Model-based approach for determining COVID-19 incidence for different testing intensities

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Introduction to the problem

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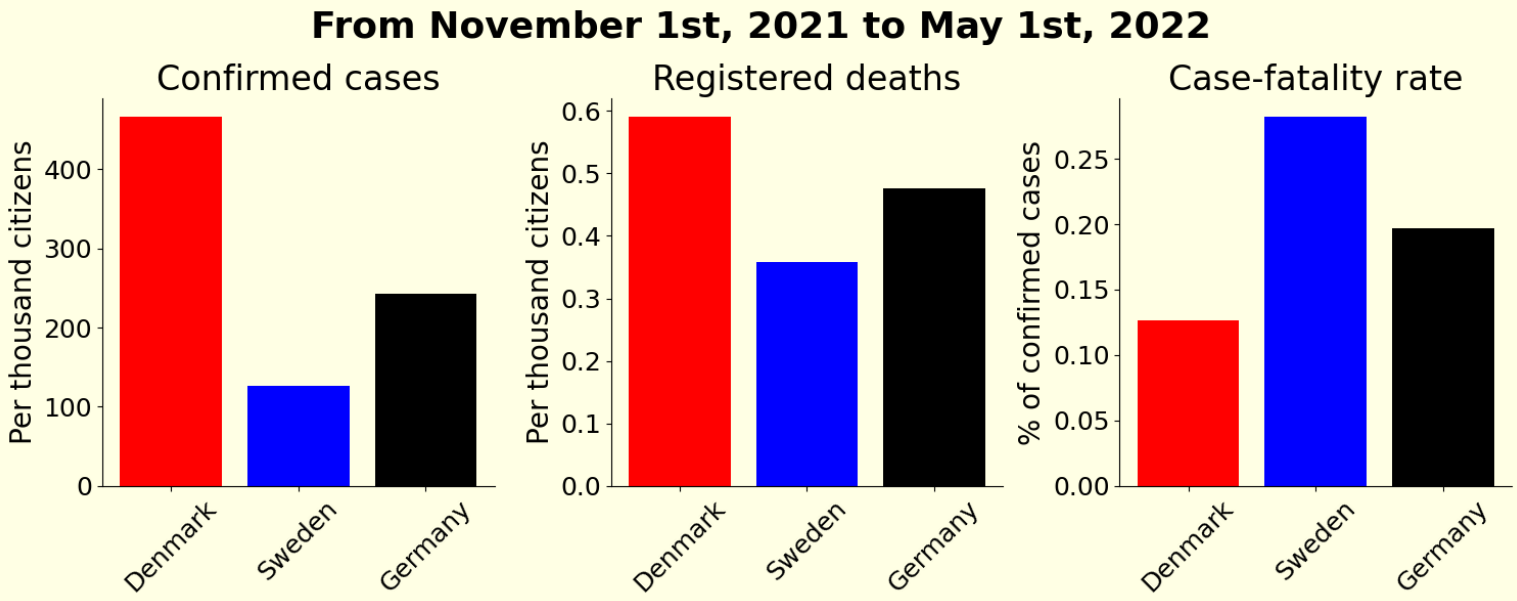
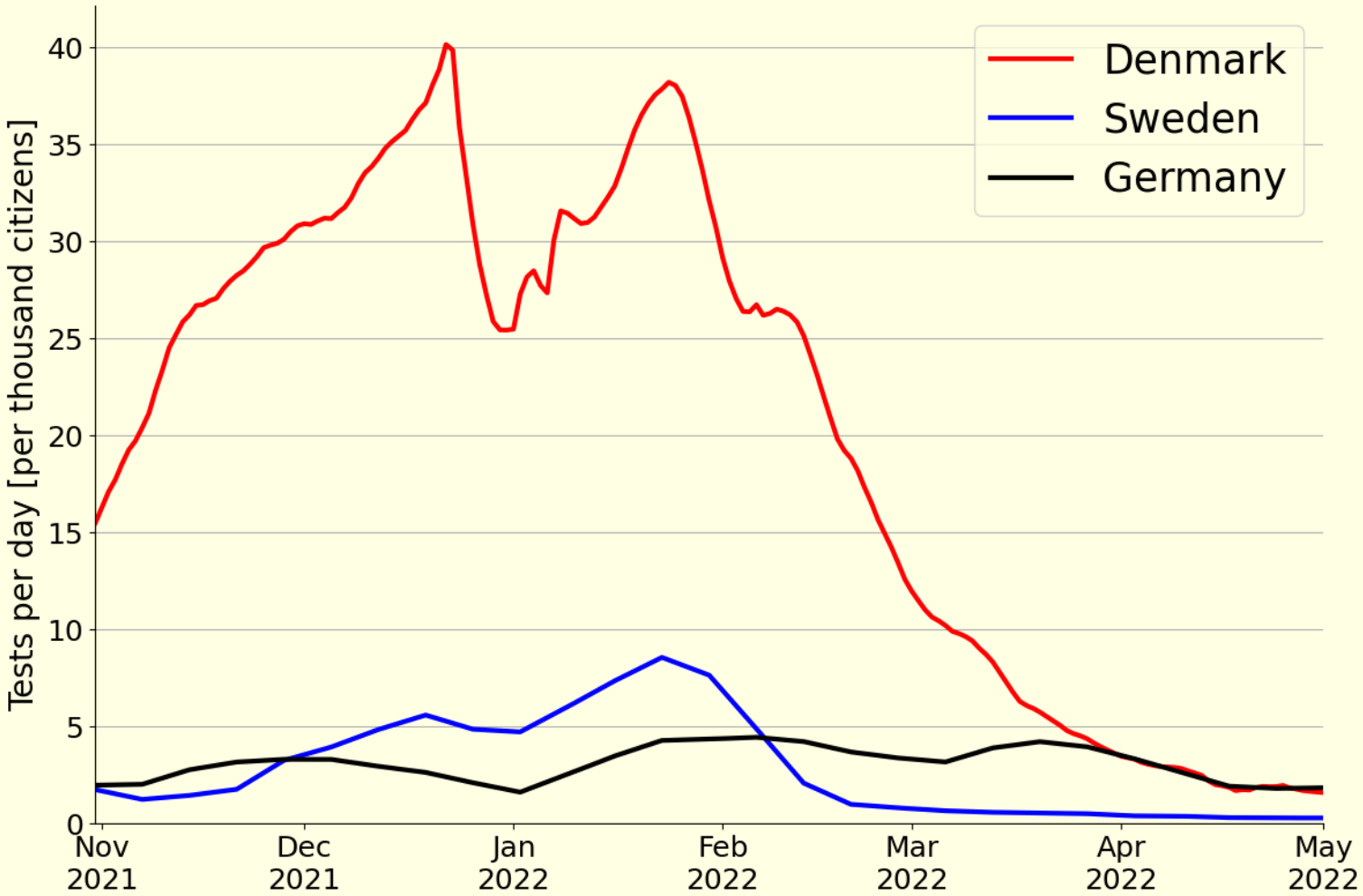
- **How do we compare case-counts between periods and places where testing activity was different?**

Let's look at some data...


From November 1st, 2021 to May 1st, 2022
Confirmed cases
Per thousand citizens
0
100
200
300
400
Denmark
Sweden
Germany
Registered deaths
Per thousand citizens
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Denmark
Sweden
Germany
Case-fatality rate
% of confirmed cases
0.00
0.05
0.10
0.15
0.20
0.25
Denmark
Sweden
Germany



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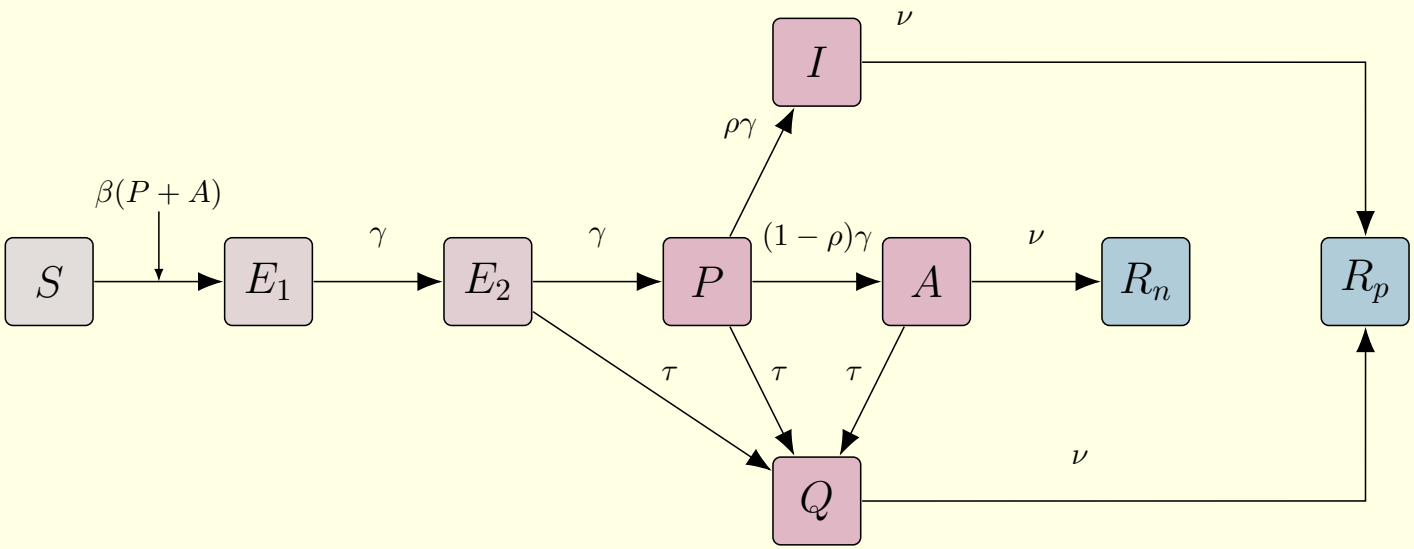
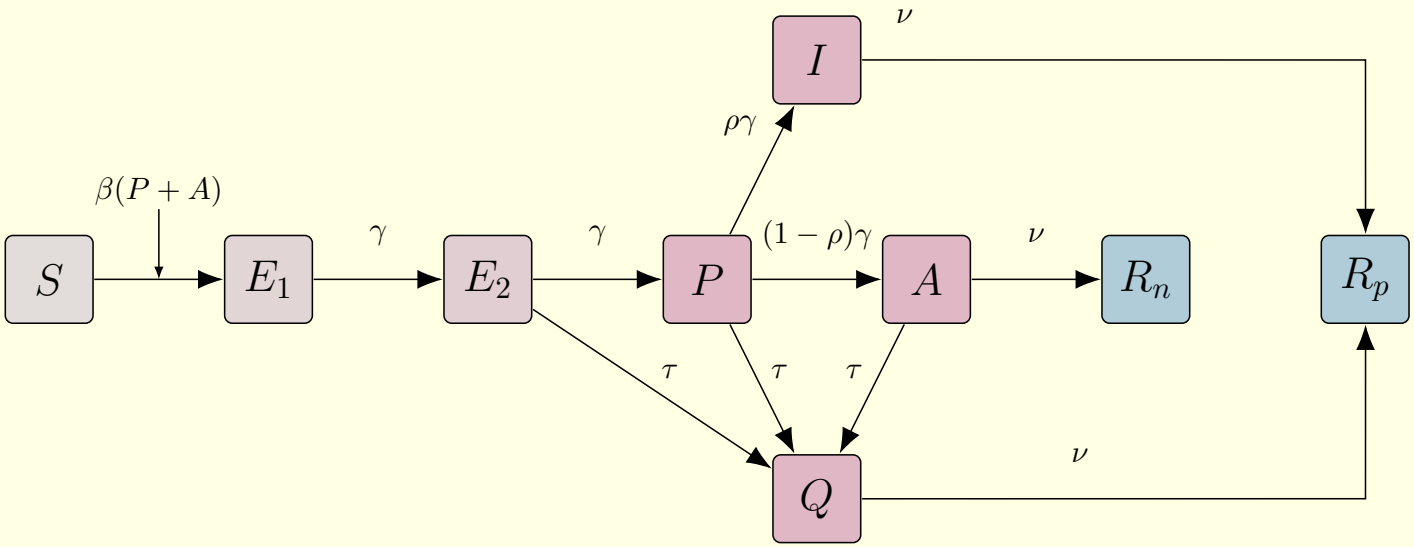
- We aim to determine the ratio between observed cases and the total number of COVID-19 cases.
- This ratio can be used as a correction-factor for observed data.
- We extend the classic SIR-model to include voluntary testing that identifies pre- and asymptomatic cases.
- This allows us to investigate the relationship between the rate of voluntary testing and the appropriate correction-factor.

The model


I
ν
$\rho\gamma$
$\beta(P+A)$
S
E_1
γ
E_2
γ
P
$(1-\rho)\gamma$
A
ν
R_n
R_p
τ
τ
τ
ν
Q

The model



$$\dot{S} = -\beta S(P+A)$$
$$\dot{E}_1 = \beta S(P+A) - \gamma E_1$$
$$\dot{E}_2 = \gamma E_1 - \gamma E_2 - \tau E_2$$
$$\dot{P} = \gamma E_2 - \gamma P - \tau P$$
$$\dot{I} = \gamma\rho P - \nu I$$
$$\dot{A} = \gamma(1-\rho)P - \nu A - \tau A$$
$$\dot{Q} = \tau(E_2 + P + A) - \nu Q$$
$$\dot{R}_p = \nu Q + \nu I$$
$$\dot{R}_n = \nu A$$

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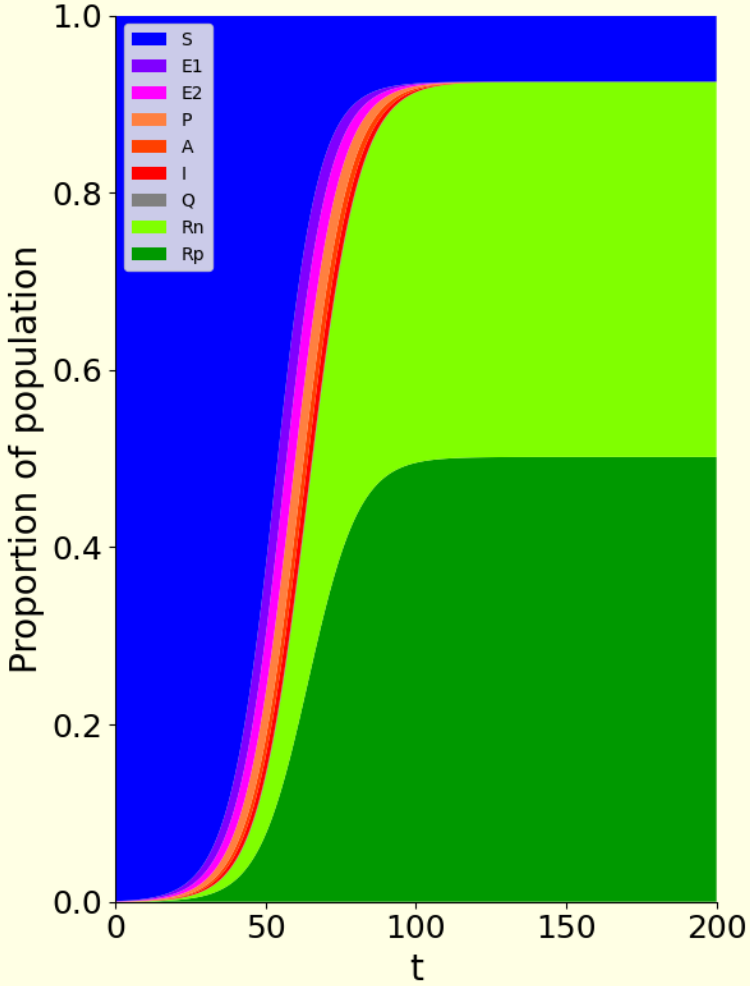
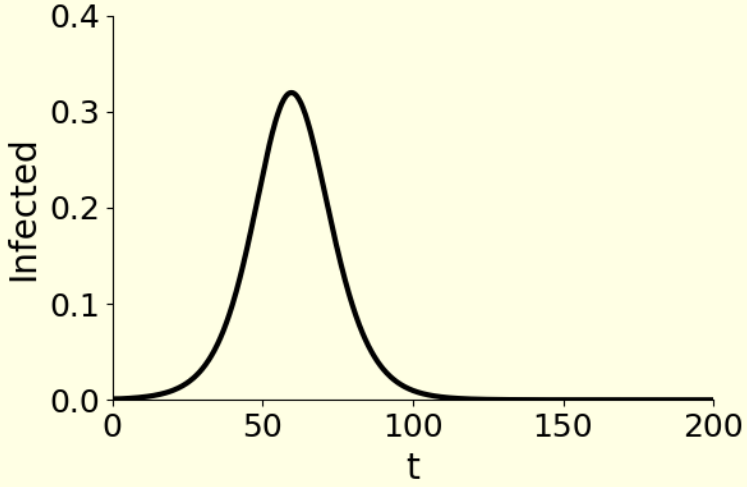
Symbol	*Description*	*Default value*
β	Infectivity	2/3
ν	Rate of recovery	1/3
γ	Rate of disease progression	1/3
ρ	Fraction of symptomatic cases	1/2
τ	Rate of testing	0 to 0.5

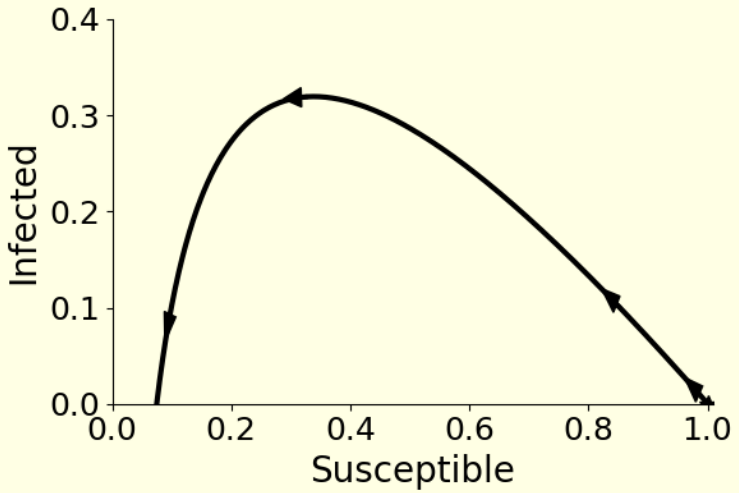
All rates units of day^{-1}. Approximate R_0 of 1.4 initially.

General model dynamics

General dynamics like classic SIR-model.







Analysis of fraction of cases identified

We consider the fraction of cases identified:

$$K = \frac{r_p}{r_p + r_n} \tag{1}$$

where $r_p = \lim_{t\to\infty} R_p(t)$ and $r_n = \lim_{t\to\infty} R_n(t)$.

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Through the methods previously applied in (Andreasen, 2018), we are able to analytically determine:

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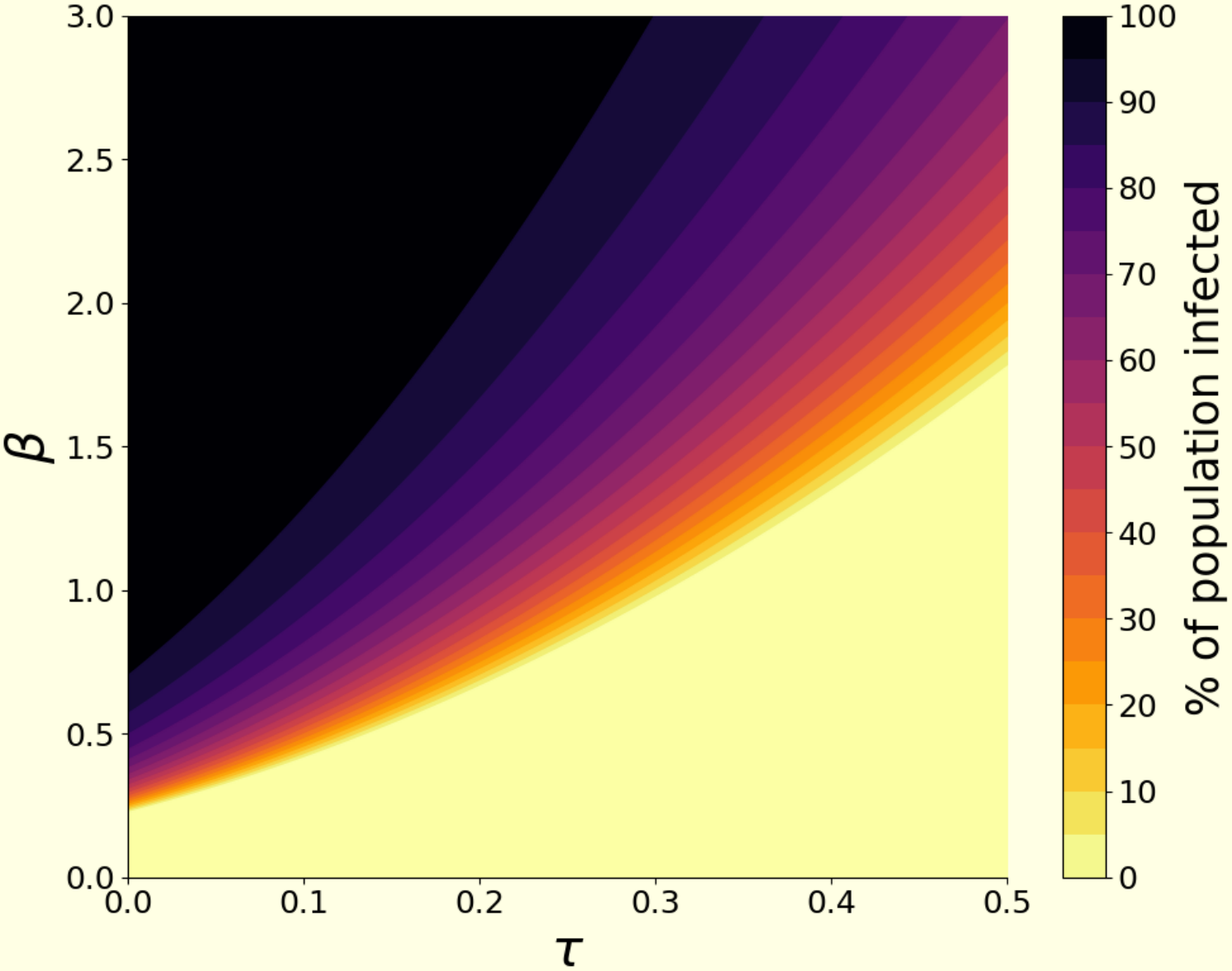
(Andreasen, V. (2018). *Epidemics in Competition: Partial Cross-Immunity. Bulletin of Mathematical Biology*, 80(11), 2957-2977. https://doi.org/10.1007/s11538-018-0495-2)

Fixed final size and (τ, β)

Although the fraction of cases identified, K, is independent of β, the epidemic final size, i.e. $r_n + r_p$, is not.

Let us take a look at the final size as a function of τ and β.

Fixed final size and (τ, β)



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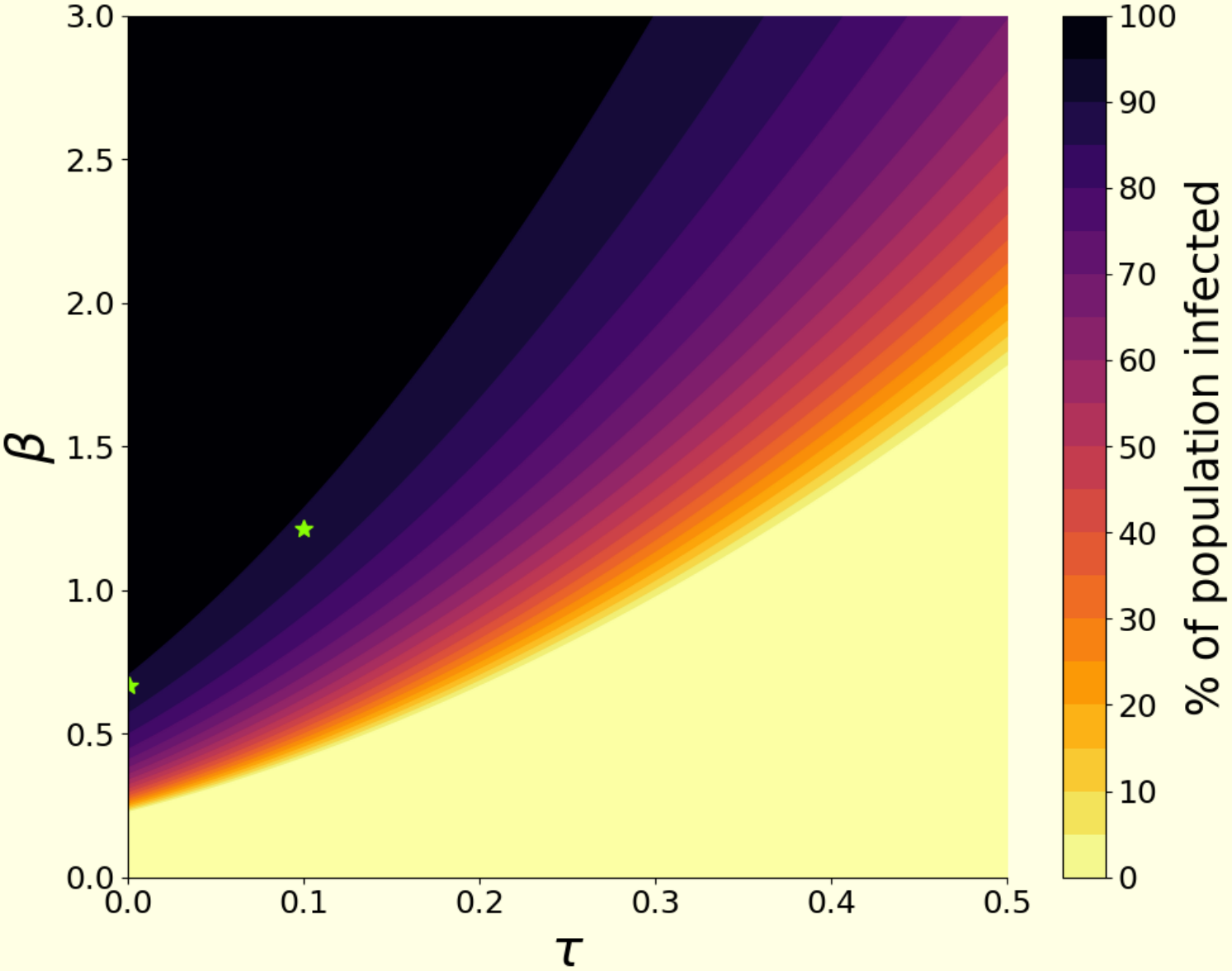

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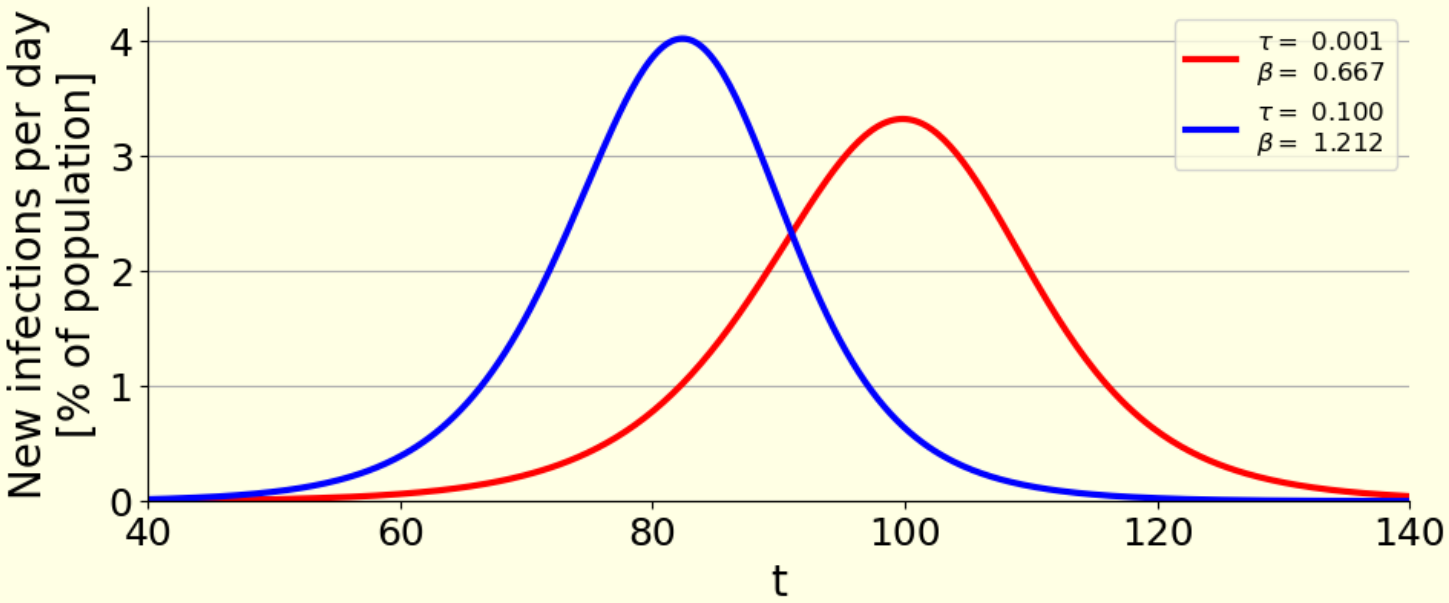

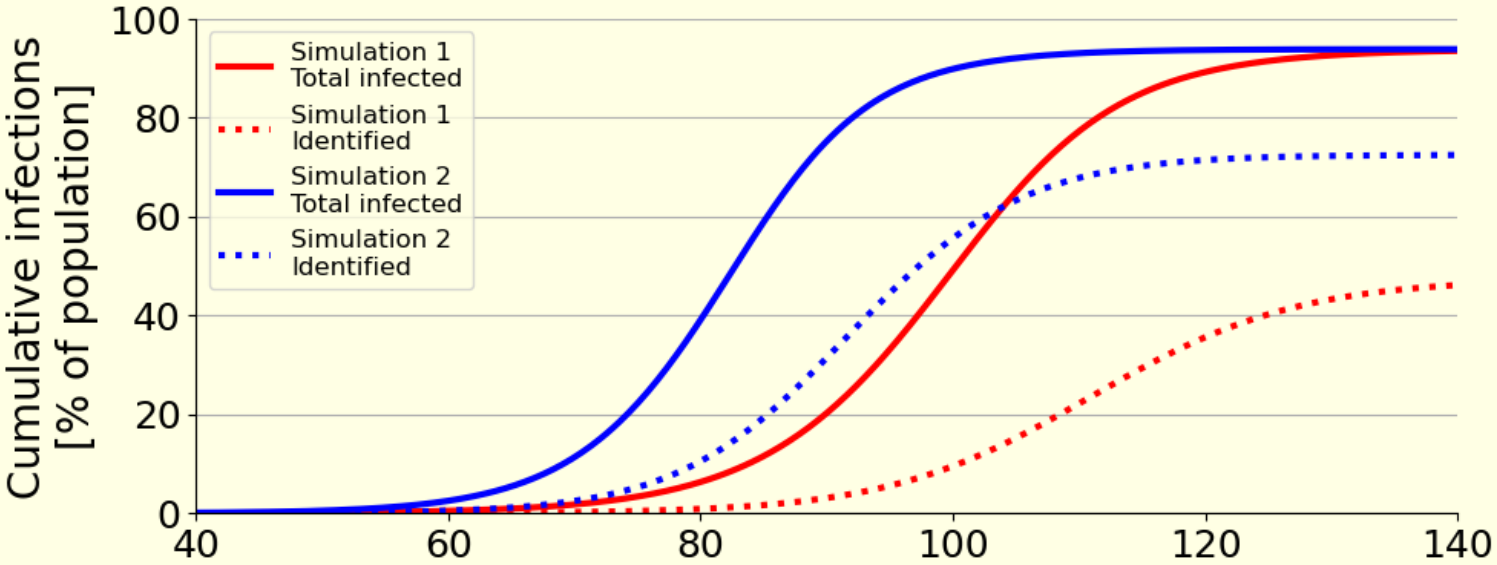

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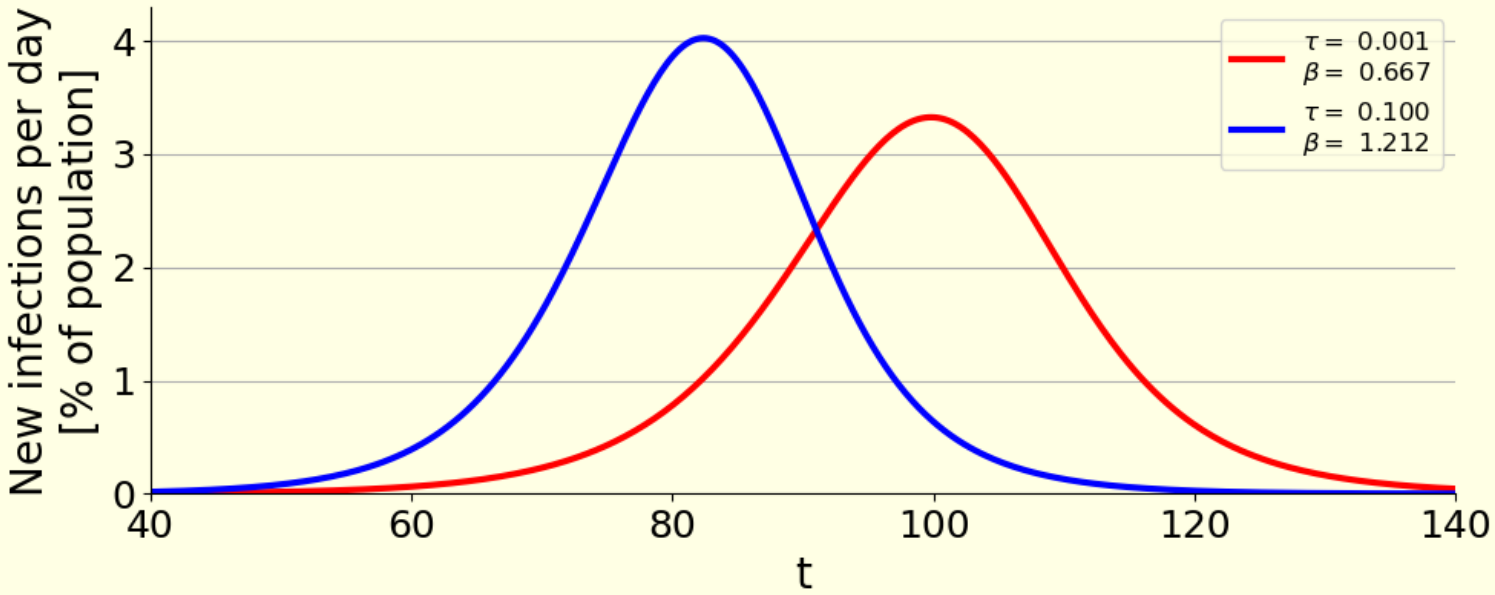

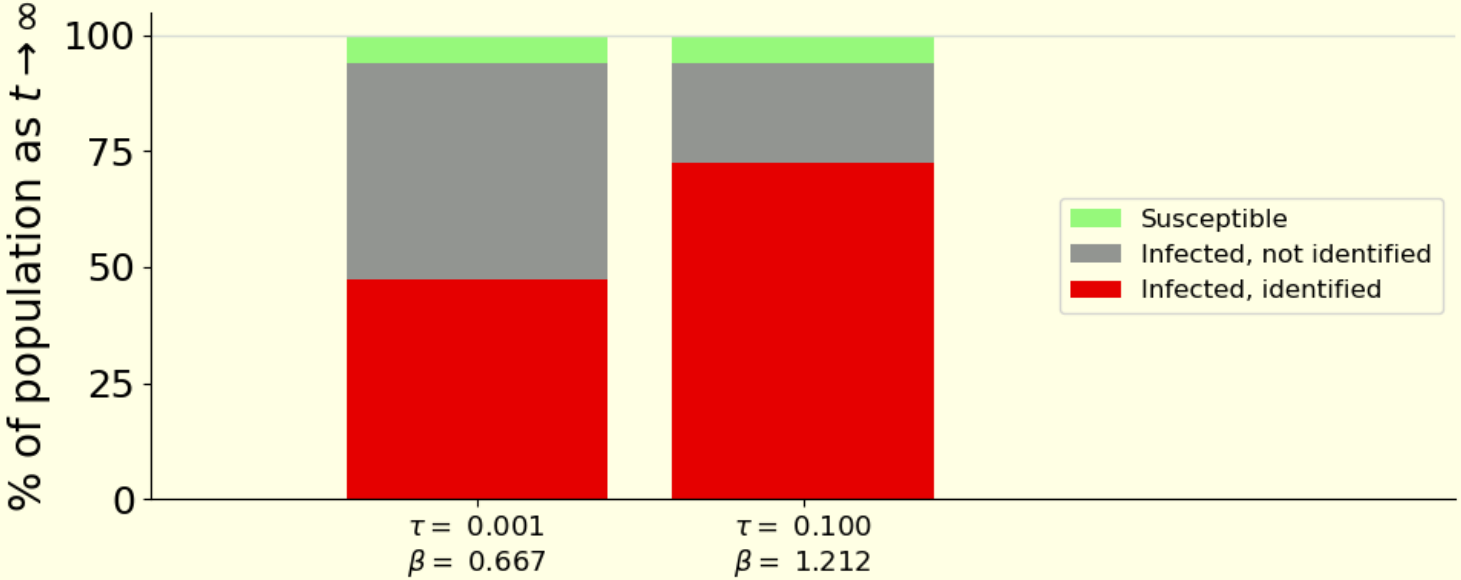

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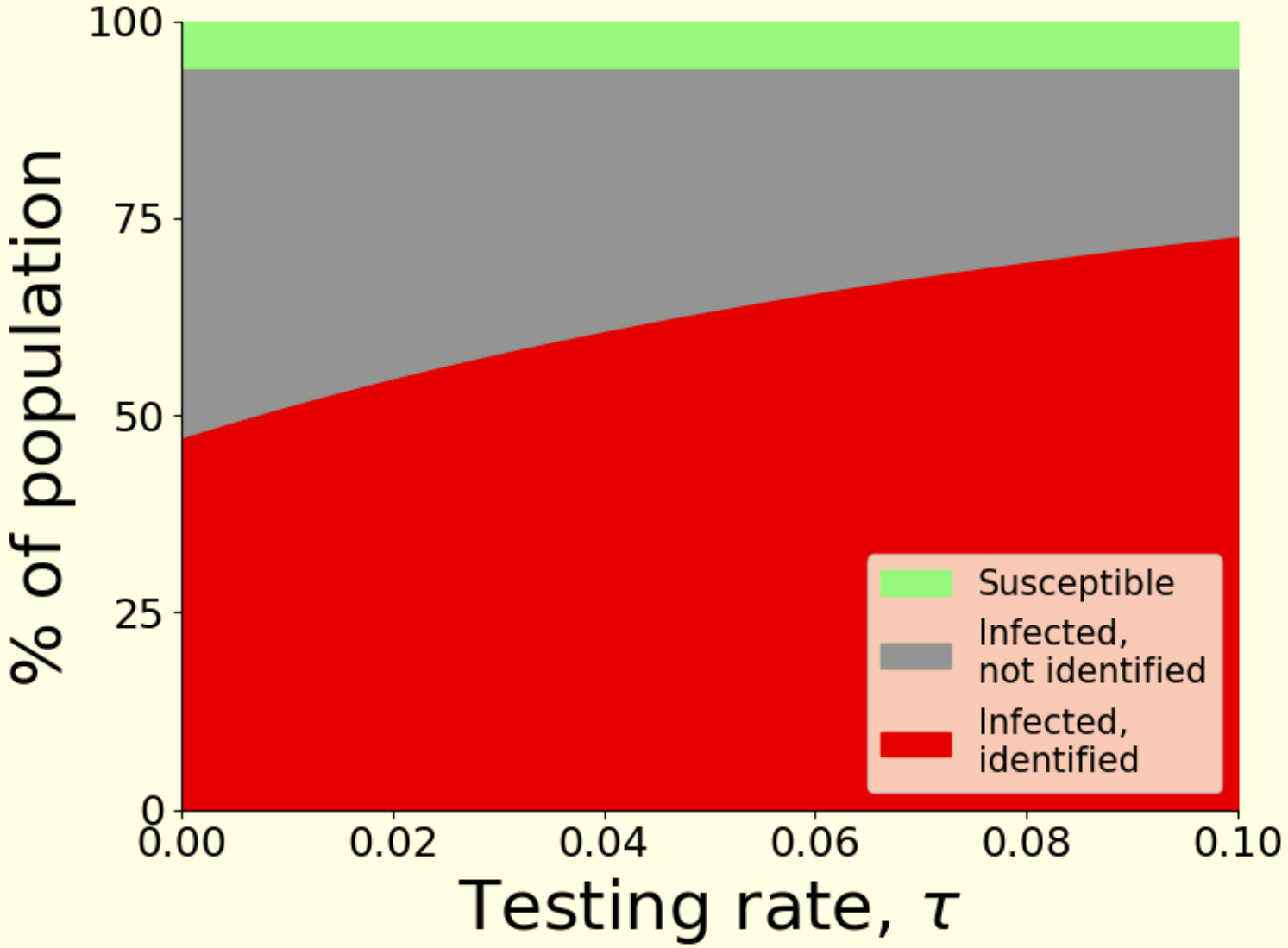

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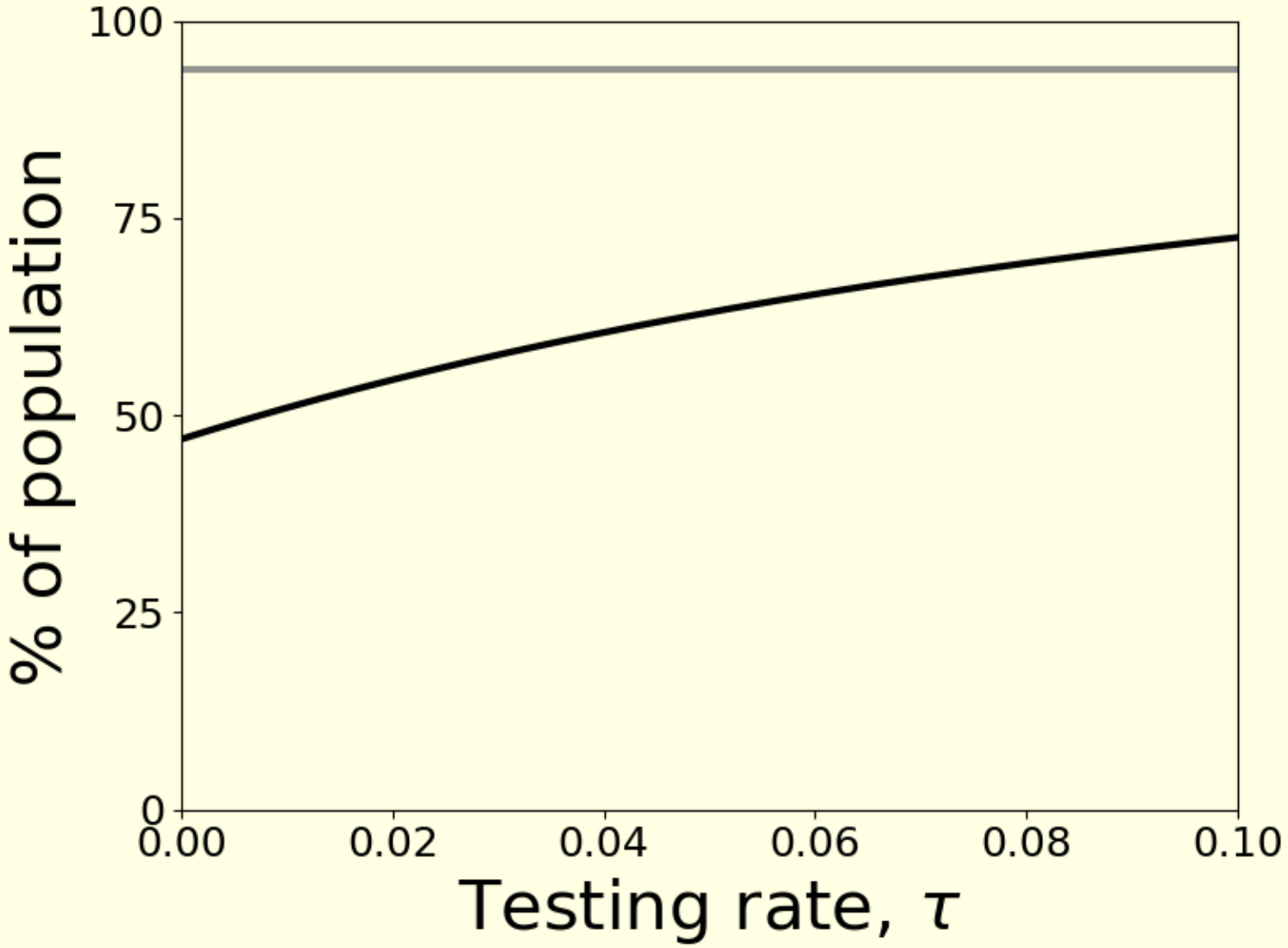

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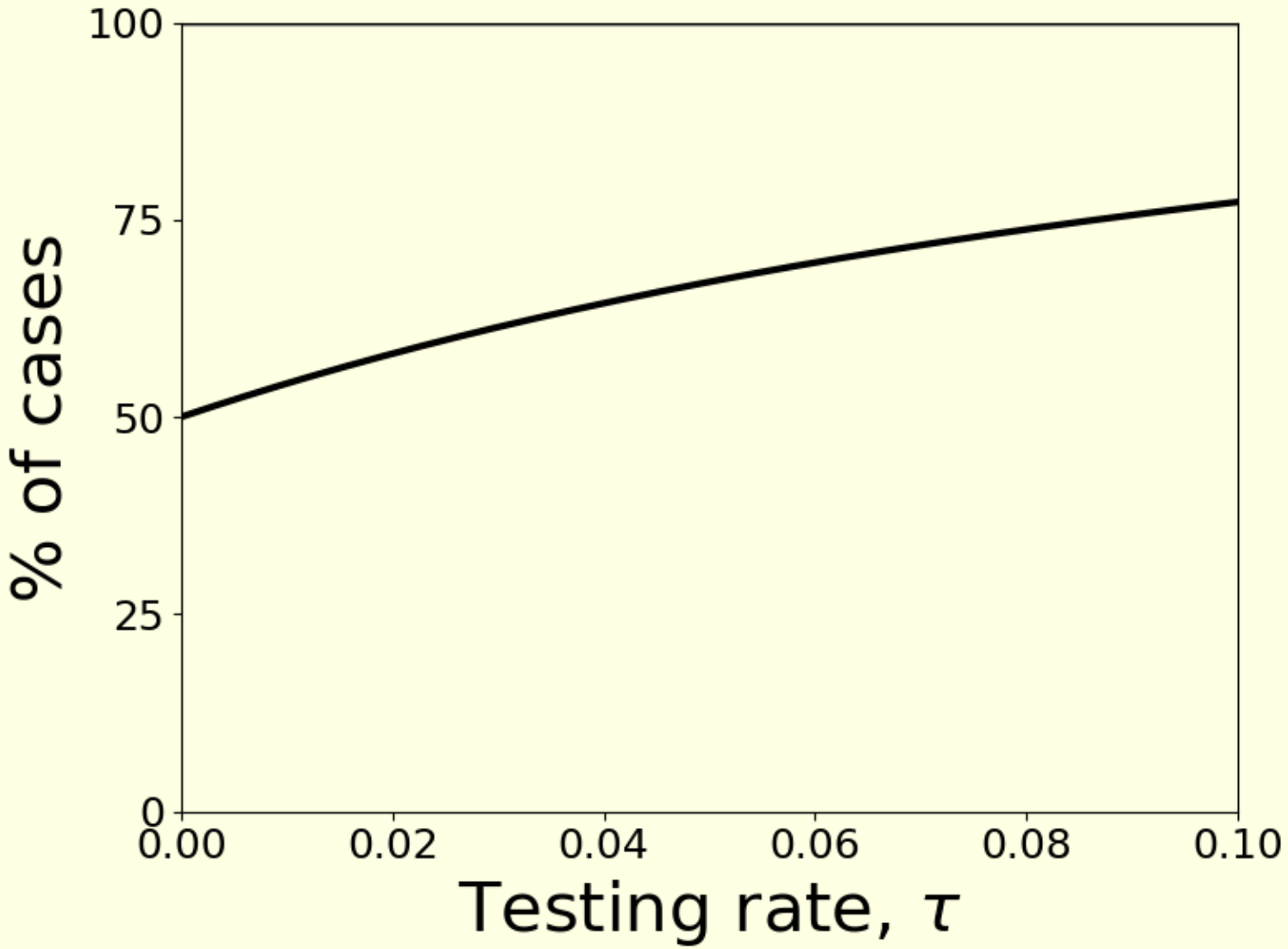

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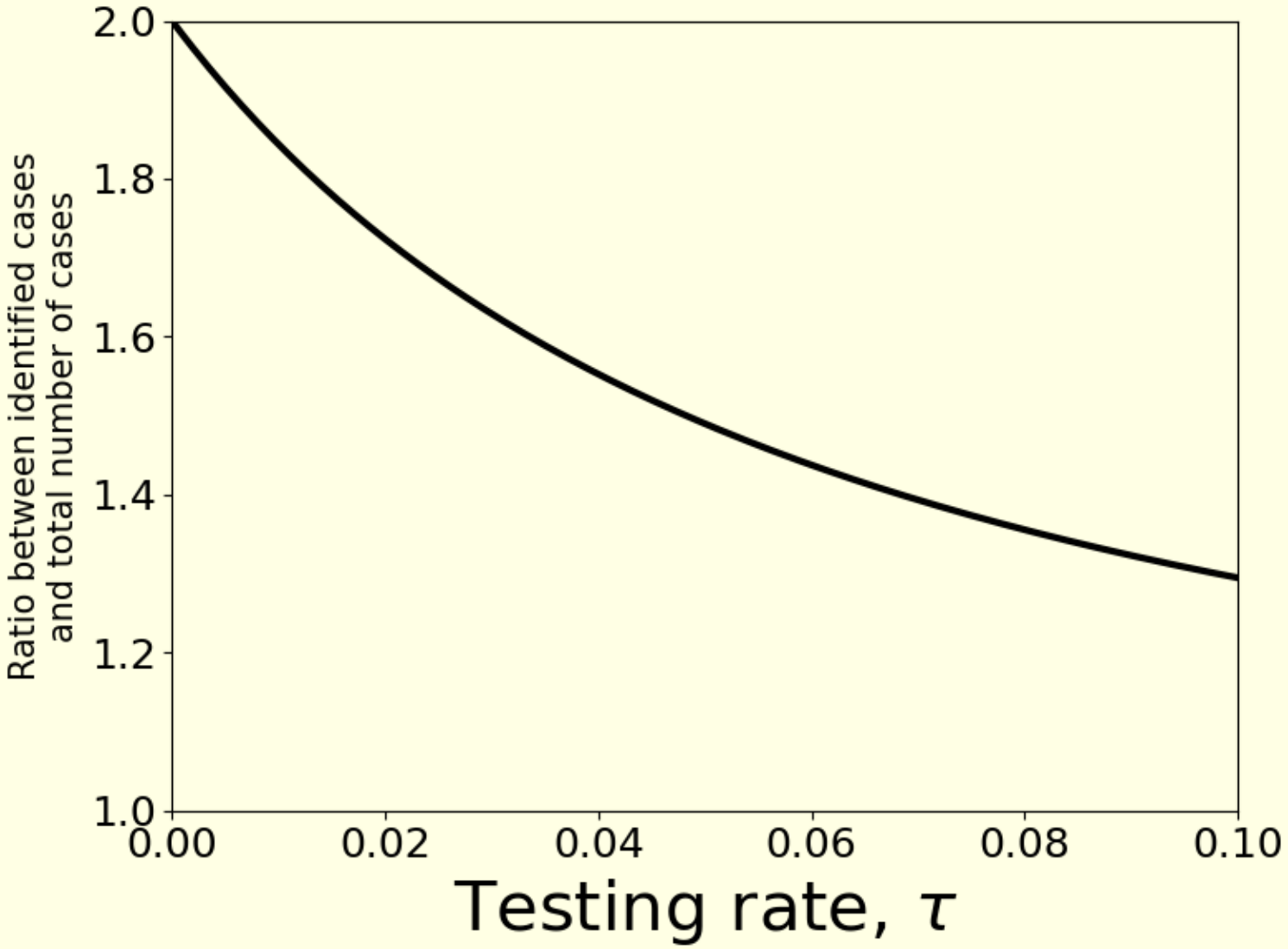
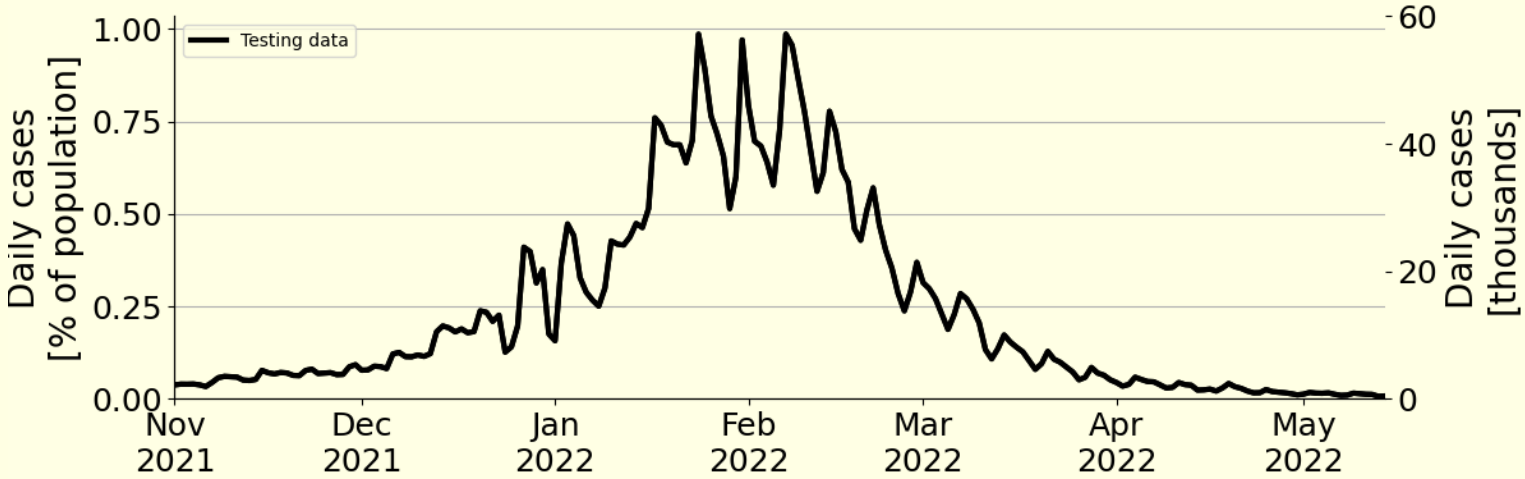
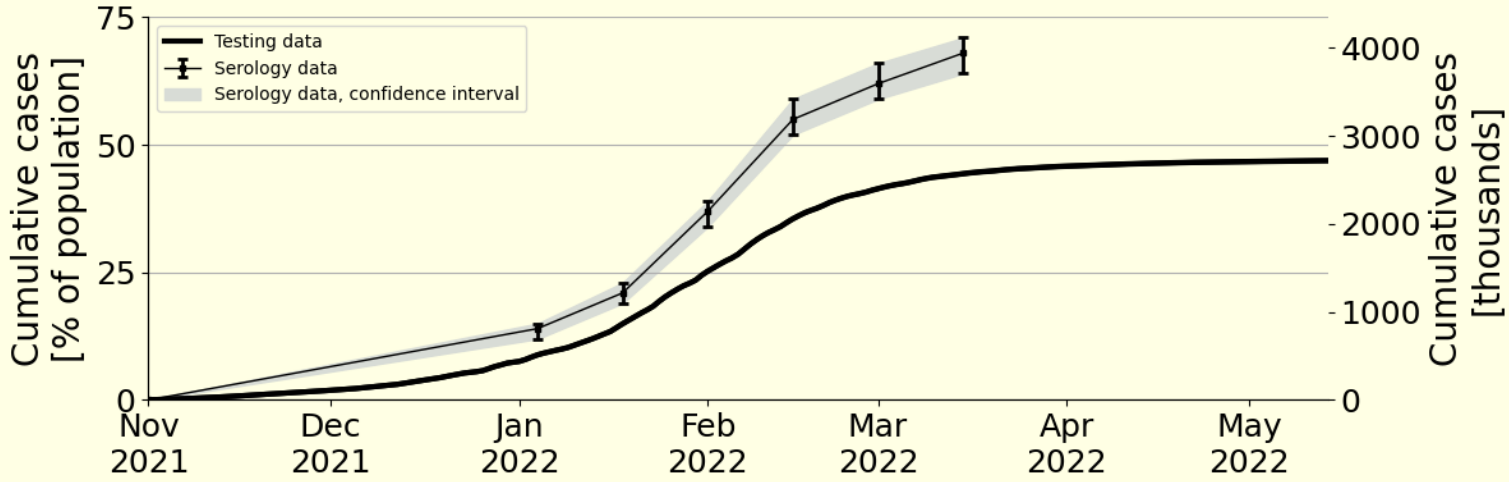


The Danish data

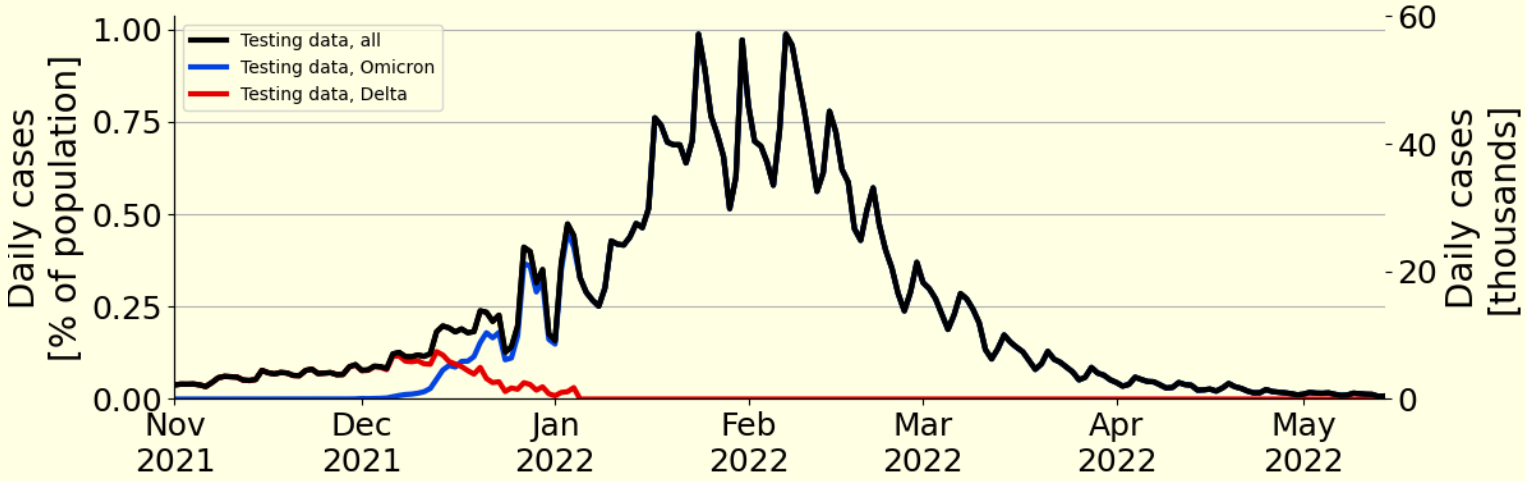
Daily cases and serology from blood-donors

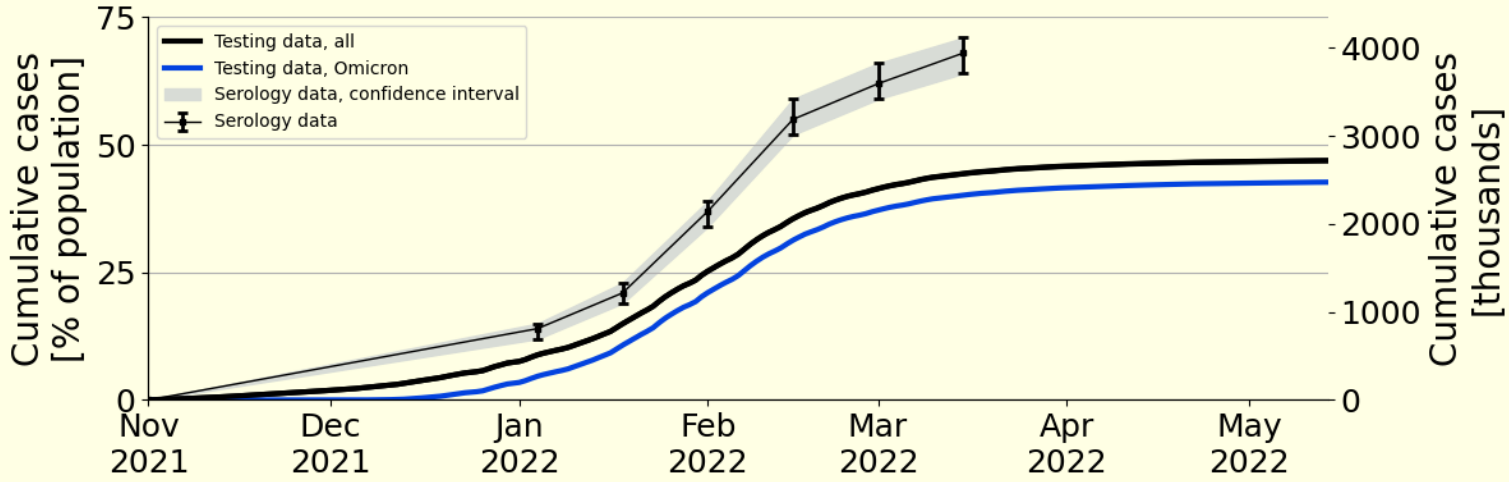




The Danish data

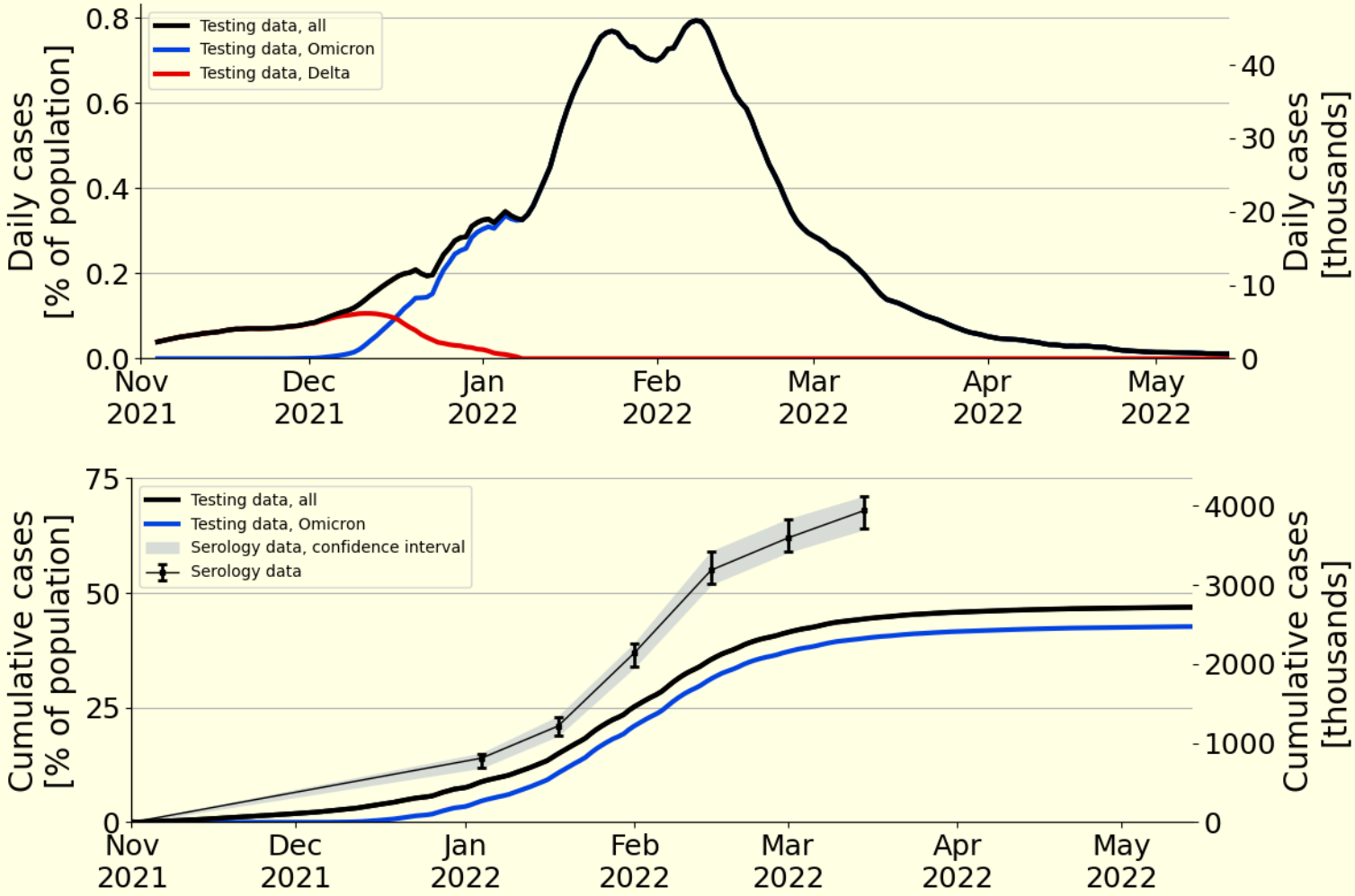
December 2021: Variant-sampling of 80 to 90% of cases.





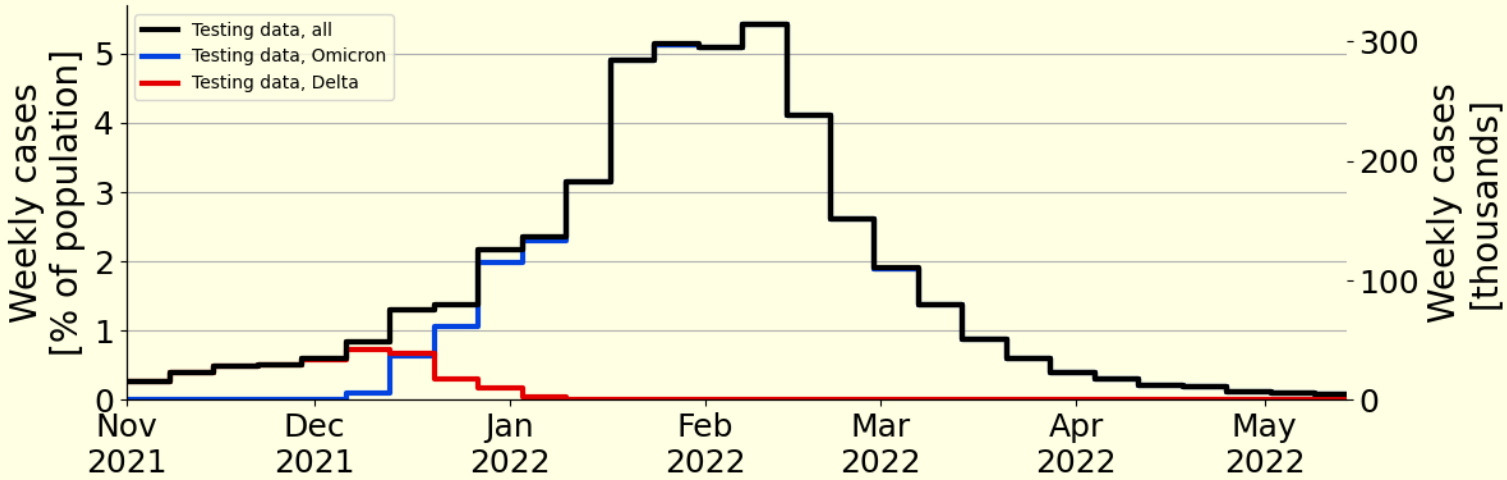
The Danish data

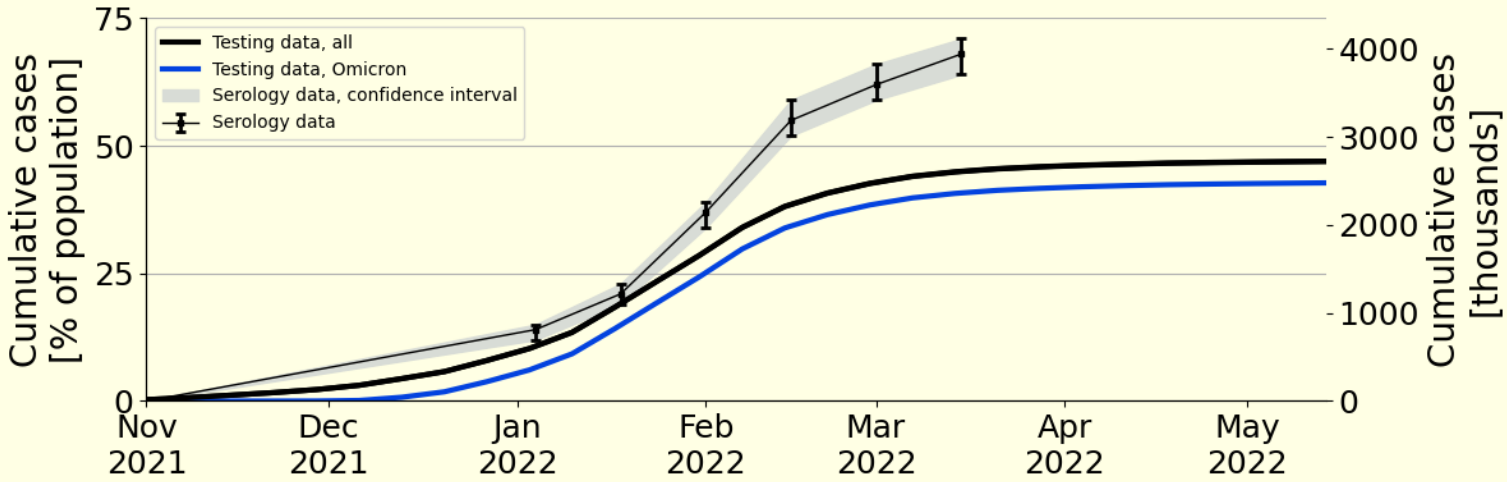
Smoothing: 7-day running mean.



The Danish data

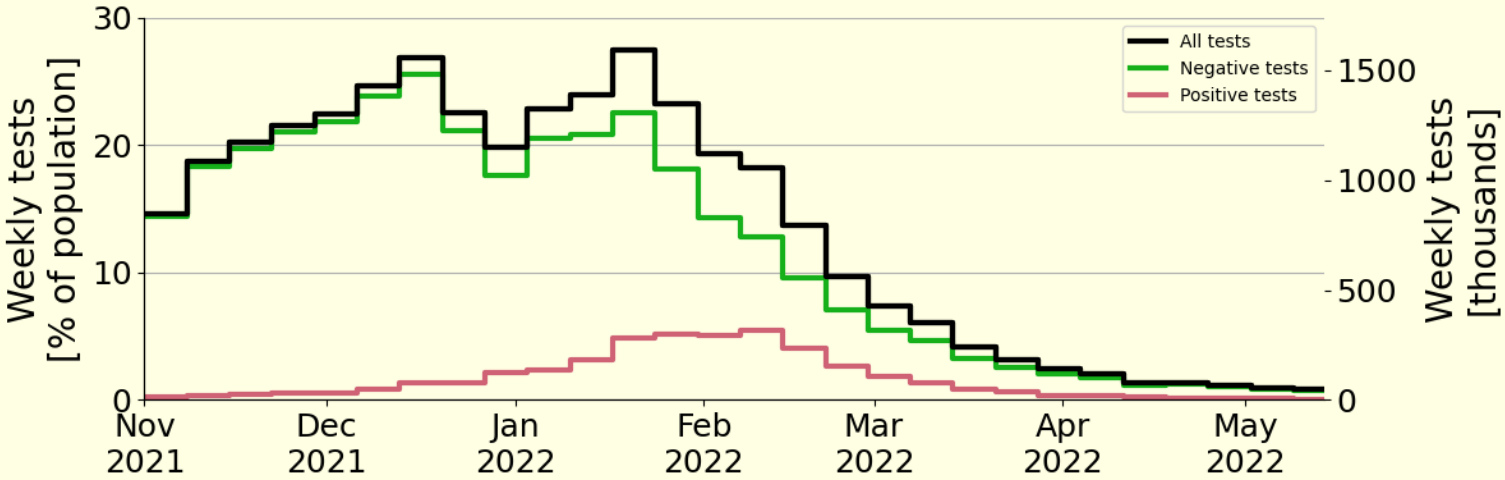
Weekly sums (Monday to Sunday)





The Danish data

Sum of weekly tests



(Only PCR shown, Antigen-tests at similar magnitude)

The Danish data

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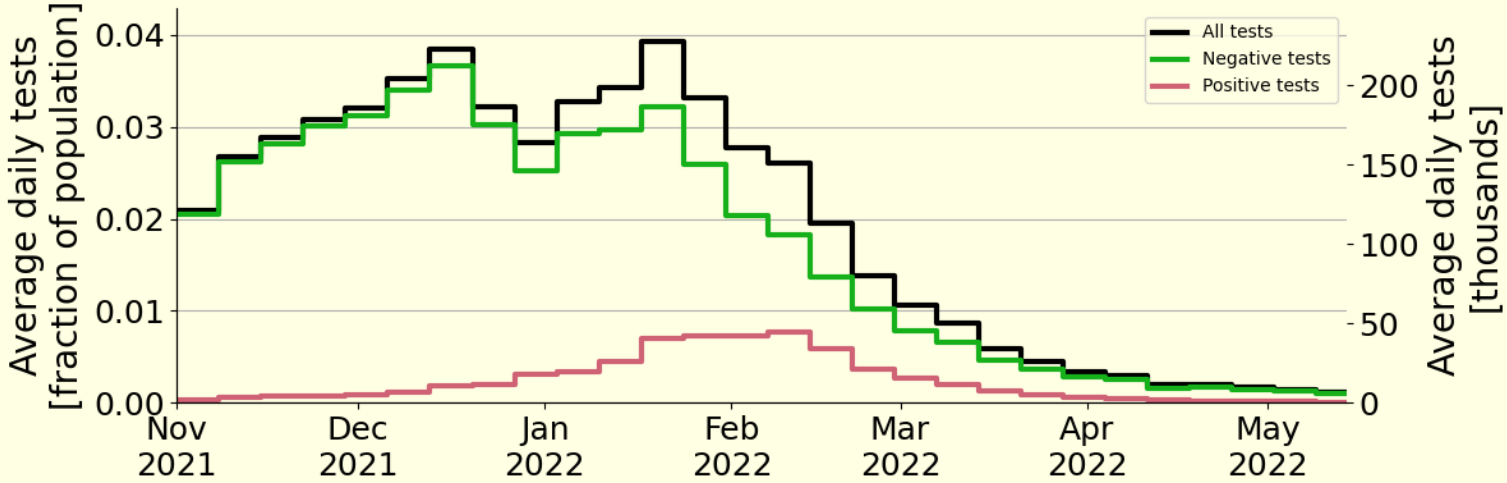
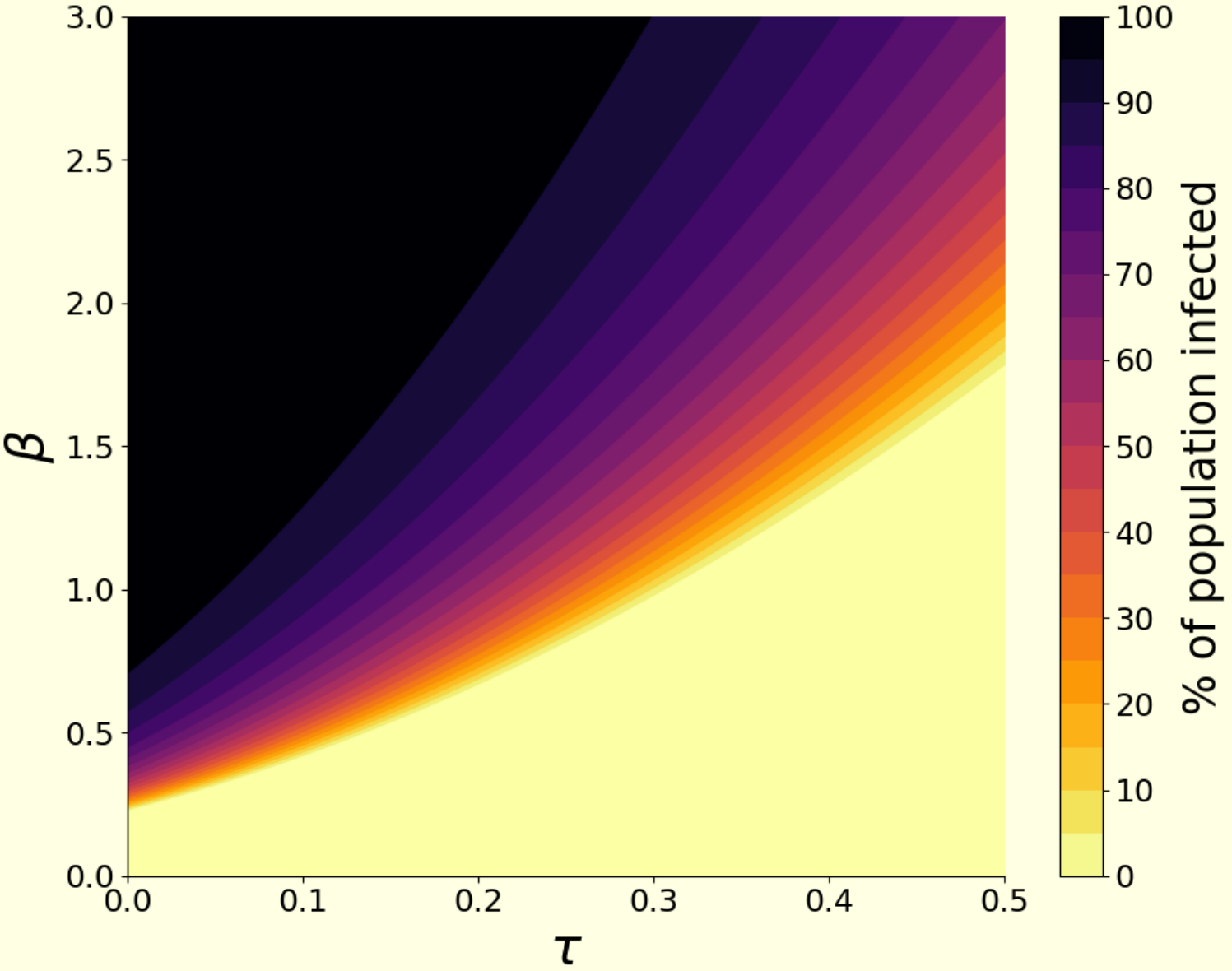


Scaled to tests per population per day (i.e. τ)

Relating to data



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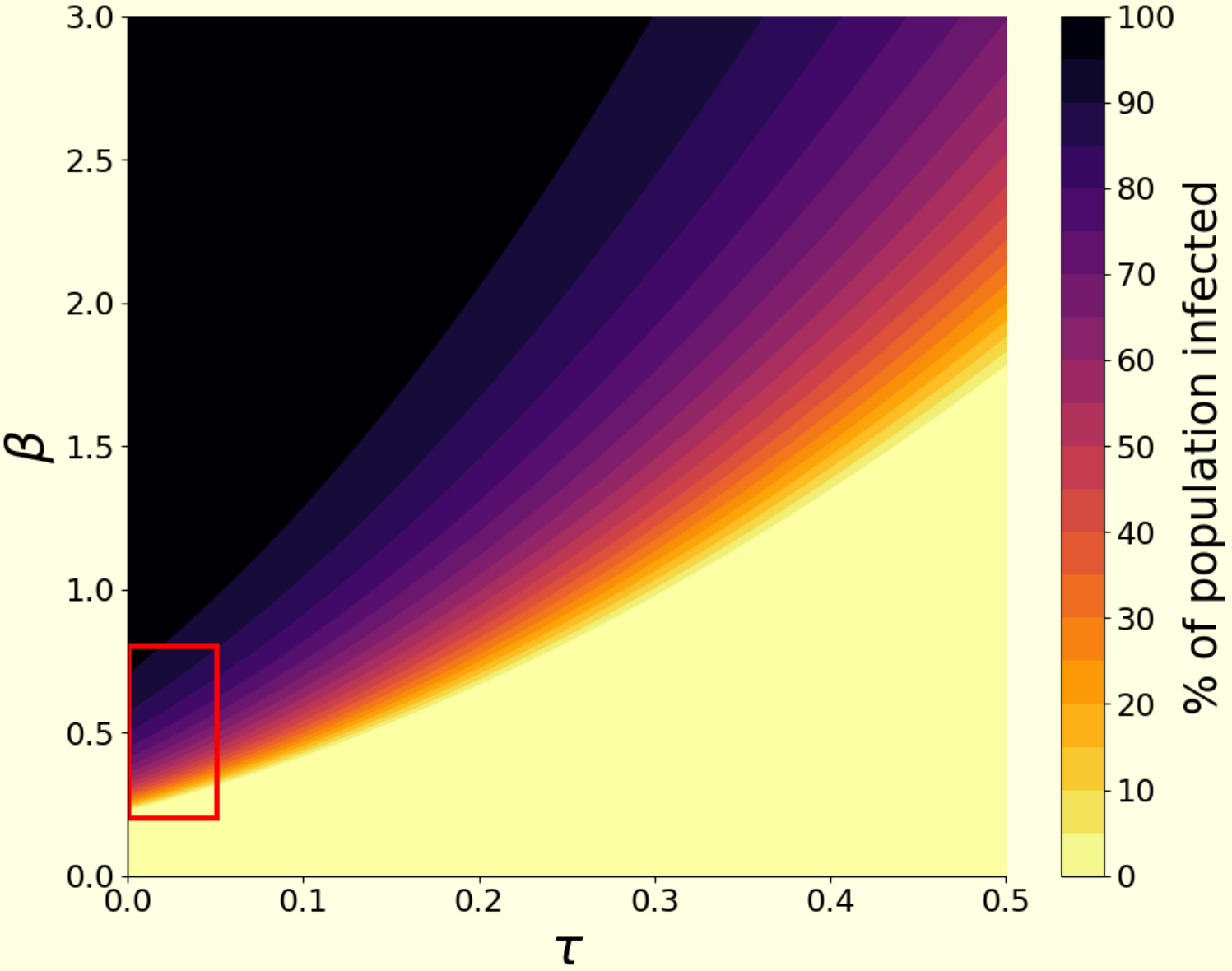

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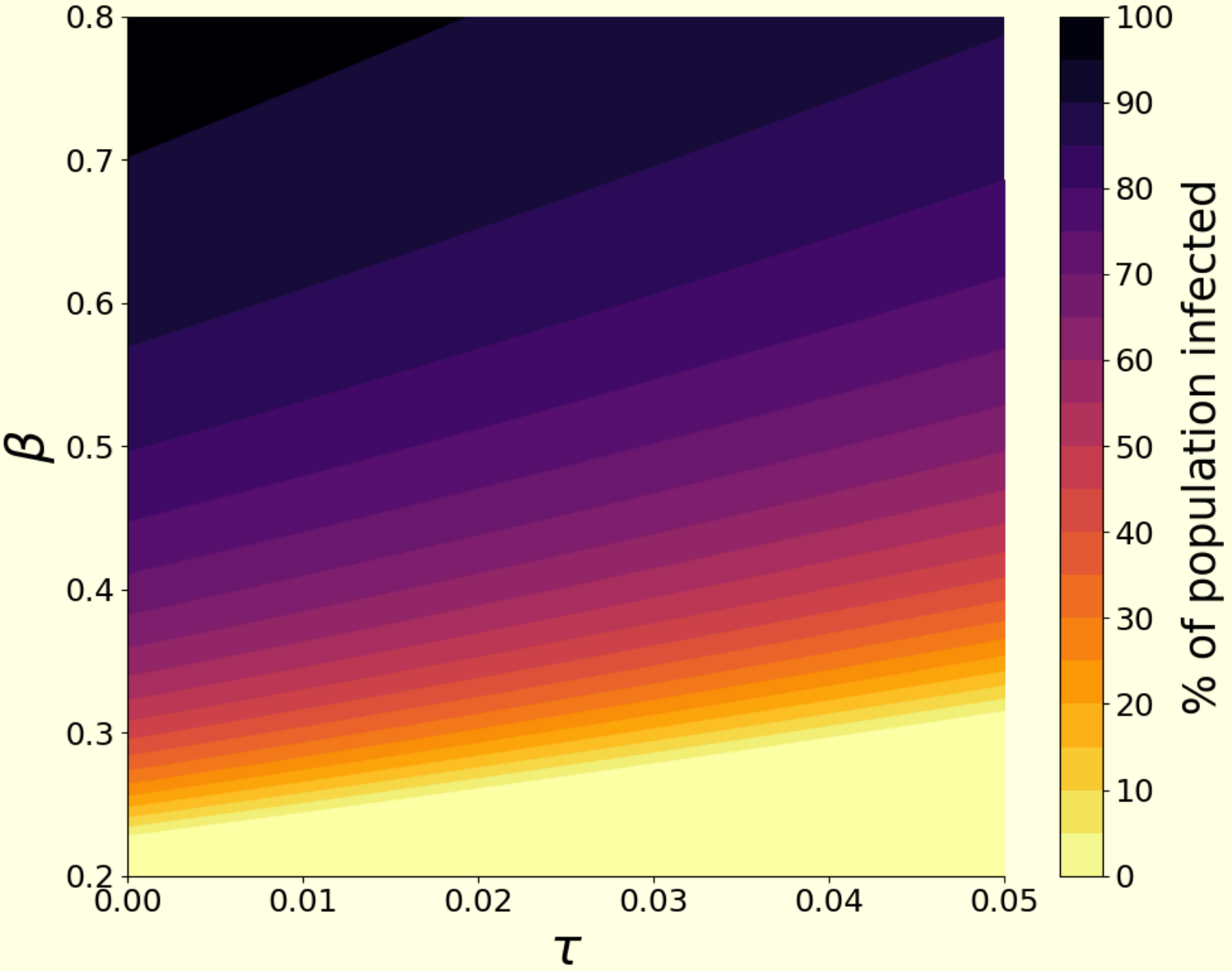

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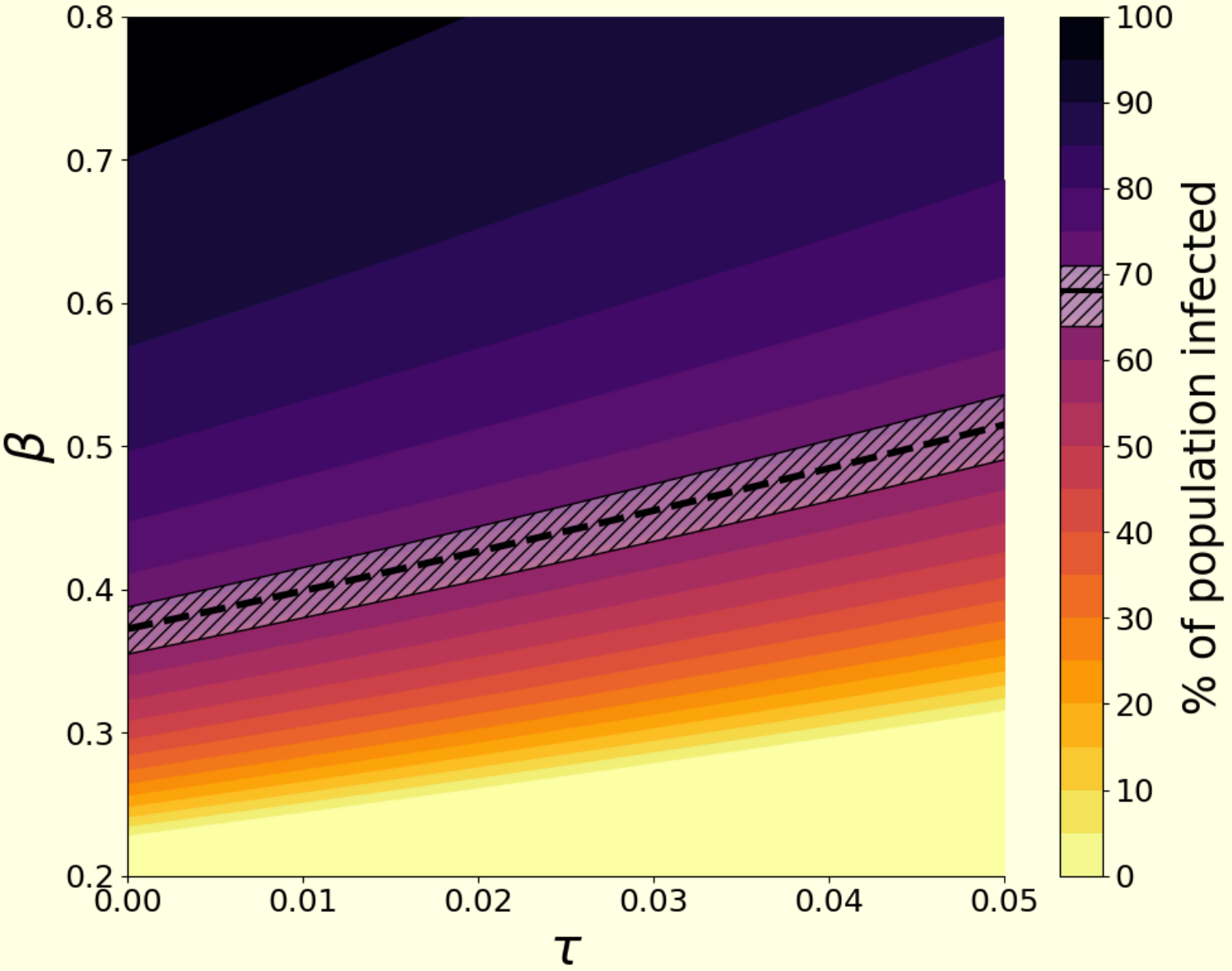

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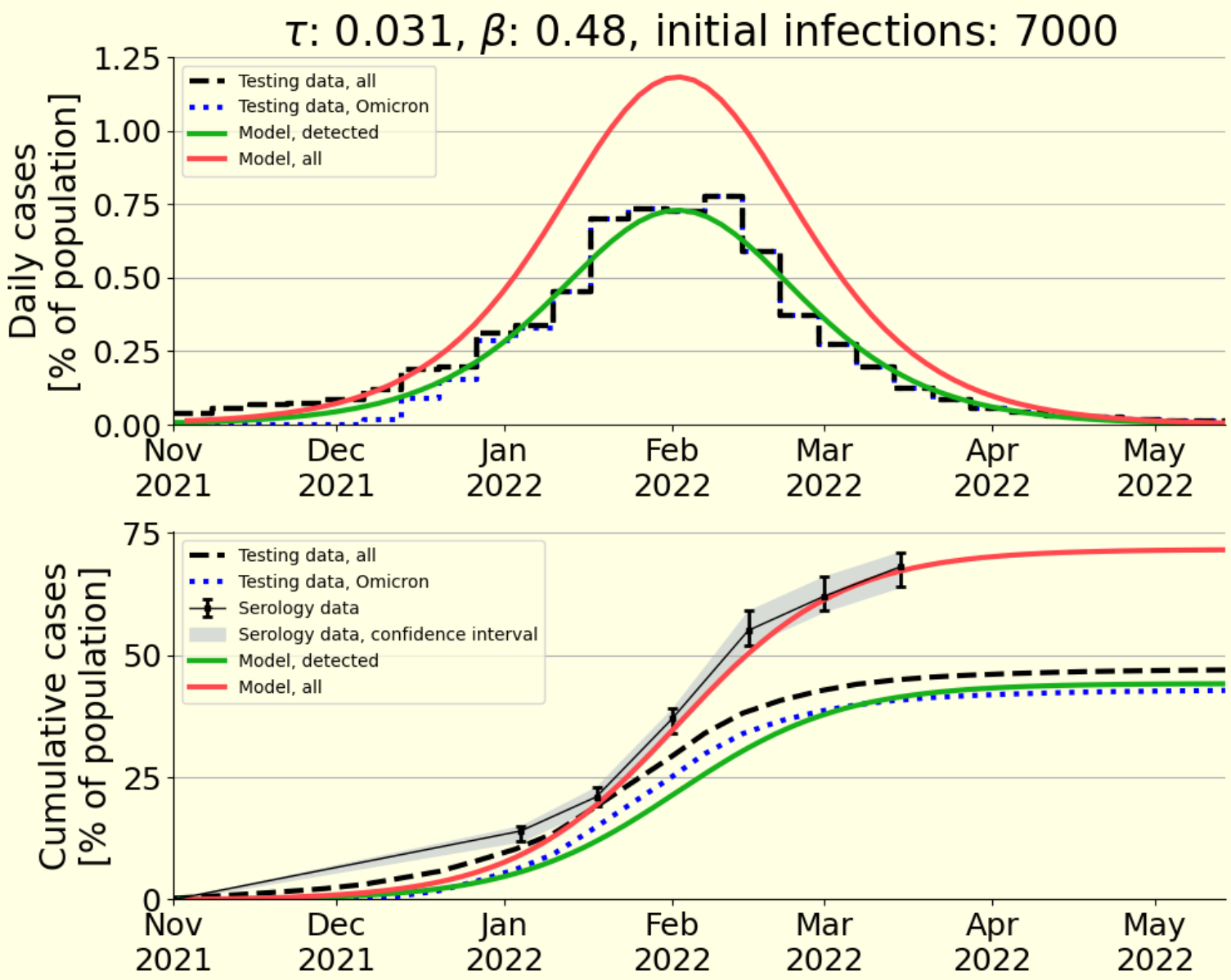

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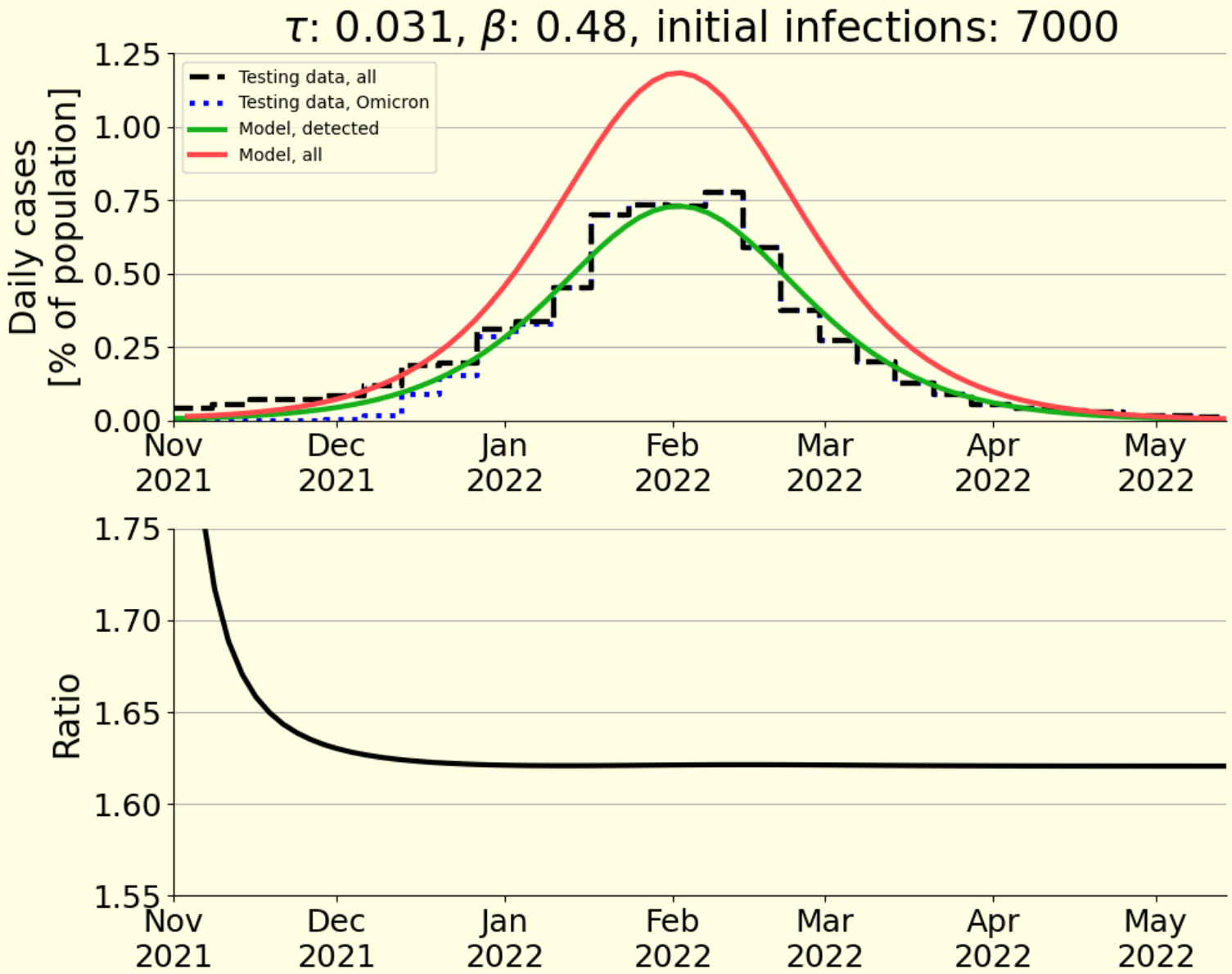

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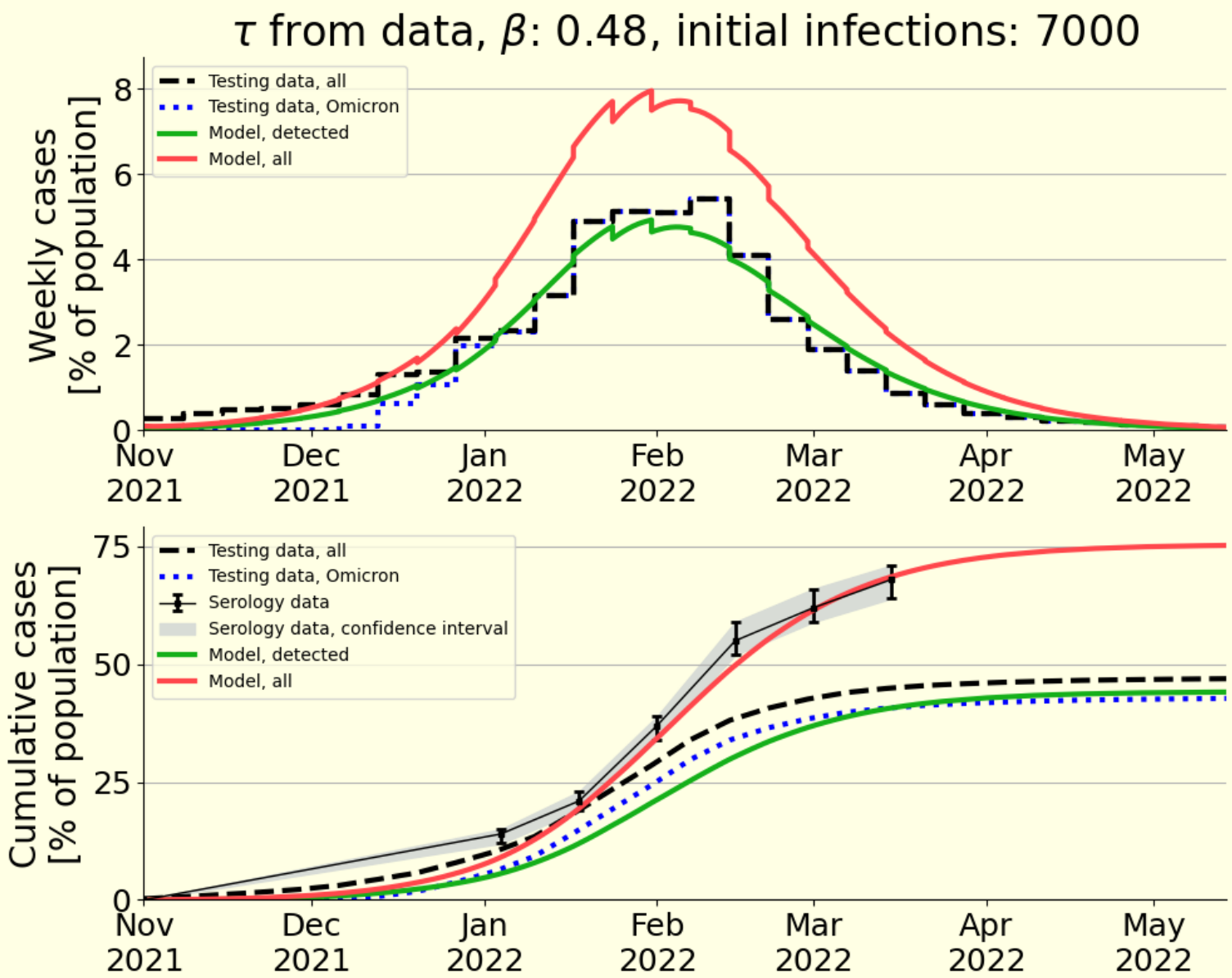

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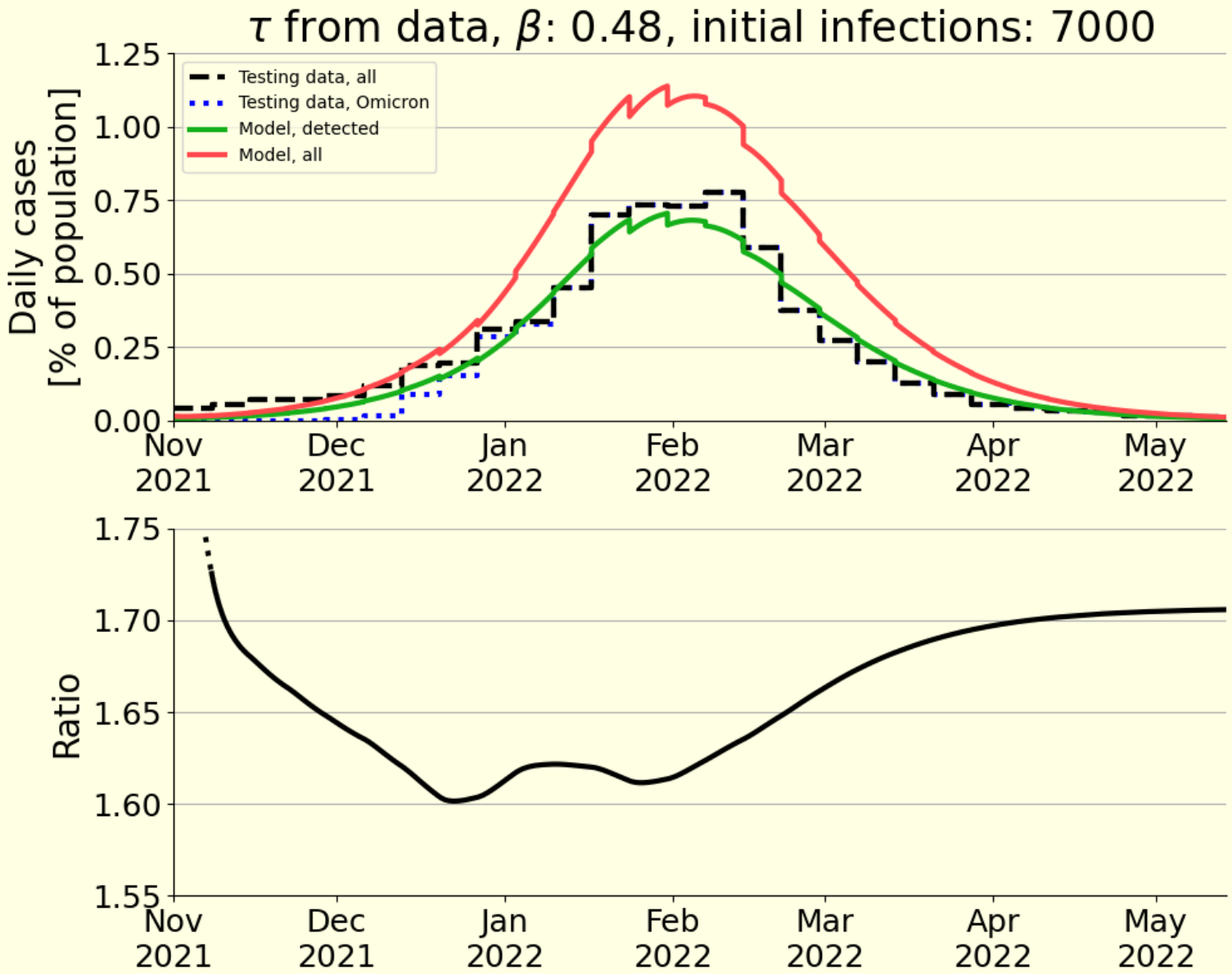

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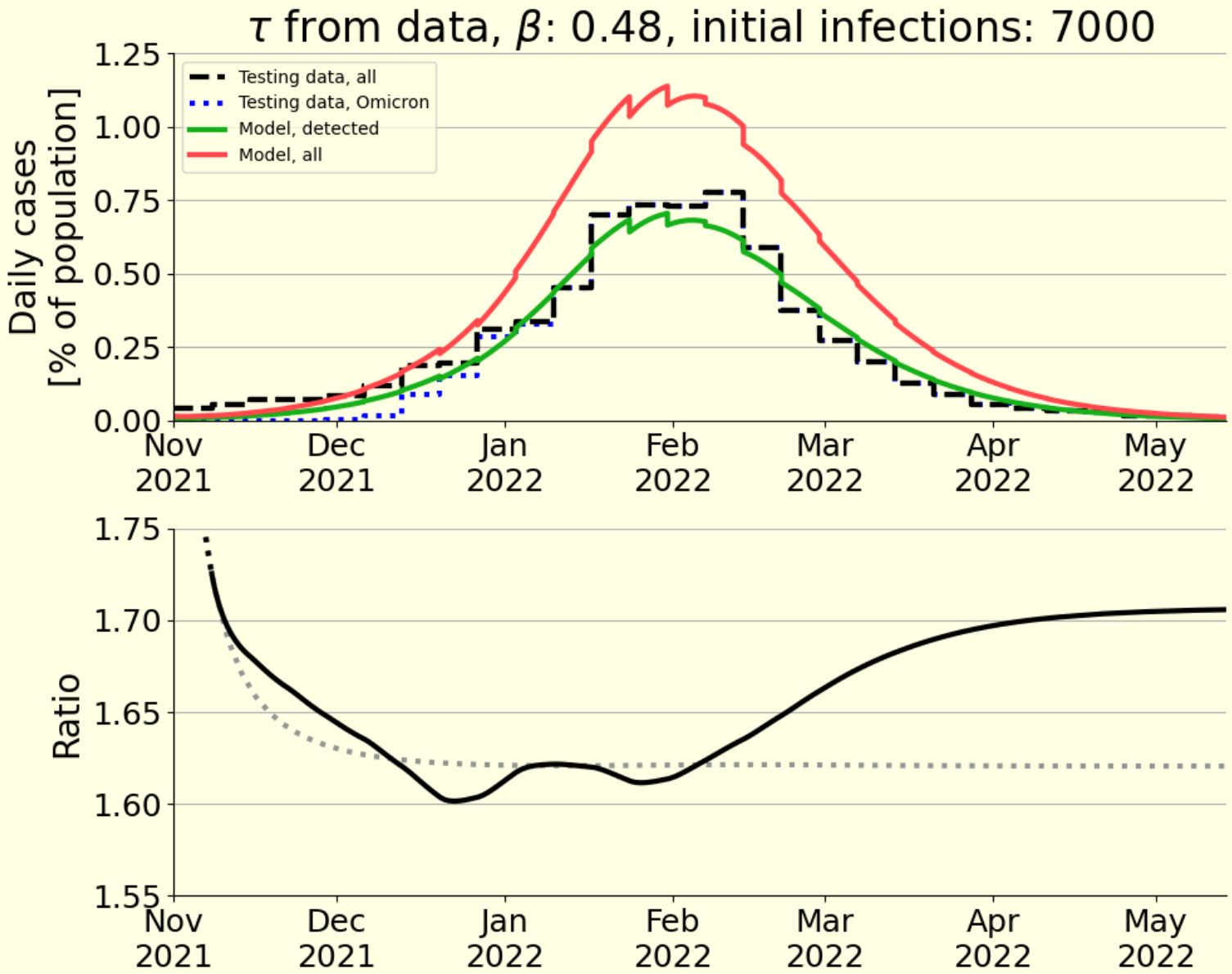

Discussion and comments

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- The simple model allows for analytical results about the epidemic final size in addition to simulations.
- Results suggest between 58% and 63% were identified, a little lower than official estimates suggesting two-thirds.
- Future work consists of further analysis, parameter-fitting and application to other countries.

Thank you for your attention.

Any questions?

Feel free to also contact me with questions or comments later

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