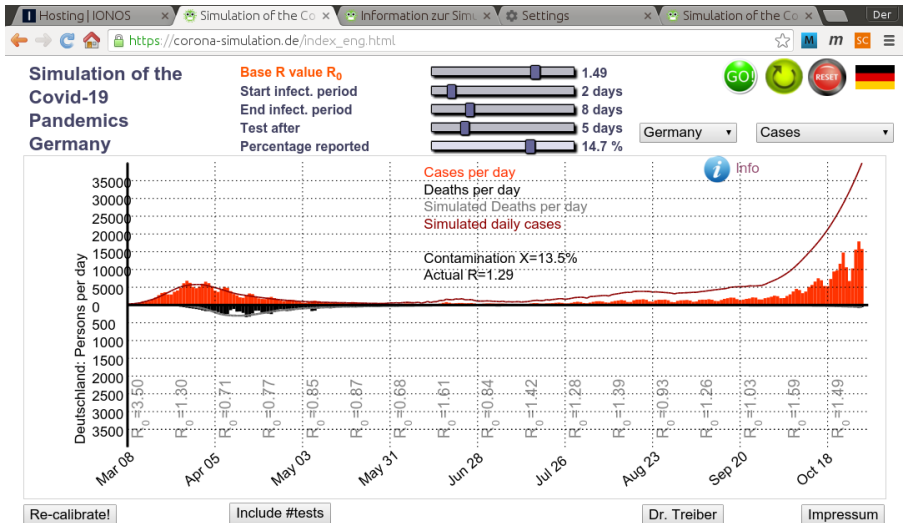




## Features III: "lockdown" shifts "wave"



## Features IV: sensitivity tests, e.g., ramping up #tests



## Summary/take-home messages

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  - ▶ tests of the model quality
  - ▶ doing useful things such as projection scenarios (do not forget Mark Twains quote about predictions!)
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