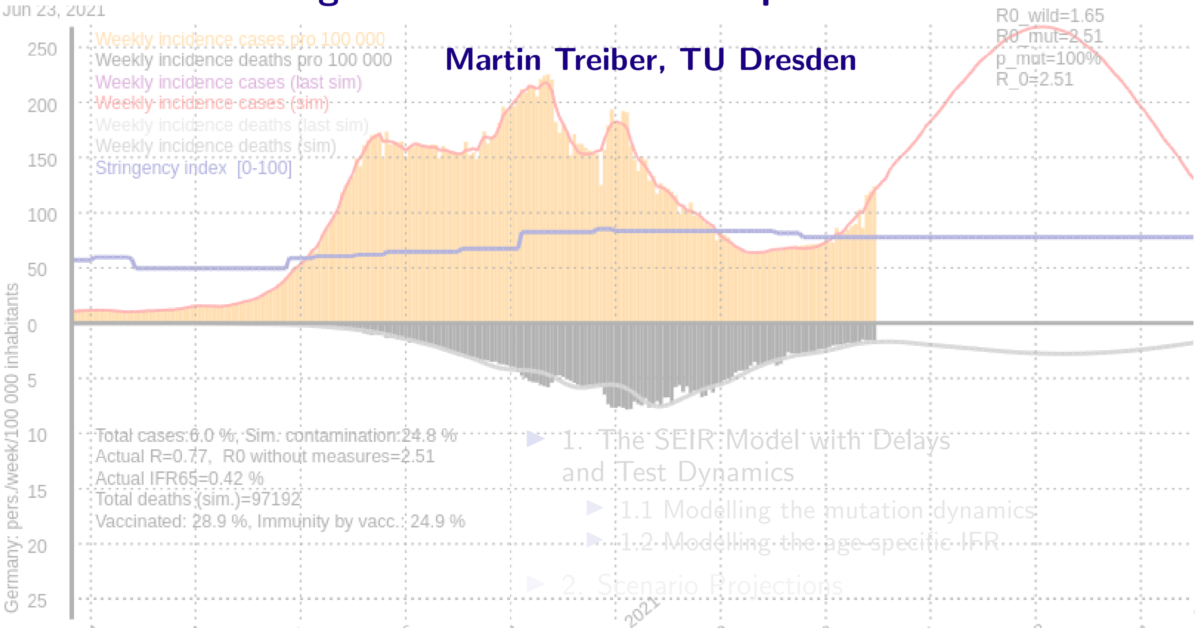
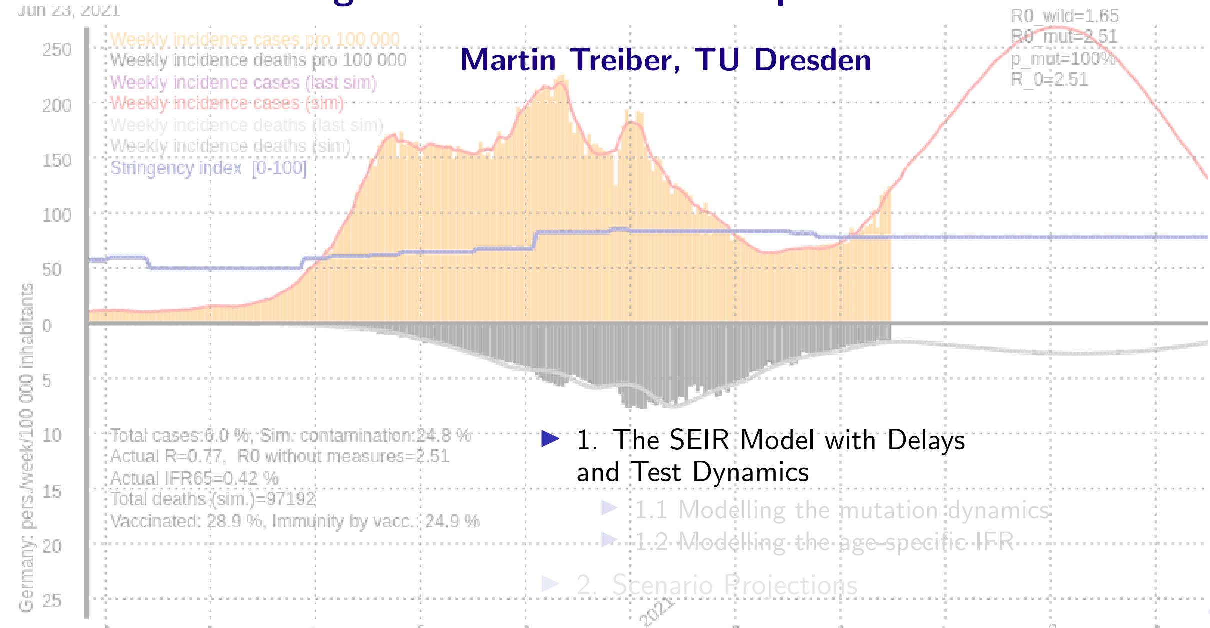
Scenario projections of the Covid-19 pandemic using a data-driven macroscopic model

Martin Treiber, TU Dresden



Scenario projections of the Covid-19 pandemic using a data-driven macroscopic model

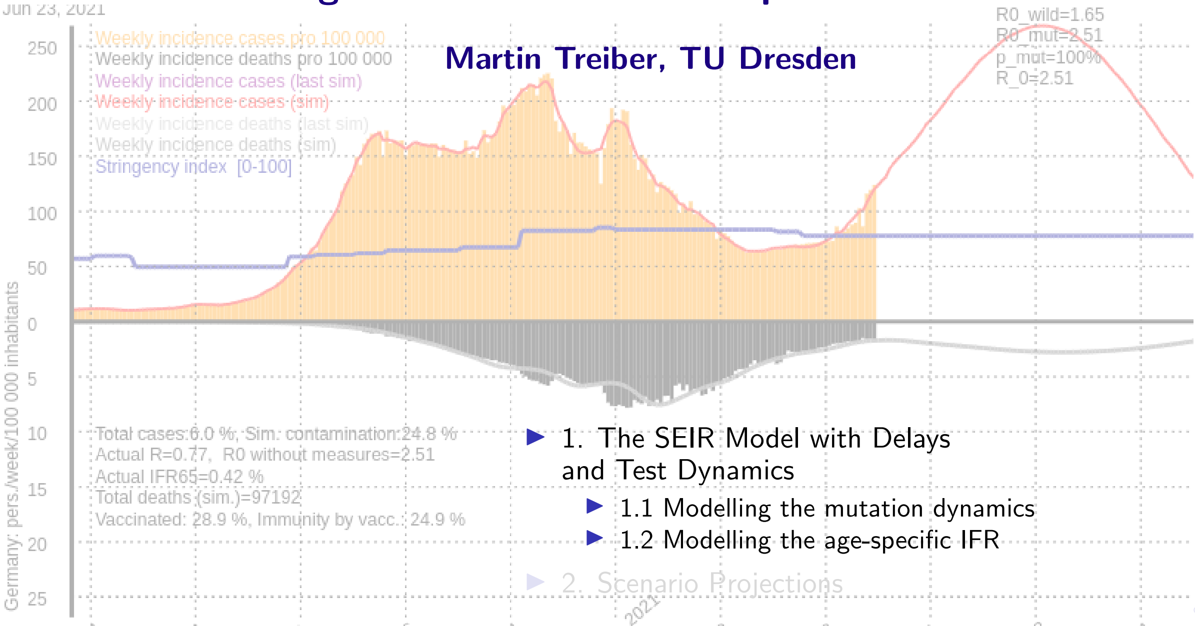
Martin Treiber, TU Dresden



- 1. The SEIR Model with Delays and Test Dynamics
  - 1.1 Modelling the mutation dynamics
  - 1.2 Modelling the age-specific IFR
- 2. Scenario Projections

Scenario projections of the Covid-19 pandemic using a data-driven macroscopic model

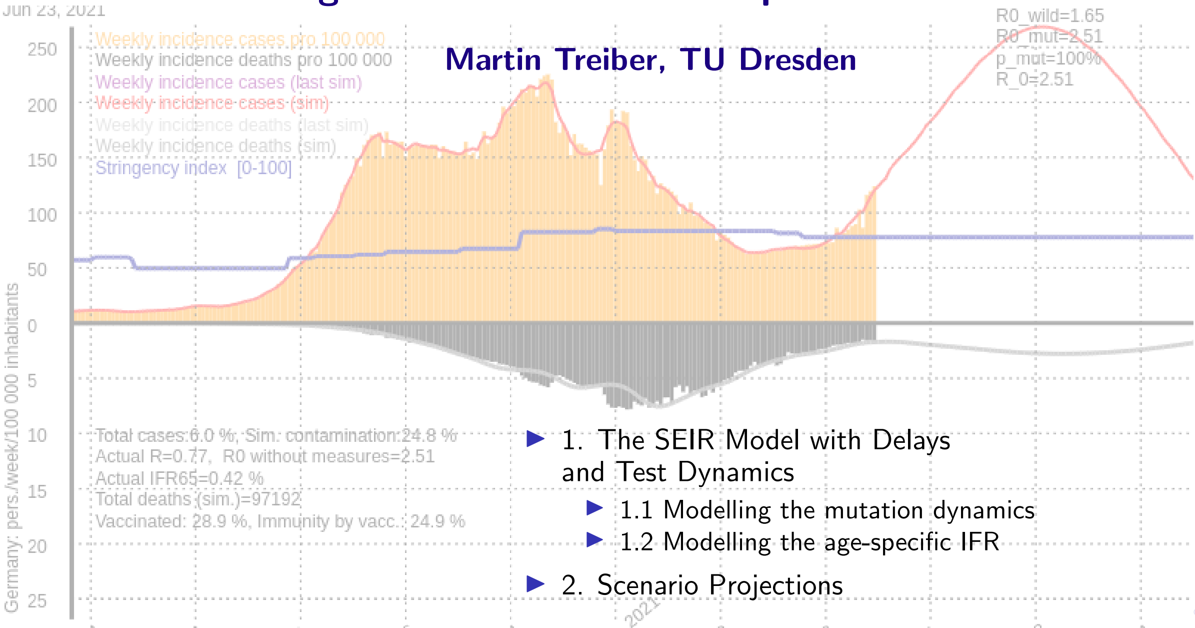
Martin Treiber, TU Dresden



- 1. The SEIR Model with Delays and Test Dynamics
  - 1.1 Modelling the mutation dynamics
  - 1.2 Modelling the age-specific IFR
- 2. Scenario Projections

Scenario projections of the Covid-19 pandemic using a data-driven macroscopic model

Martin Treiber, TU Dresden



- 1. The SEIR Model with Delays and Test Dynamics
  - 1.1 Modelling the mutation dynamics
  - 1.2 Modelling the age-specific IFR
- 2. Scenario Projections

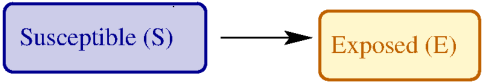
1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartments

Susceptible (S)

1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartments

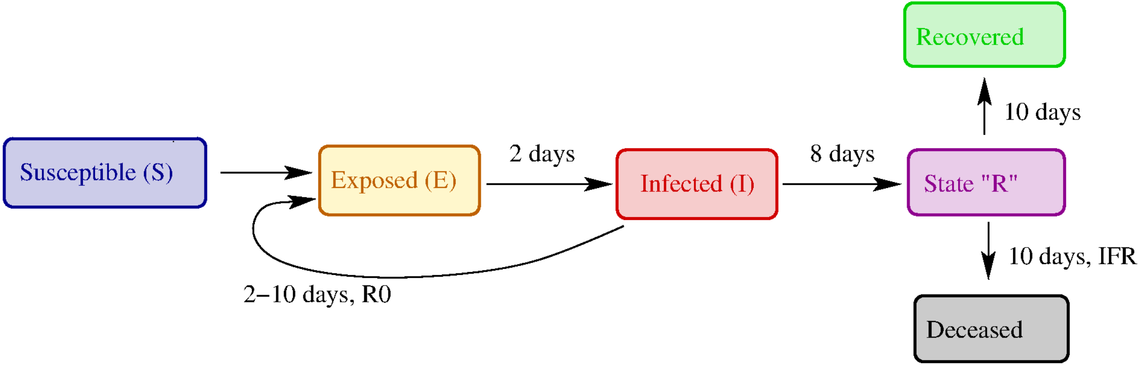


1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartments

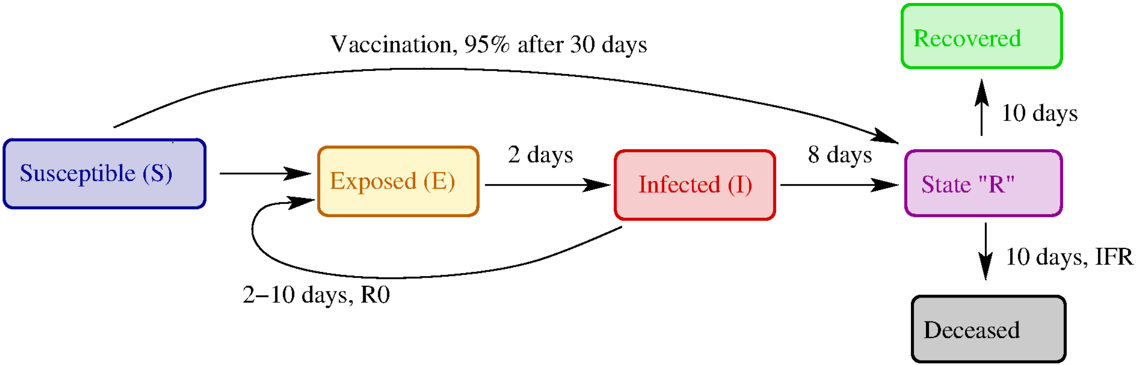
1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartments



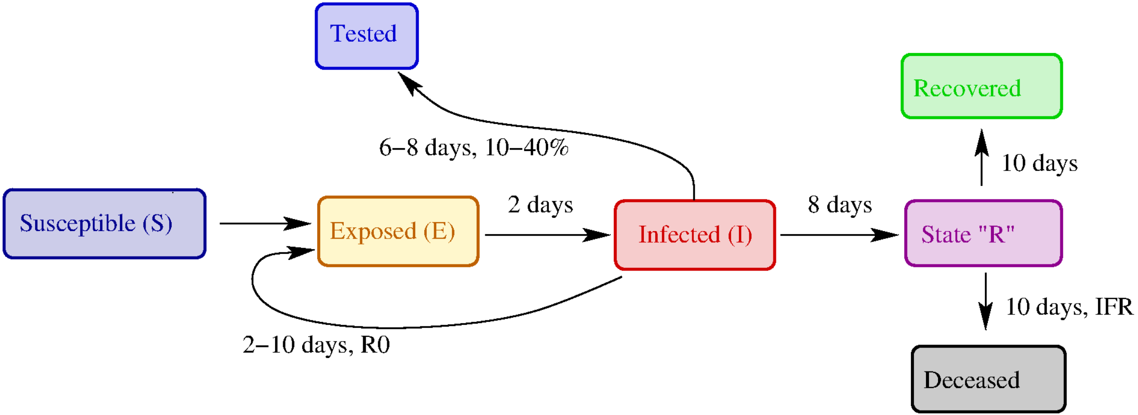
1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartiments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartiments



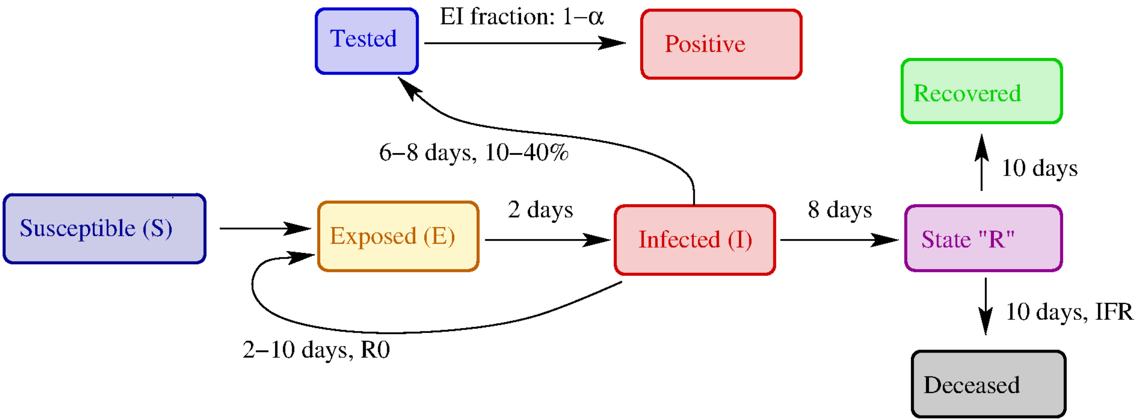
1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartiments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartiments



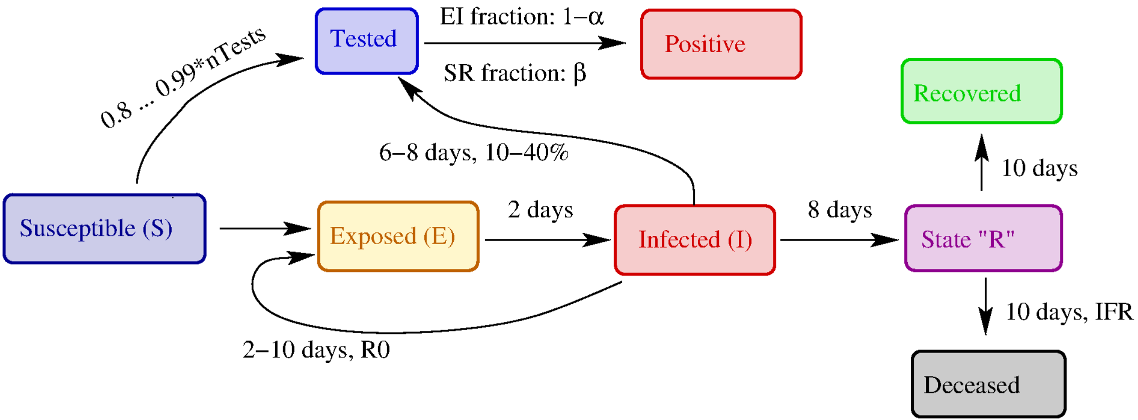
1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartiments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartiments



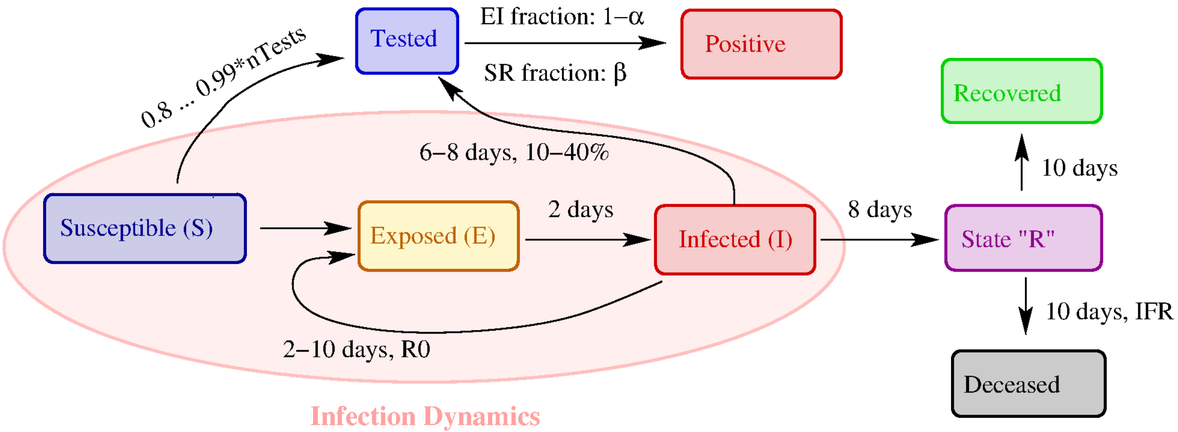
1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartiments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartiments



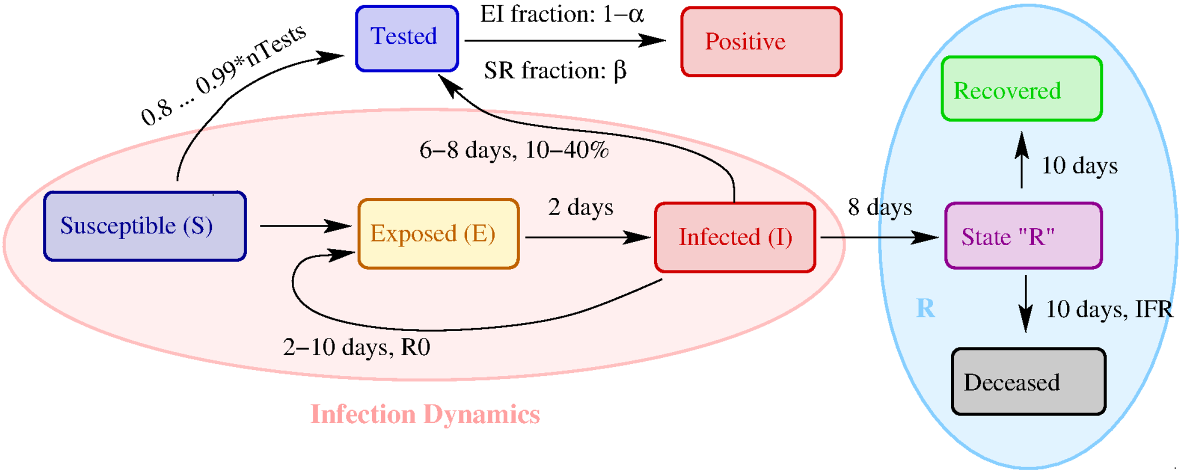
1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartments



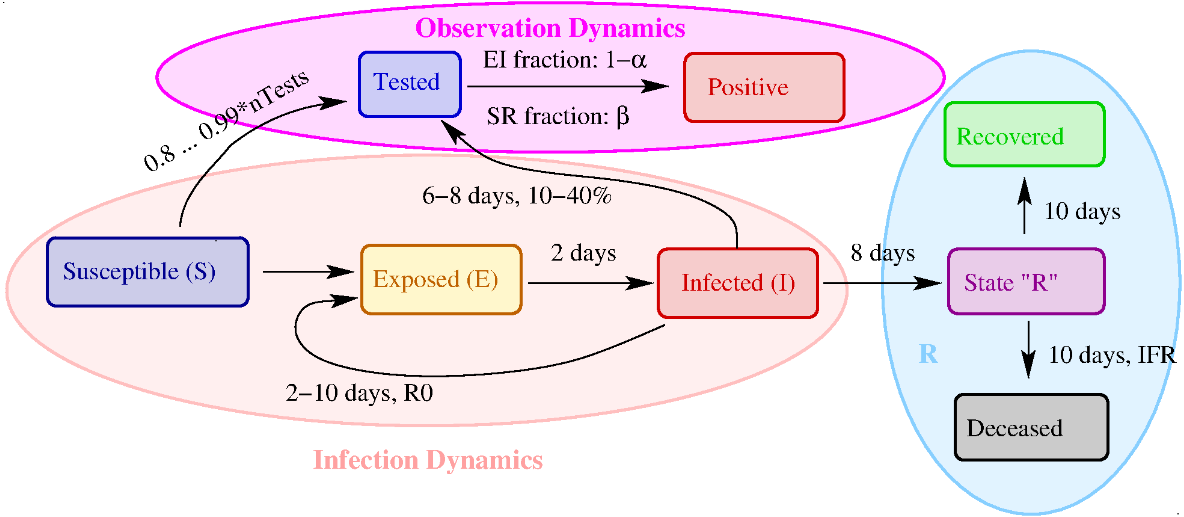
1. Macroscopic SEIR model with explicit delays and test dynamics

- Different infection *phases* (compartiments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartiments

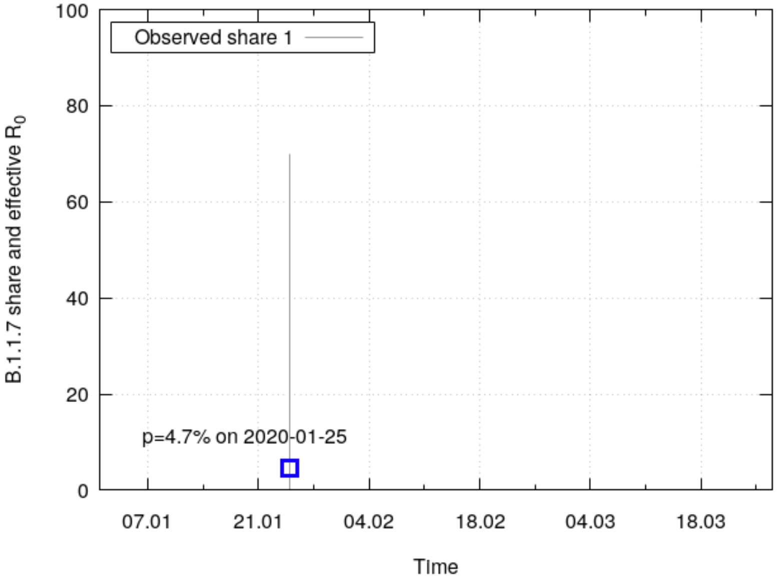


1. Macroscopic SEIR model with explicit delays and test dynamics

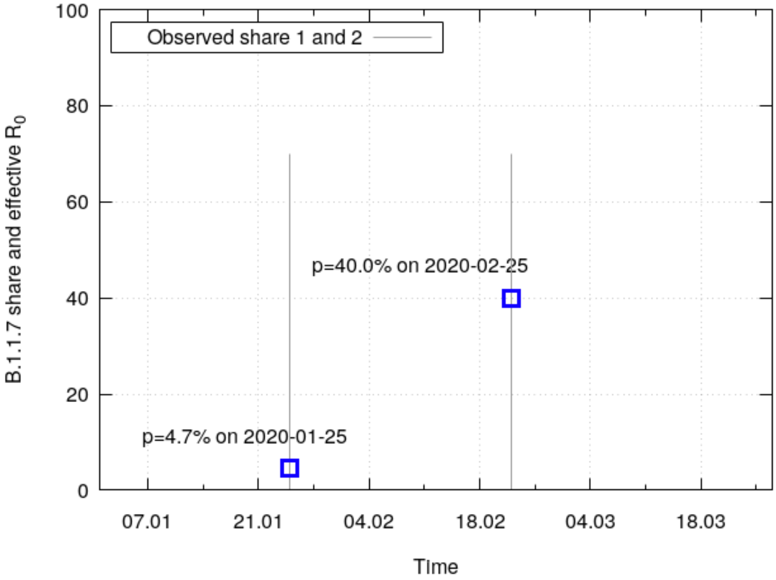
- Different infection *phases* (compartments) and their *transitions*
- Macroscopic dynamic variables: fractions of the population in the compartments



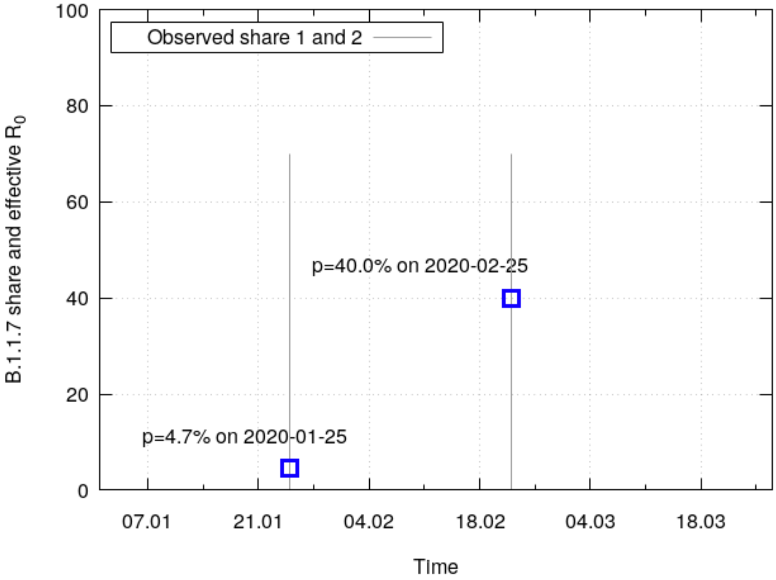
1.1 Modelling the mutation dynamics



1.1 Modelling the mutation dynamics



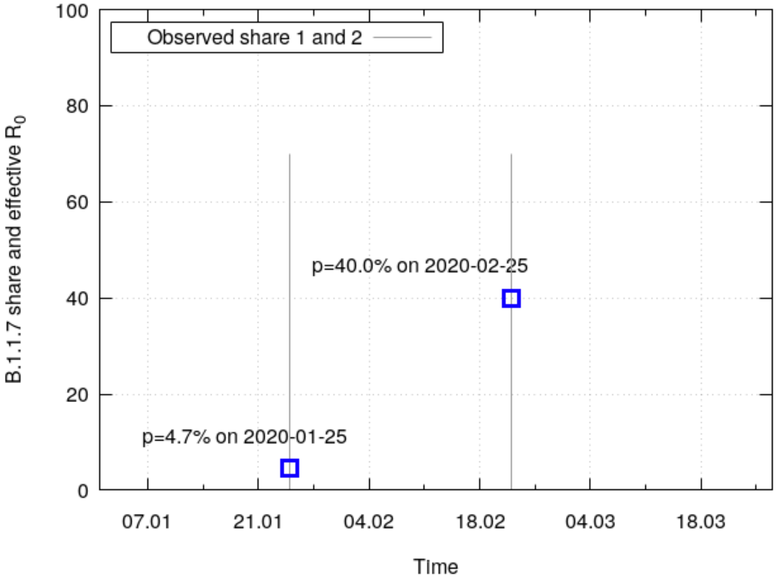
1.1 Modelling the mutation dynamics



Odds ratio

$$y = \frac{p}{1-p}$$

1.1 Modelling the mutation dynamics

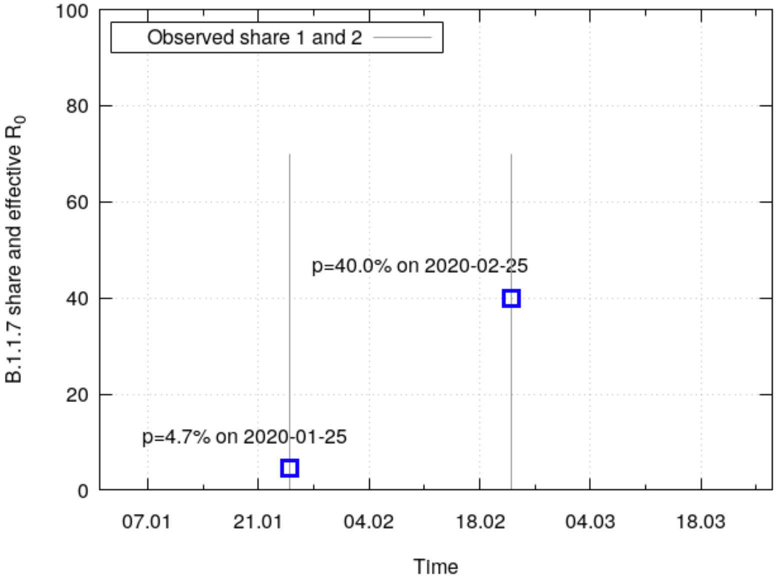


Odds ratio

$$y = \frac{p}{1-p}$$

$$y = y_0 e^{r_y t}$$

1.1 Modelling the mutation dynamics



Odds ratio

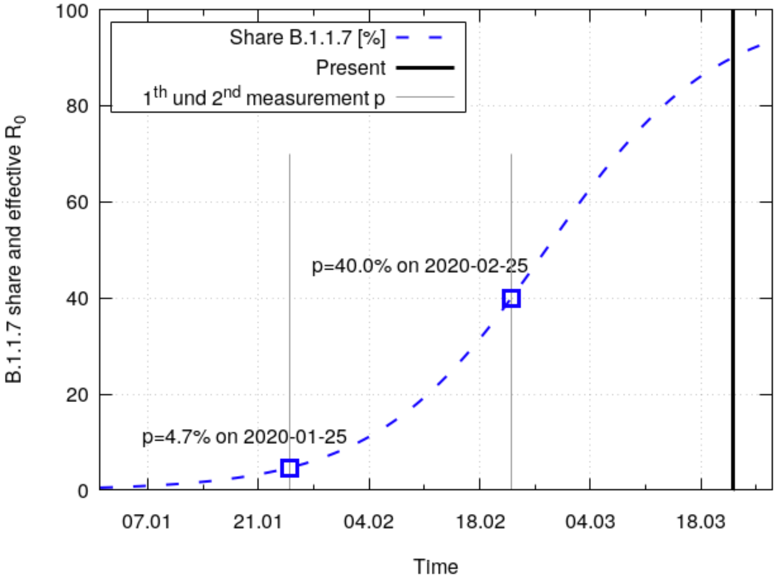
$$y = \frac{p}{1-p}$$

$$y = y_0 e^{r_y t}$$

Estimation growth rate

$$r_y \approx \frac{\ln y(t_2) - \ln y(t_1)}{t_2 - t_1}$$

1.1 Modelling the mutation dynamics



Odds ratio

$$y = \frac{p}{1-p}$$

$$y = y_0 e^{r_y t}$$

Estimation growth rate

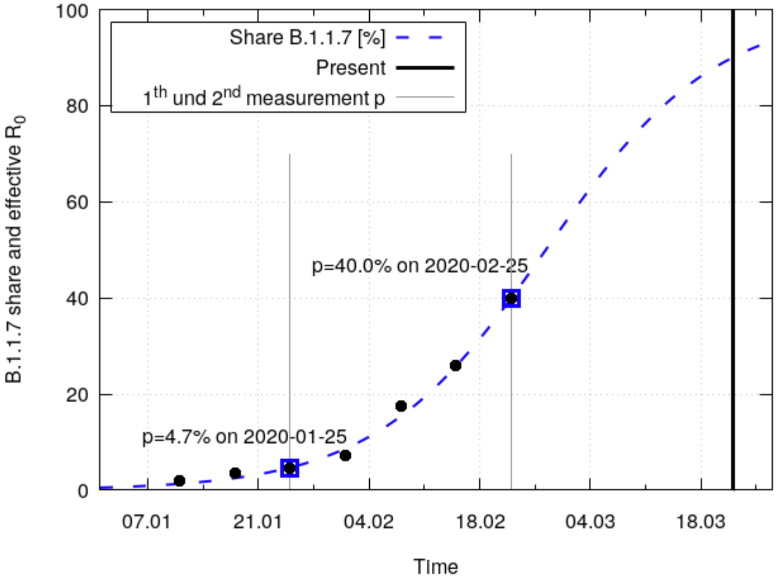
$$r_y \approx \frac{\ln y(t_2) - \ln y(t_1)}{t_2 - t_1}$$

Estimation B.1.1.7 share

$$p = \frac{y}{1+y}$$

$$= \frac{p_0 e^{r_y t}}{1 + p_0 \left(e^{r_y t} - 1\right)}$$

1.1 Modelling the mutation dynamics



Odds ratio

$$y = \frac{p}{1-p}$$

$$y = y_0 e^{r_y t}$$

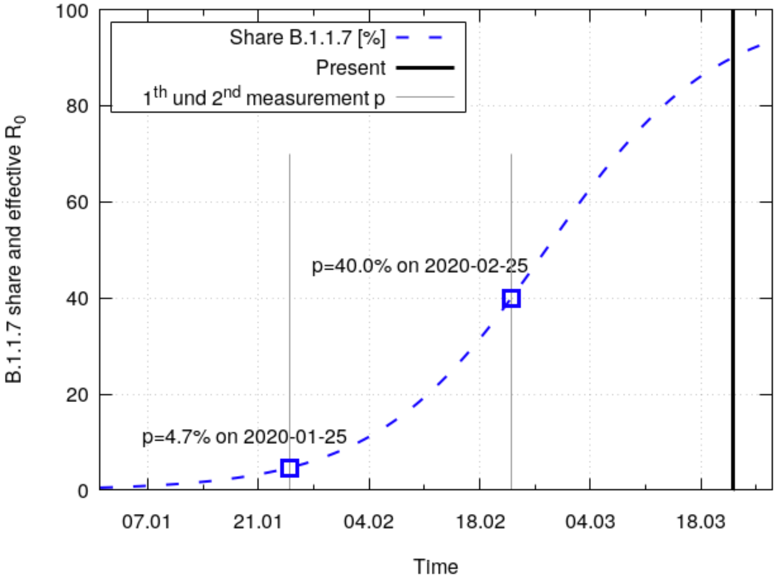
Estimation growth rate

$$r_y \approx \frac{\ln y(t_2) - \ln y(t_1)}{t_2 - t_1}$$

Estimation B.1.1.7 share

$$p = \frac{y}{1+y} = \frac{p_0 e^{r_y t}}{1 + p_0 \left(e^{r_y t} - 1\right)}$$

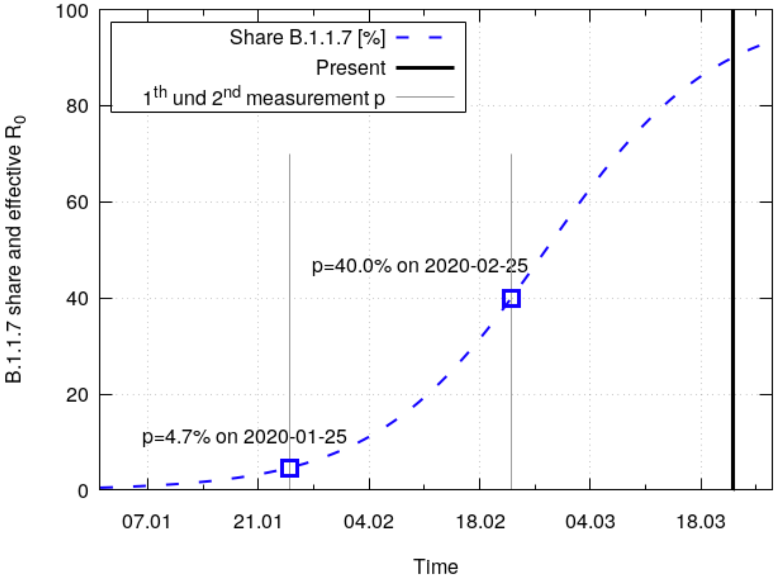
1.1 Modelling the mutation dynamics



τ: generation time

$$R_0^{\text{mut}}/R_0^{\text{wild}} = \tau r_y + 1$$

1.1 Modelling the mutation dynamics



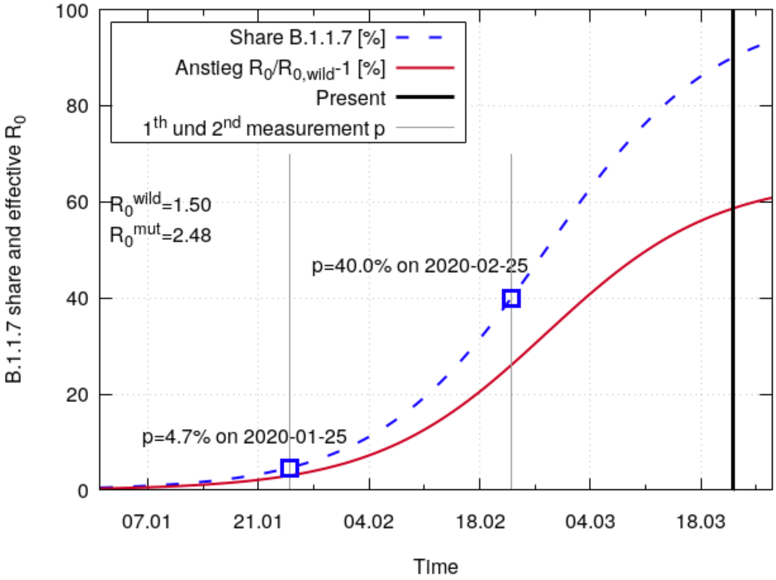
τ: generation time

$$R_0^{\text{mut}}/R_0^{\text{wild}} = \tau r_y + 1$$

Effective R_0:

$$R_0 = (1-p)R_0^{\text{wild}} + pR_0^{\text{mut}}$$

1.1 Modelling the mutation dynamics



τ: generation time

$$R_0^{\text{mut}}/R_0^{\text{wild}} = \tau r_y + 1$$

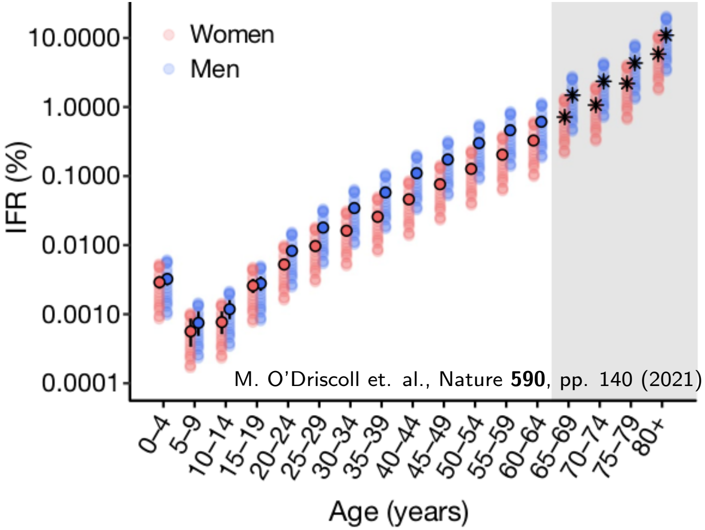
Effective R_0:

$$R_0 = (1-p)R_0^{\text{wild}} + pR_0^{\text{mut}}$$

$\Rightarrow$ $R_0^{\text{wild}}, R_0^{\text{mut}}$ known

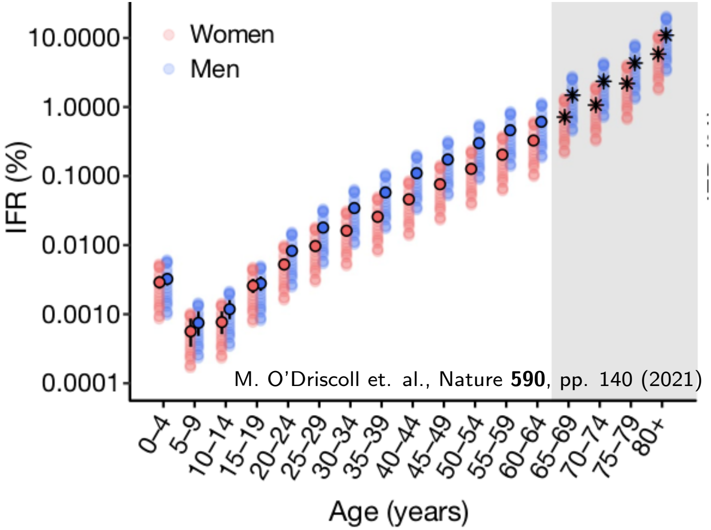
$\Rightarrow$ forecast $R_0(t)$

1.2 Modelling the age-specific infection fatality rate (IFR)



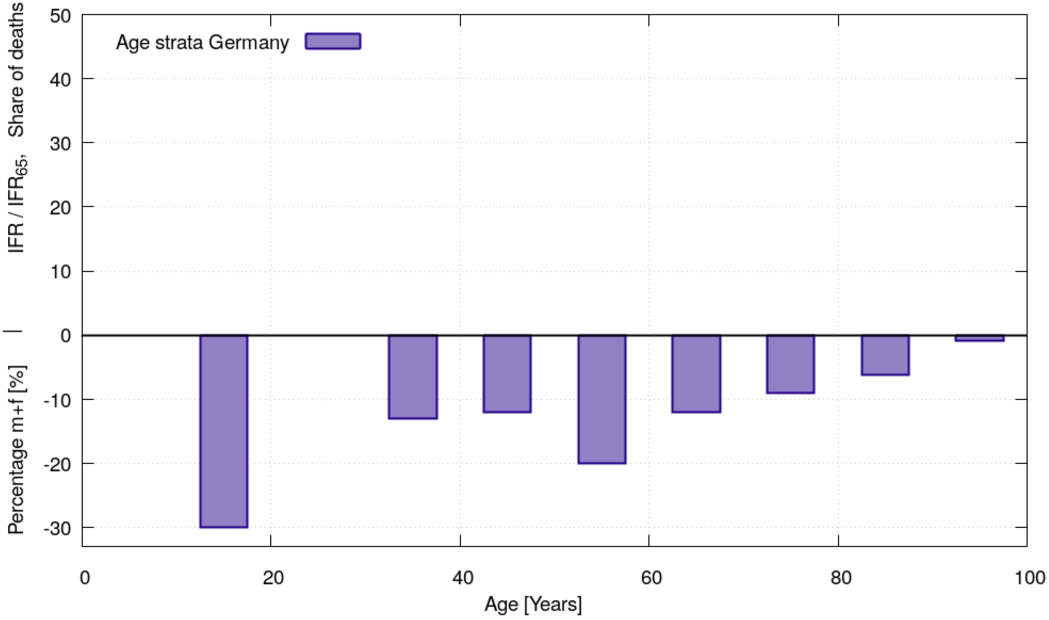
- The IFR exhibits a nearly exponential growth with the age
- The same is true for the case fatality rate (CFR) and for the total one-year fatality
- The gender difference is weak (corresponds to ≈ 5 years)
- The infection probability exhibts a much weaker age dependency
- ⇒ leave infection spread model unchanged (enables interactive just-in-time calibration) and calculate the IFR in age strata afterwards

1.2 Modelling the age-specific infection fatality rate (IFR)

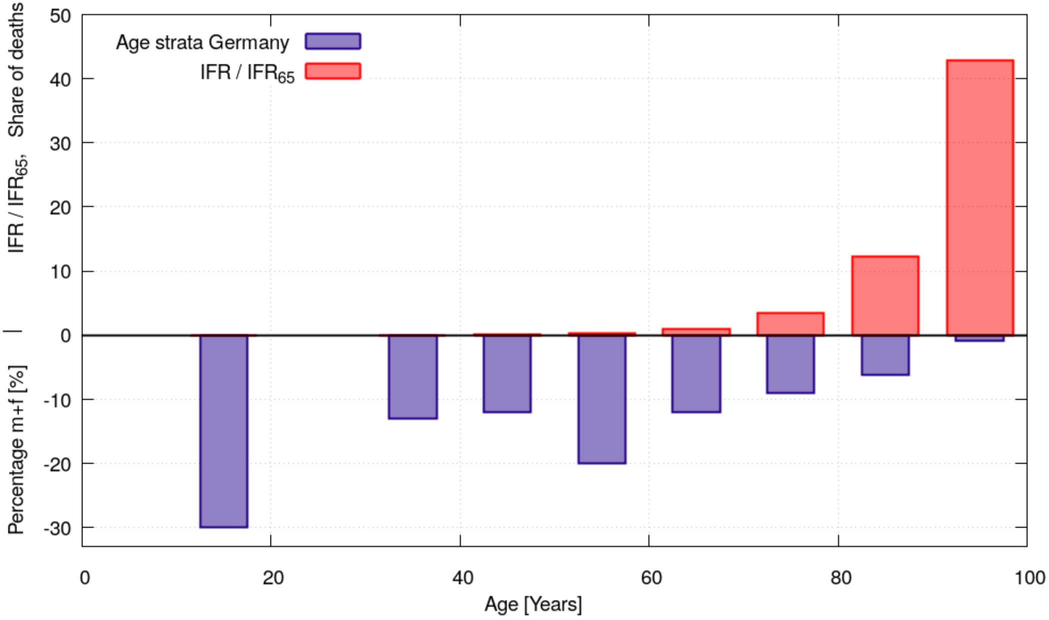


- The IFR exhibits a nearly exponential growth with the age
- The same is true for the case fatality rate (CFR) and for the total one-year fatality
- The gender difference is weak (corresponds to $\approx$ 5 years)
- The infection probability exhibts a much weaker age dependency
- $\Rightarrow$ leave infection spread model unchanged (enables interactive just-in-time calibration) and calculate the IFR in age strata afterwards

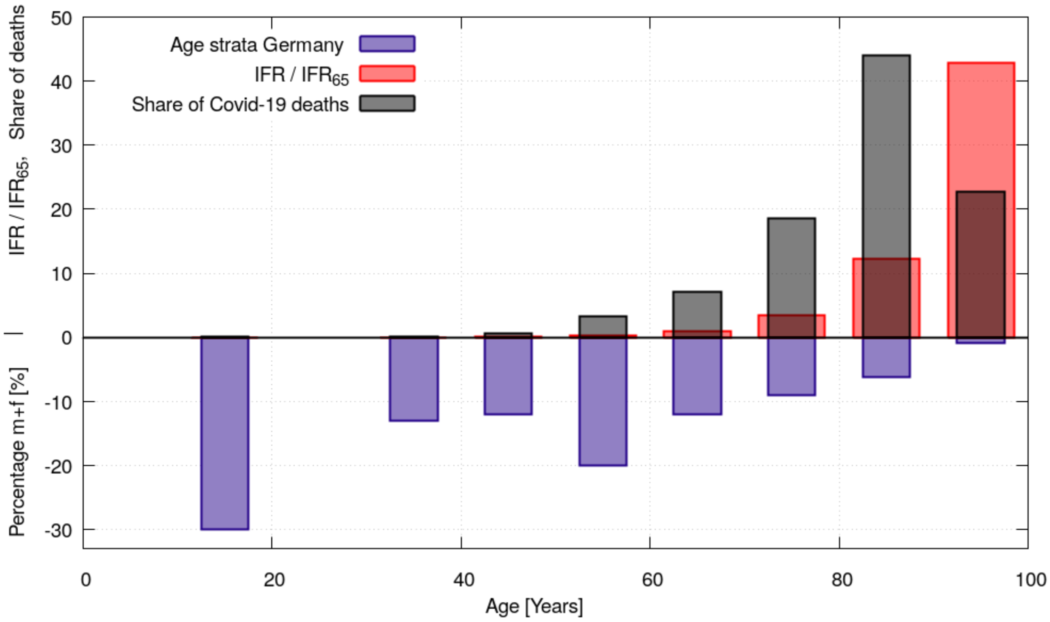
Calculating the global IFR as multiple of IFR_{65}



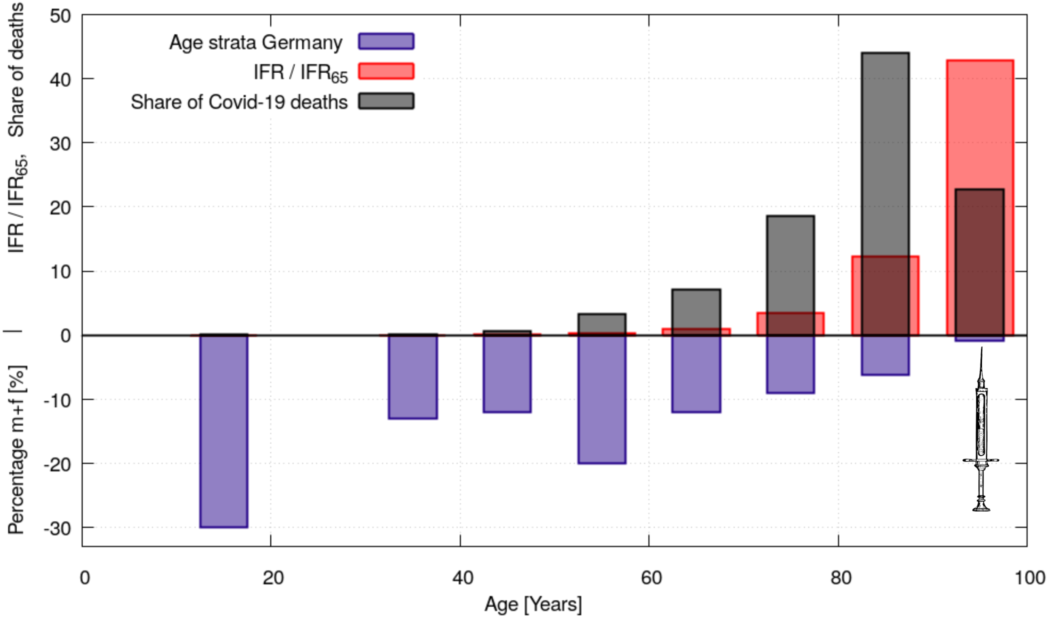
Calculating the global IFR as multiple of IFR_{65}



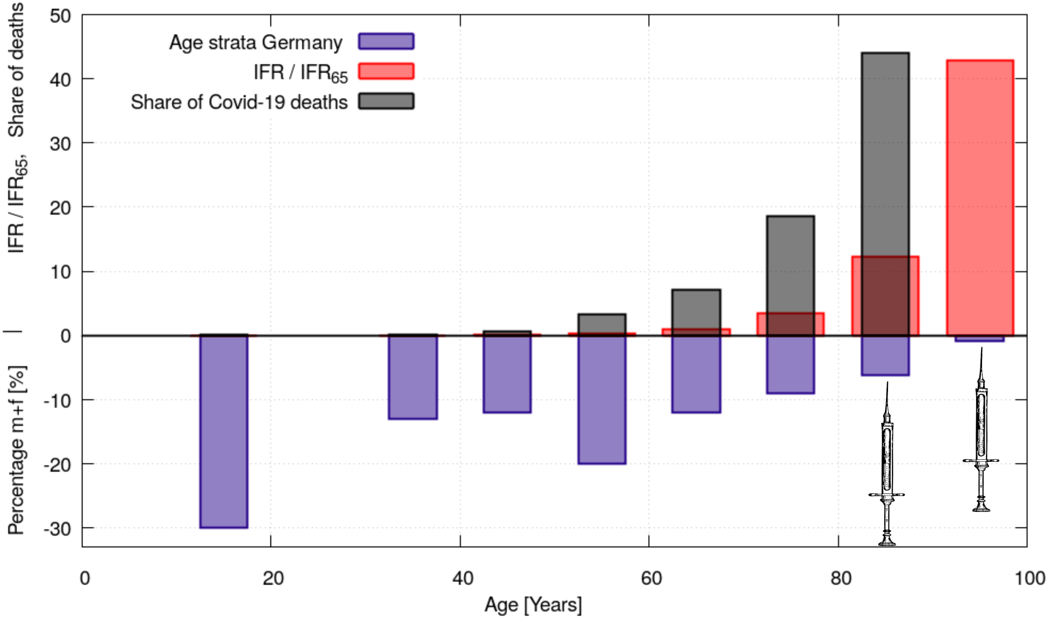
Calculating the global IFR as multiple of IFR_{65}



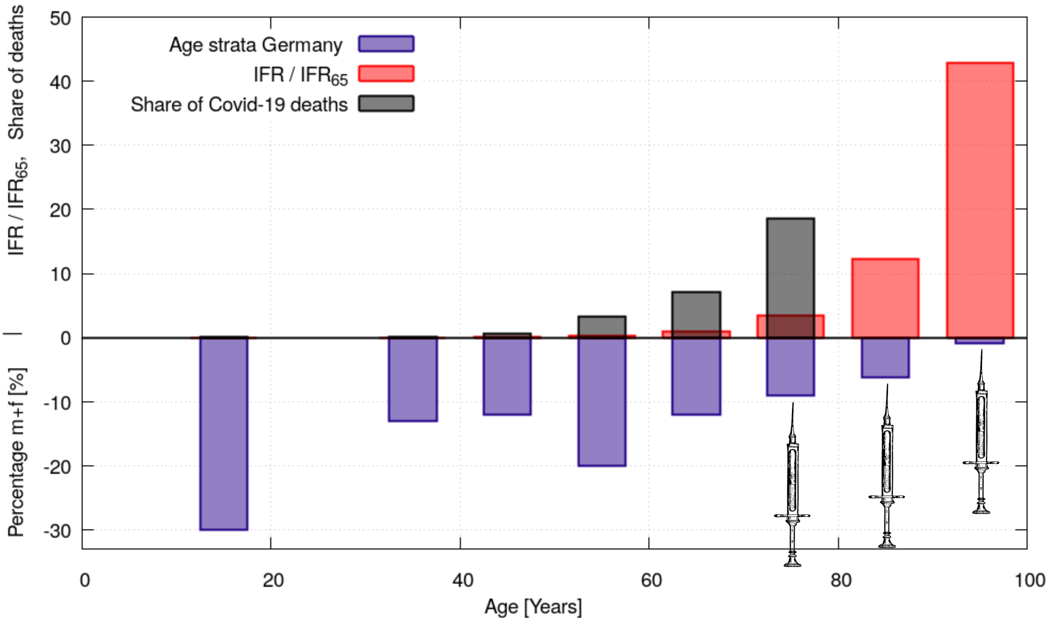
Calculating the global IFR as multiple of IFR_{65}



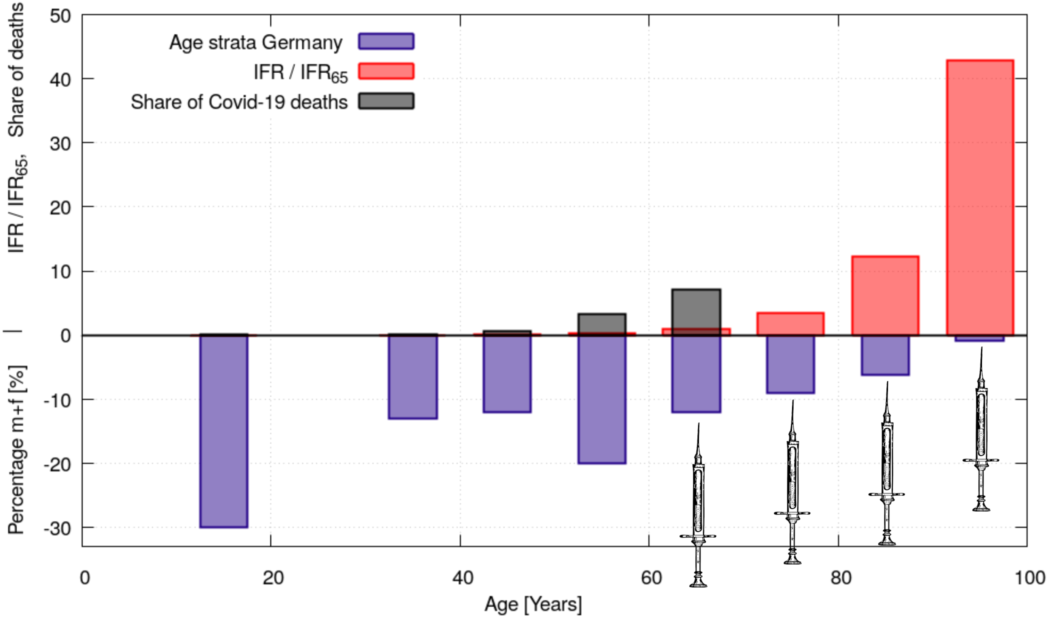
Calculating the global IFR as multiple of IFR_{65}



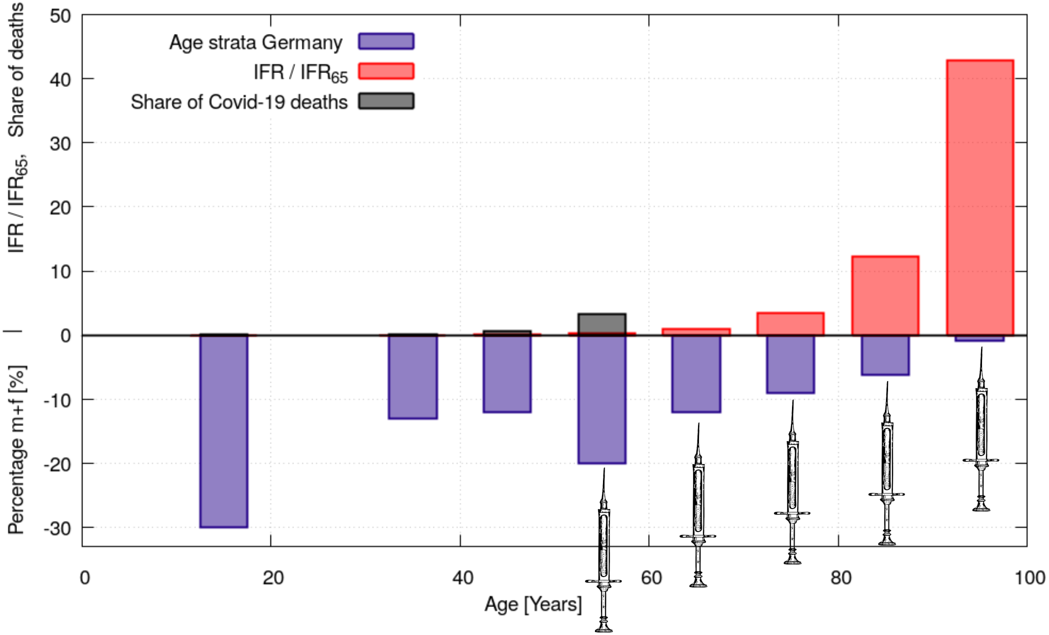
Calculating the global IFR as multiple of IFR_{65}



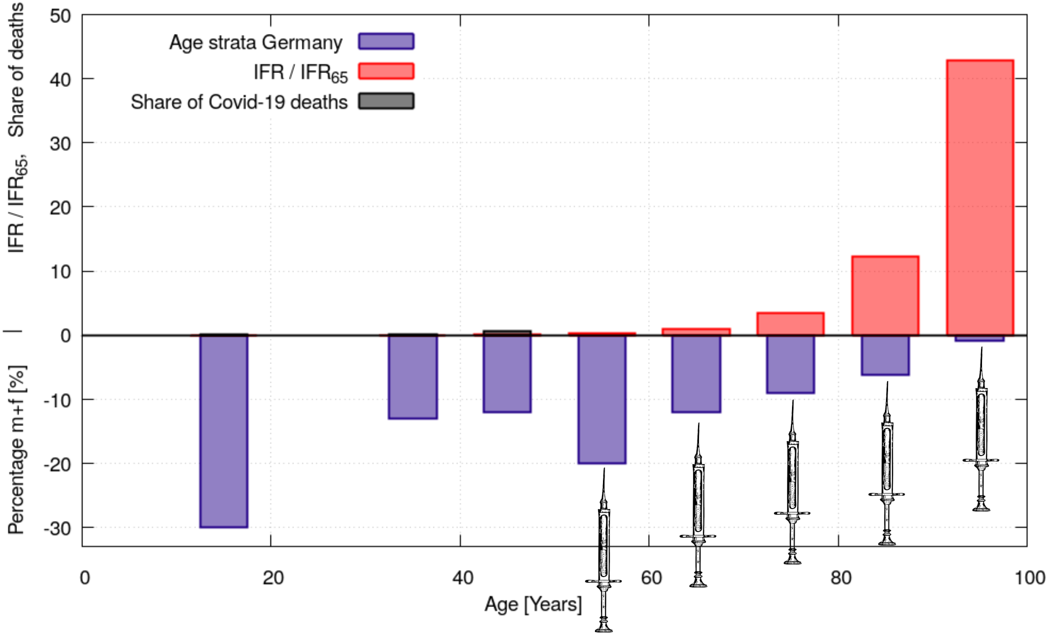
Calculating the global IFR as multiple of IFR_{65}



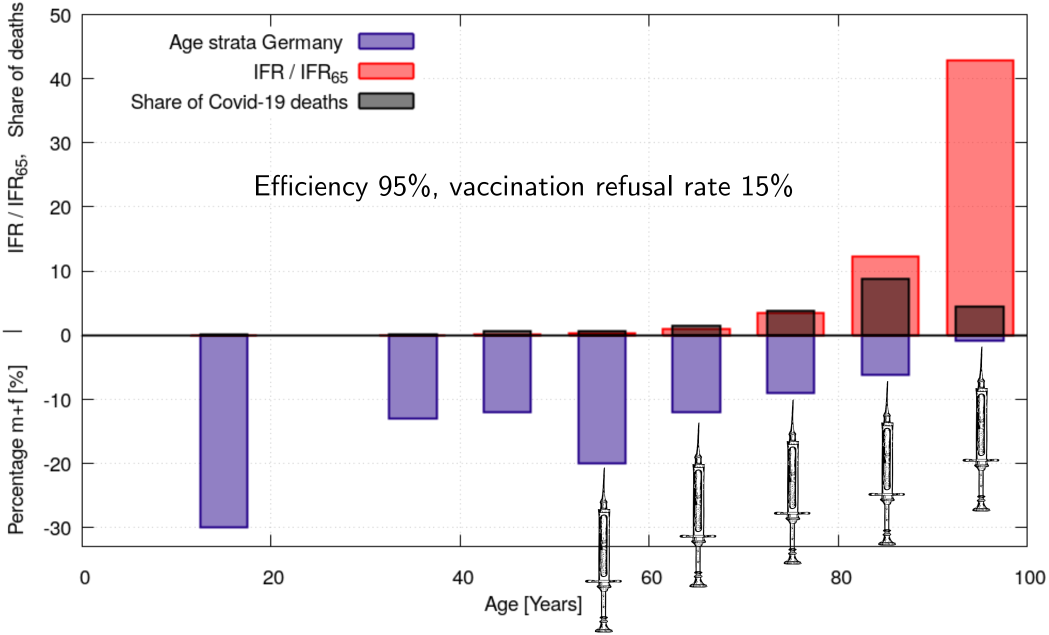
Calculating the global IFR as multiple of IFR_{65}



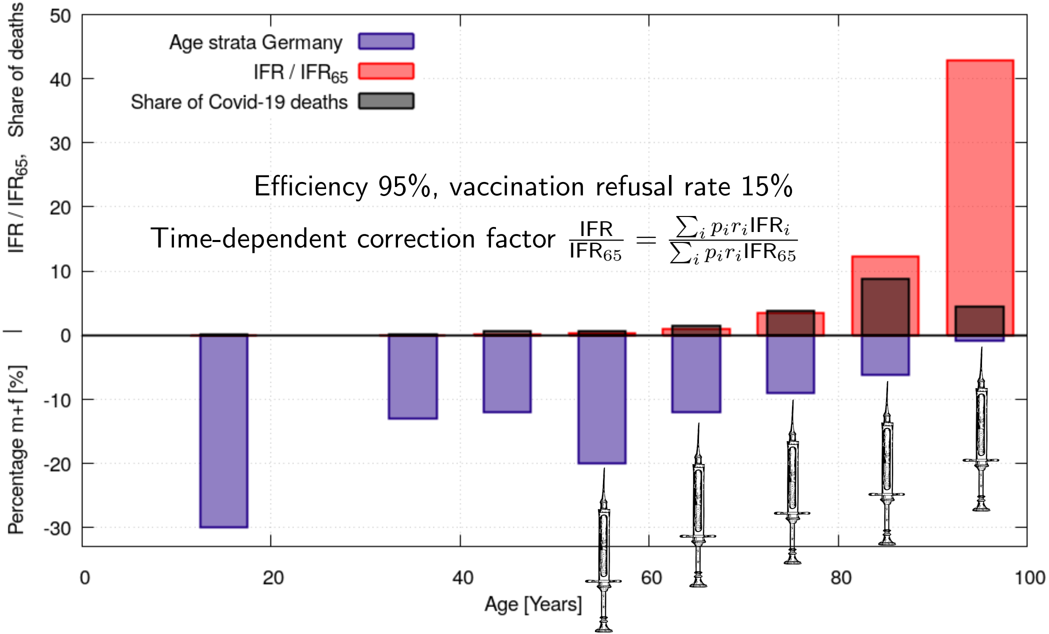
Calculating the global IFR as multiple of IFR_{65}



Calculating the global IFR as multiple of IFR_{65}



Calculating the global IFR as multiple of IFR_{65}



Interactive simulations