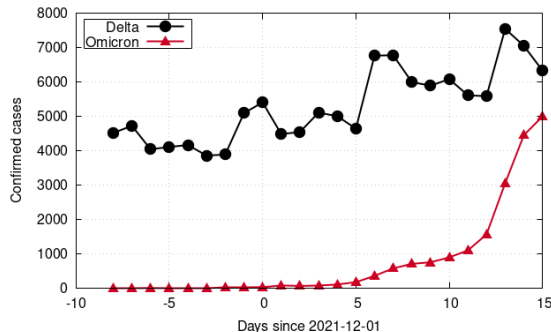
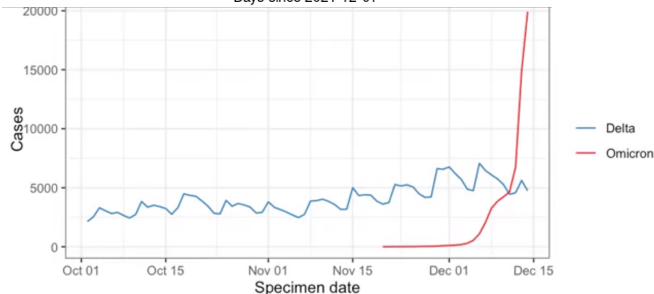


# 1. Delta and Omicron: Observations

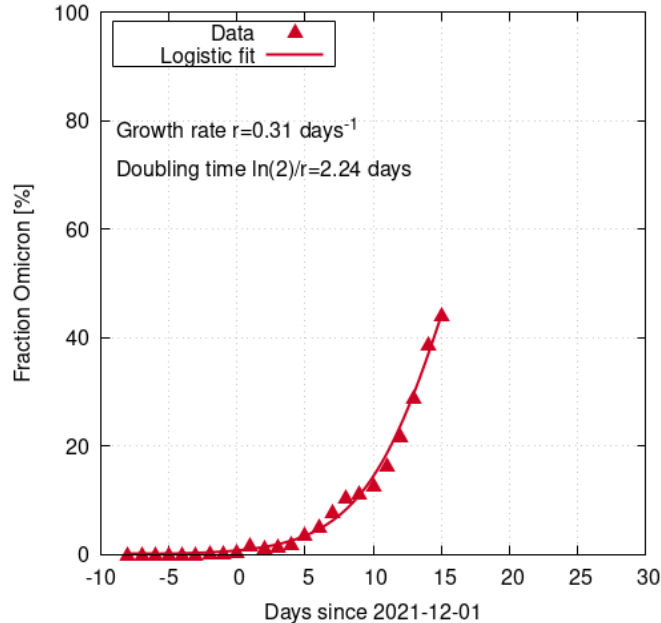


- ▶ Data from Danmark and London
- ▶ The Delta and Omicron variants coexist without directly affecting each other
- ▶ Indirect interaction via competing for common resources, i.e., *first come, first served*



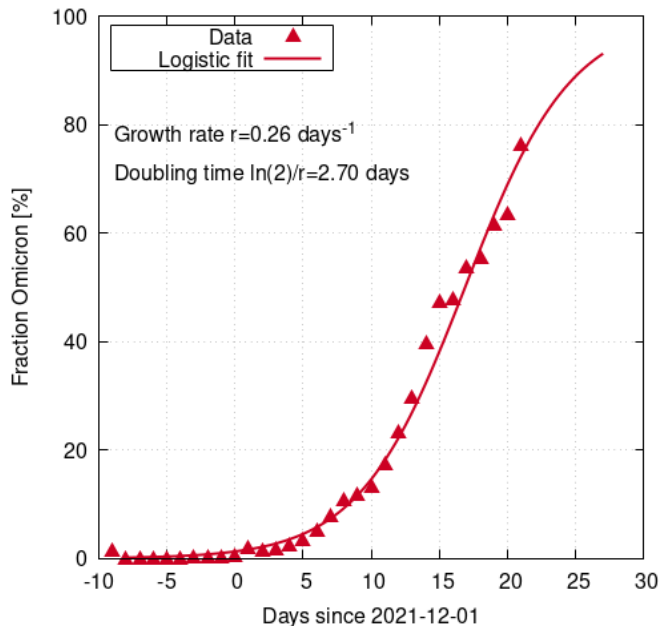
Data: UKHSA. SGTF proportions from daily update combined with case numbers from coronavirus.data.gov.uk.

## 2. Rate $r$ of the logistic growth of the Omicron share



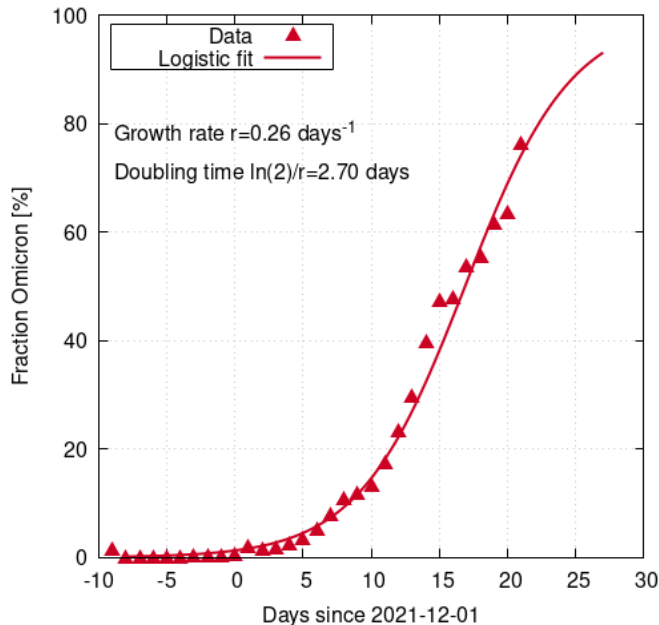
- The share of Omicron can be well described by a logistic function with growth rate  $r$

## Update and: how to determine the rate $r$



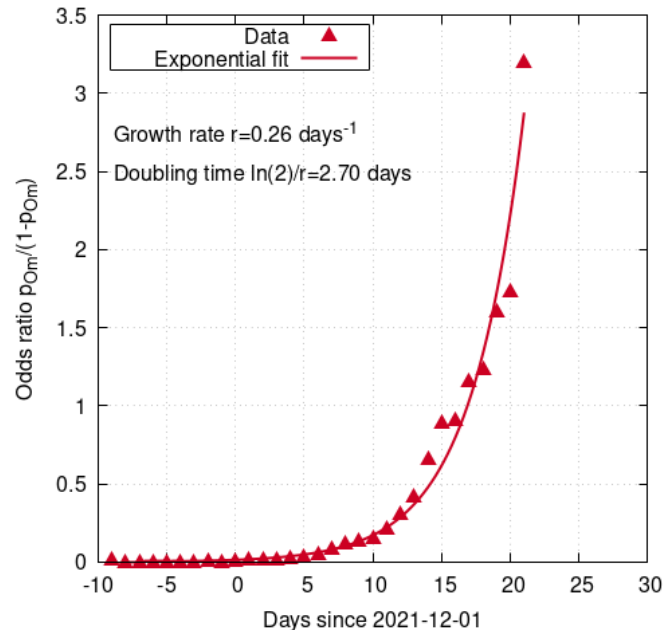
► Data update.

## Update and: how to determine the rate $r$



► Data update. How to get the curve?

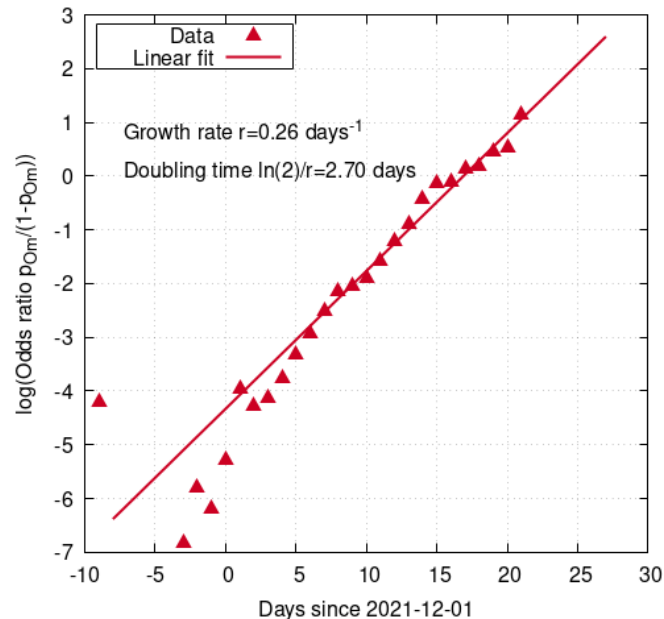
## Update and: how to determine the rate $r$



- Data update. How to get the curve?
- Transform the observed Omicron share  $p$  into the **odds ratio**  $y = p/(1 - p)$
- From Observation 1 (coexistence), it follows that the odds ratio grows exponentially:

$$y(t) = y_0 e^{rt}$$

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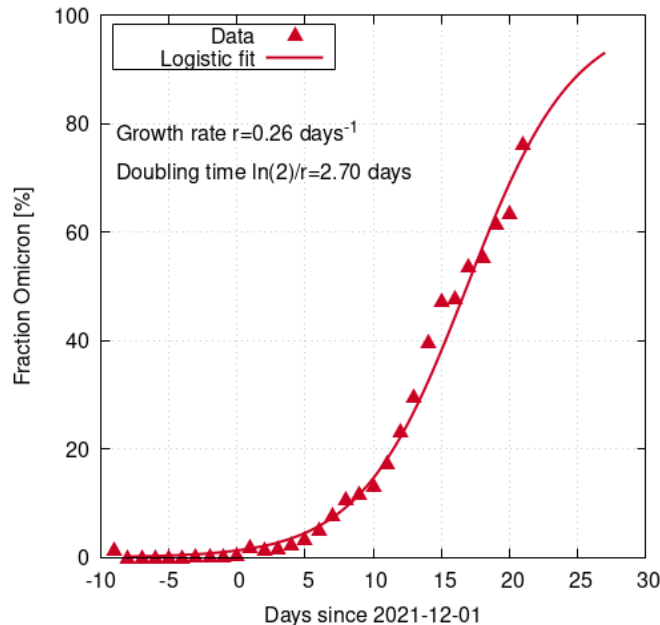
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- Transforming back gives the s-shaped predicted Omicron share (logistic function)

$$p(t) = \frac{y(t)}{1 + y(t)}$$

### 3. Relation between the logistic growth rate $r$ and the reproduction numbers

Assumptions:

- ▶ Neither positive nor negative **cross effects**: Each variant acts on its own (using common resources of susceptible humans)
- ▶ The Delta and Omicron variants have different **base reproduction numbers**  $R_{10}$  and  $R_{20}$  and different **generation times**  $T_1$  and  $T_2$ , respectively (e.g.,  $R_{10} = 5$ ,  $T_1 = 5$  days,  $T_2 = 4$  days)
- ▶ The **immunities**  $I_1$  and  $I_2$  (including vaccinations and past infections) against Delta and Omicron are generally different
- ▶ The **reduction factors**  $f_m$  by isolation measures and the **seasonal factor**  $f_s$  are common
- ▶ All factors influencing the effective reproduction number  $R$  are multiplicative. Daily new infections  $x_1$  (Delta) and  $x_2$  (Omicron) develop according to following

$$\begin{array}{ll} \text{Infection dynamics} & x_1(t_0 + T_1) = R_1 x_1(t_0) = R_{10}(1 - I_1) f_m f_s x_1(t_0), \\ \text{as } f(R_{01}, R_{02}, \text{ factors}): & x_2(t_0 + T_2) = R_2 x_2(t_0) = R_{20}(1 - I_2) f_m f_s x_2(t_0) \end{array} \quad (1)$$



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Assuming continuous infections (slowly varying rates), we can write (1) as

$$x_1(t) = x_1(0)R_1^{t/T_1} = x_1(0) \exp\left(\frac{t}{T_1} \ln R_1\right) \equiv x_1(0) \exp(r_1 t),$$

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How does the odds  $y = x_2/x_1$  evolve?

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## 4. Determining the Omicron base reproduction rate from the logistic growth rate

Just use Relation (3) and insert the dependence of the actual growth rates  $R_1$  and  $R_2$  as a function of the base reproduction numbers  $R_{01}$ ,  $R_{02}$  and factors from (1)

After some manipulations ...

$$\text{Observed Omicron } R_{02}: \quad R_{20} = e^{rT_2} (f_m f_s)^{\gamma-1} \frac{(R_{10}(1 - I_1))^\gamma}{1 - I_2}, \quad \gamma = \frac{T_2}{T_1} \quad (4)$$

- For equal generation times  $T_1 = T_2 = T$ , the measures and the seasonal effects drop out and  $r$  depends only on the past infection and vaccination immunities (remains time dependent since the immunities change):

$$T_1 = T_2 = T \quad \Rightarrow \quad R_{20} = e^{rT} \frac{R_{10}(1 - I_1)}{1 - I_2}$$

Example:  $e^{rT} = 3$ ,  $R_{10} = 4$ ,  $I_1 = 0.6$ ,  $I_2 = 0.2$ ,  $R_{20} = 3/2 R_{10} = 6$

- With neither immunities nor measures nor season effects but  $T_2 = 0.5T_1$  ( $\gamma = 0.5$ ), we have  $R_{20} = e^{rT_2} \sqrt{R_{10}}$ , e.g., for  $e^{rT_2} = 2$  and  $R_{01} = 4$ , we have  $R_{02} = R_{01} = 4$
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Example:  $e^{rT} = 3$ ,  $R_{10} = 4$ ,  $I_1 = 0.6$ ,  $I_2 = 0.2$ ,  $R_{20} = 3/2 R_{10} = 6$

- With neither immunities nor measures nor season effects but  $T_2 = 0.5T_1$  ( $\gamma = 0.5$ ), we have  $R_{20} = e^{rT_2} \sqrt{R_{10}}$ , e.g., for  $e^{rT_2} = 2$  and  $R_{01} = 4$ , we have  $R_{02} = R_{01} = 4$
- With measures/season effects and immunities as above, we may have  $R_{02} < R_{01}$

## 4. Determining the Omicron base reproduction rate from the logistic growth rate

Just use Relation (3) and insert the dependence of the actual growth rates  $R_1$  and  $R_2$  as a function of the base reproduction numbers  $R_{01}$ ,  $R_{02}$  and factors from (1)

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## 5. Effective infection growth rate and reproduction number

The **effective growth rate**  $r_{\text{eff}}$  of the infection dynamics (not to be confused with the logistic growth rate  $r$  of the Omicron shares  $p$ ) comes directly from (2):

$$\dot{x} = \dot{x}_1 + \dot{x}_2 = r_1 x_1 + r_2 x_2 = [(1-p)r_1 + pr_2]x \equiv r_{\text{eff}}x$$

Associating  $r_{\text{eff}}$  with  $\ln R_{\text{eff}}/T_1$ , we get the

$$\text{Effective reproduction number: } R_{\text{eff}} = R_1^{1-p} R_2^{p/\gamma} \quad (5)$$

- ▶ Because  $1/\gamma = T_1/T_2 > 1$ , influence factors influencing  $R_1$  and  $R_2$  according to (1) have a more sensitive effect on Omicron than on Delta: If  $T_1/T_2 = 1/\gamma = 2$  and measures lead to a factor  $1/\sqrt{2} \approx 0.7$  on Delta ( $R_1$ ), they simultaneously lead to a factor  $1/2$  on Omicron ( $R_2$ )
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## 5a. Effective infection growth rate vs Omicron spreading rate

From (3), we obtain

$$e^{rT_1} = R_2^{1/\gamma} R_1^{-1}$$

Eliminating  $R_2$  with (5), we get a relation between the effective infection growth rate  $R_{\text{eff}}$ , the Omicron spreading rate  $r$ , and the actual reproduction number  $R_1$  of the “old” variant:

$$R_{\text{eff}} = R_1 e^{rT_1 p} \quad (6)$$

## 5b. Determining dynamics based on Dutch reference

- ▶ Dutch has excellent time series for Omicron share  $p$  from which to determine  $r$  and incidences from which to estimate  $R_{\text{eff}}$ .
- ▶ For other countries, only  $R_{\text{eff}}$  can be estimated while  $r$  (which varies with the country as a function of  $I_1$ ,  $I_2$  and  $f_m$ ) is not known
- ▶ From (1) and (3), we obtain for Holland (preferably at a time where  $p \approx 0.5$ ) the base reproduction ratio

$$\frac{R_{20}}{R_{10}^\gamma} = \frac{e^{rT_2}(1 - I_1)^\gamma (f_m f_s)^{\gamma-1}}{1 - I_2} \equiv \alpha \quad (7)$$

- ▶ For other countries,  $R_{01}$  and  $R_{02}$  may be different (because of behavior, pop density etc) but we assume  $\alpha = \text{const.}$ , so using (5), (1), and (7), we get at mutation initialisation, independent from  $r$  (but of course we need  $p$ )

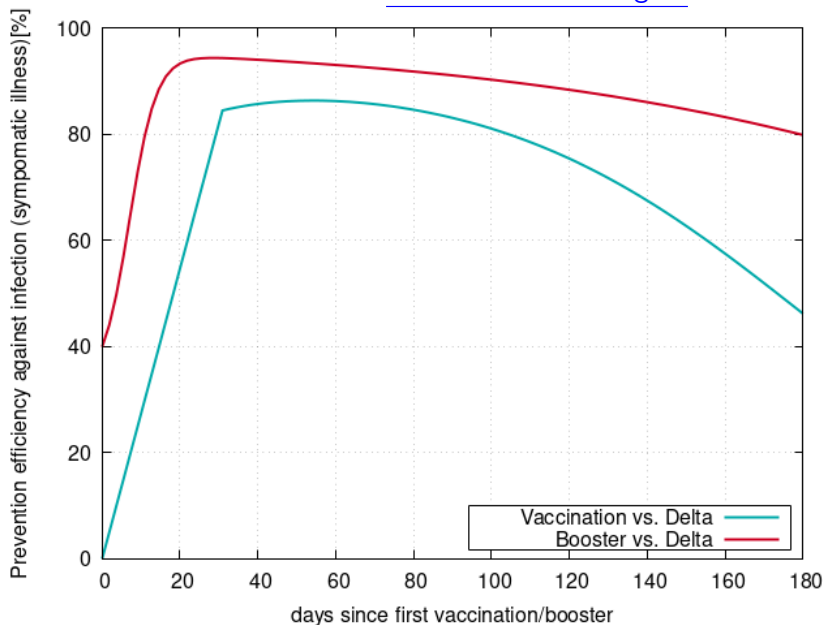
$$\frac{R_{\text{eff}}}{R_{10}} = (\alpha(1 - I_2))^{p/\gamma} (1 - I_1)^{1-p} (f_m f_s)^{p(1/\gamma-1)+1}, \quad R_{20} = \alpha R_{10}^\gamma \quad (8)$$

- ▶ After initialisation, just calculate  $R_1$ ,  $R_2$  from (1),  $r$  from (3), the new Omicron share via the odds update  $\dot{y} = ry$ ,  $p = y/(1 + y)$ , and the new effective reproduction number  $R_{\text{eff}}$  from (5).



## 6. Immunity I: vaccinations/boosters vs. Delta variant

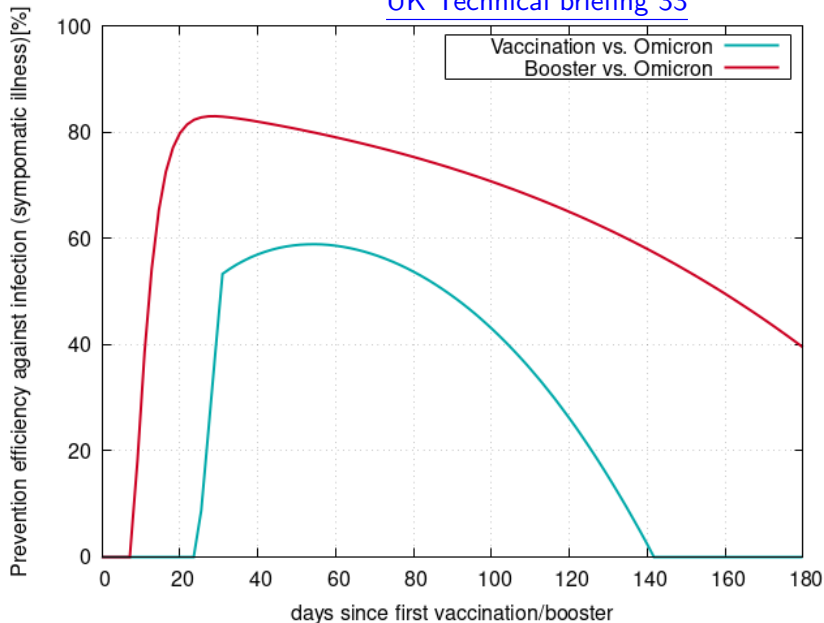
UK Technical briefing 33



“First vaccinated-  
first boosted”  
principle

## 6. Immunity II: vaccinations/boosters vs. Omicron variant

[UK Technical briefing 33](#)



Only fresh  
full vaccinations  
or boosters  
help against  
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## 6. Immunity III: past infections

- ▶ 100 % immunity of Delta against Delta reinfections
- ▶ 100 % immunity of Omicron against Omicron reinfections
- ▶ 100 % no cross immunity (people can get both Delta and Omicron infections)

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## 7. Determining the population immunities in the simulator I: vaccinations

Here, I make following assumptions

- ▶ Vaccination efficiency curves  $I_1^v(\tau)$  and  $I_2^v(\tau)$  against Delta and Omega as shown,
- ▶ corresponding booster efficiencies  $I_1^b(\tau)$  and  $I_2^b(\tau)$ ,
- ▶ *First vaccinated-first boosted*

Since the protection depends on the vaccination times, I sum up the different histories weighted with the past daily vaccination and booster rates  $r_{t'}^v$  and  $r_{t'}^b$  (fraction of the population per day):

$$I_1^{\text{vacc}}(t) = \sum_{t'=t_v}^t r_{t'}^v I_1^v(t-t') + \sum_{t'=t_b}^t r_{t'}^b I_1^b(t-t')$$

where  $t_b$  is the time of the first booster shot, and  $t_v$  the oldest time of the first vaccination of any person who is not yet boosted.

The vaccination immunity  $I_2$  is calculated in analogy.

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## Determining the population immunities in the simulator II: infections and total

- Everybody can only be infected once with any variant but there is no cross immunity, so the immunity is just equal to the total percentage  $X_1$  and  $X_2$  of people infected with either variant:

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*Notice:*  $X_i$  is not just the cumulated number of cases divided by the population because any infection, whether detected or not detected, counts

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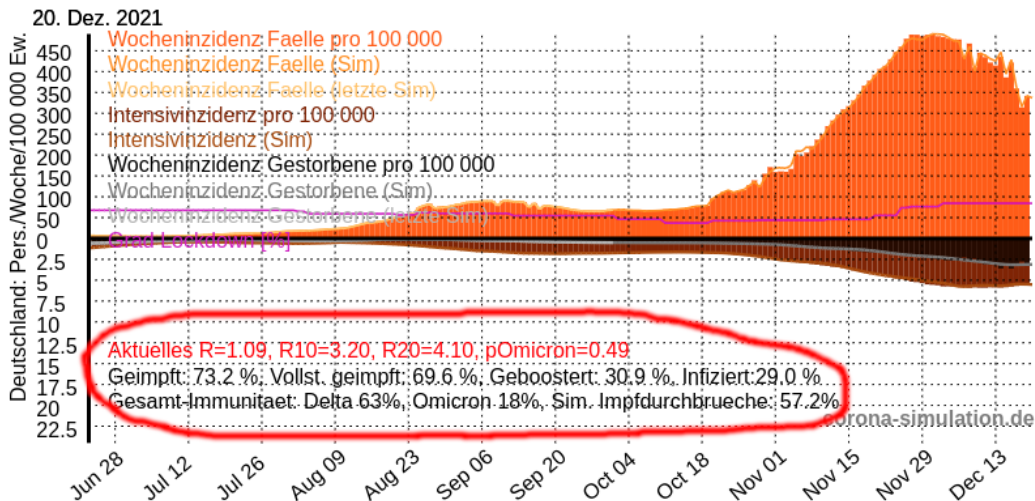
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- There is no correlation between vaccinations and infections:

$$1 - I_1 = (1 - I_1^v)(1 - I_1^x), \quad 1 - I_2 = (1 - I_2^v)(1 - I_2^x) \quad (9)$$

## Simulation



All items  $I_1$ ,  $I_2$ ,  $p$ ,  $R_{10}$ ,  $R_{20}$ ,  $f_{\text{season}}$  and  $f_{\text{stringency}}$  are displayed in the simulation