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

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the world

▶ Different approaches to COVID-19 mitigation througout

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▶ Different approaches to COVID-19 mitigation througout the world

► The impact of differences in data-collection must be understood, also for future research.

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▶ Different approaches to COVID-19 mitigation througout the world

- ► The impact of differences in data-collection must be understood, also for future research.
- ► In particular: For each reported case of COVID-19, how many unidentified cases?

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- ▶ Different approaches to COVID-19 mitigation througout the world
- ► The impact of differences in data-collection must be understood, also for future research.
- ► In particular: For each reported case of COVID-19, how many unidentified cases?
- ► The role of testing: Confirmation of symptoms, required for various activities or entirely voluntary?

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- ▶ Different approaches to COVID-19 mitigation througout the world
- ► The impact of differences in data-collection must be understood, also for future research.
- ▶ In particular: For each reported case of COVID-19, how many unidentified cases?
- ▶ The role of testing: Confirmation of symptoms, required for various activities or entirely voluntary?
- ► How do we compare case-counts between periods and places where testing activity was different?

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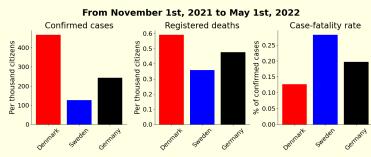
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▶ Different approaches to COVID-19 mitigation througout the world

- ► The impact of differences in data-collection must be understood, also for future research.
- ▶ In particular: For each reported case of COVID-19, how many unidentified cases?
- ▶ The role of testing: Confirmation of symptoms, required for various activities or entirely voluntary?
- ► How do we compare case-counts between periods and places where testing activity was different?

Let's look at some data...



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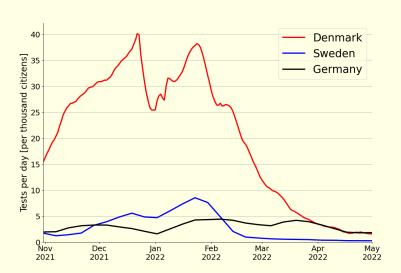
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▶ We aim to determine the ratio between observed cases

and the total number of COVID-19 cases.

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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.

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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.

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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.

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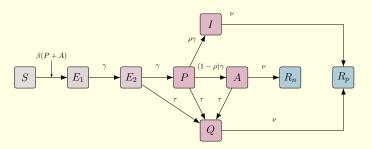
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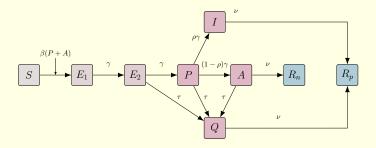
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$$\dot{S} = -\beta S(P+A) \qquad \dot{A} = \gamma (1-\rho)P - \nu A - \tau A$$

$$\dot{E}_1 = \beta S(P+A) - \gamma E_1 \qquad \dot{Q} = \tau (E_2 + P+A) - \nu Q$$

$$\dot{E}_2 = \gamma E_1 - \gamma E_2 - \tau E_2 \qquad \dot{R}_p = \nu Q + \nu I$$

$$\dot{P} = \gamma E_2 - \gamma P - \tau P \qquad \dot{R}_n = \nu A$$

$$\dot{I} = \gamma \rho P - \nu I$$

The model

 $S = -\beta S(P + A)$

 $\dot{E}_1 = \beta S(P+A) - \gamma E_1$

 $\dot{E}_2 = \gamma E_1 - \gamma E_2 - \tau E_2$

 $\dot{D} = \alpha F$, $\alpha D = \pi D$

Rate of testing

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$K_n = V_1 - V_1 - V_2$		
$\dot{I} = \gamma \rho P - \nu I$		
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

 $A = \gamma(1-\rho)P - \nu A - \tau A$

 $\dot{Q} = \tau(E_2 + P + A) - \nu Q$

0 to 0.5

 $R_p = \nu Q + \nu I$

All rates units of day⁻¹. Approximate R_0 of 1.4 initially.

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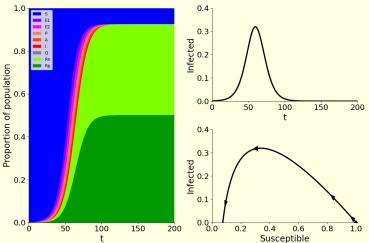
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We consider the fraction of cases identified:

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

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

Analysis of fraction of cases identified

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We consider the fraction of cases identified:

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

where $r_p = \lim_{t\to\infty} R_p(t)$ and $r_n = \lim_{t\to\infty} R_n(t)$. The correction-factor we want is K^{-1} .

Analysis

Fraction identified

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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 $r_n = \lim_{t \to \infty} R_n(t)$.

The correction-factor we want is K^{-1} .

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

$$K = 1 - \left(\frac{\nu}{\nu + \tau}\right) \left(1 - \frac{\tau}{\gamma + \tau}\right) \left(1 - \frac{\gamma \rho + \tau}{\gamma + \tau}\right) \quad (2)$$

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We consider the fraction of cases identified:

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Note that K is independent of β .

We consider the fraction of cases identified:

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 $K = \frac{r_p}{r_p + r_n}$ (1)

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

The correction-factor we want is K^{-1} .

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

$$K = 1 - \left(\frac{\nu}{\nu + \tau}\right) \left(1 - \frac{\tau}{\gamma + \tau}\right) \left(1 - \frac{\gamma \rho + \tau}{\gamma + \tau}\right) \tag{2}$$

Note that K is independent of β .

(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)

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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 .

0.5

0.0

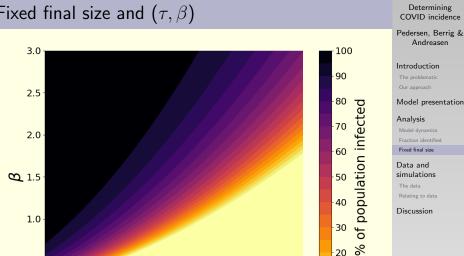
0.1

0.2

0.3

τ

0.4



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20

-10

0.5

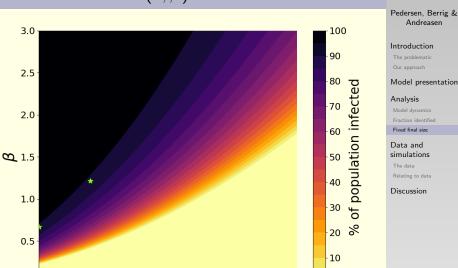
0.0

0.1

0.2

0.3

τ



0.4

0.5

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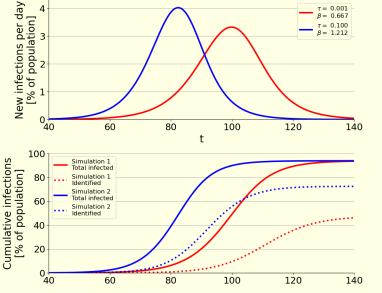
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 $\tau = 0.001$ B = 0.667

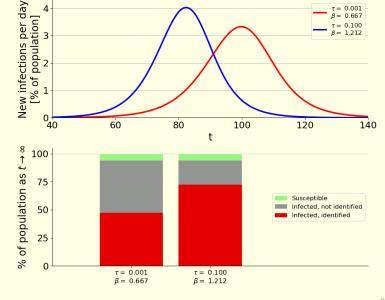
 $\tau = 0.100$

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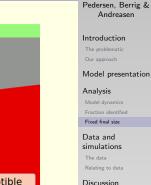
Fixed final size

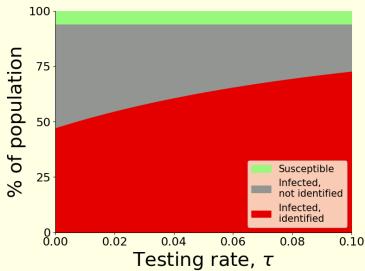
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(β chosen such that final size is fixed)



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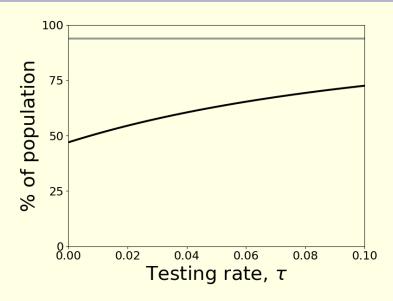
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(β chosen such that final size is fixed)

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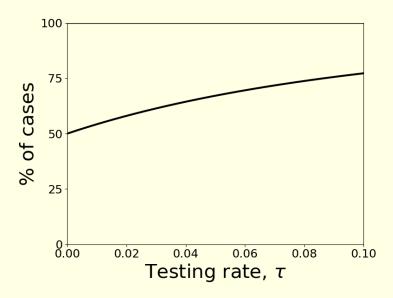
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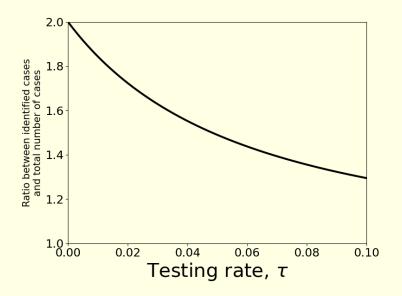
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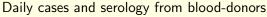
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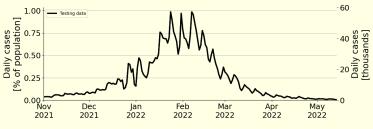
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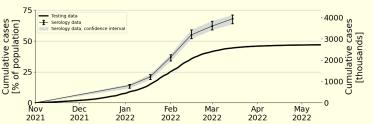
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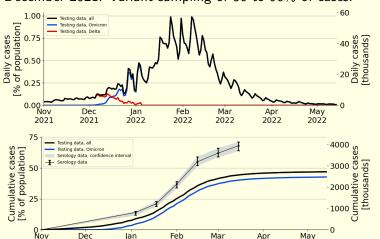


2021

2021

Andreasen

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



2022

2022

2022

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-40

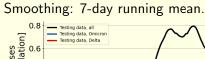
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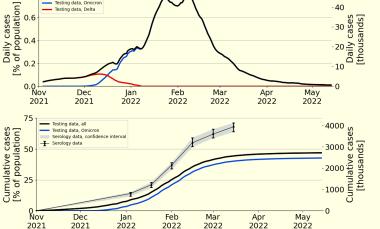
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Weekly cases

May

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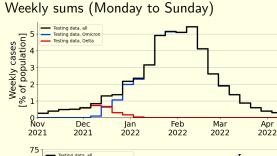
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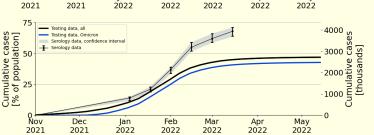
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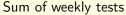
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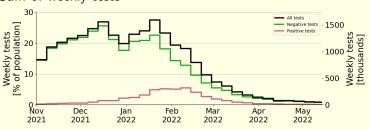
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(Only PCR shown, Antigen-tests at similar magnitude)

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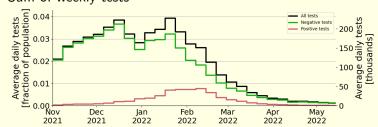
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Scaled to tests per population per day (i.e. τ)





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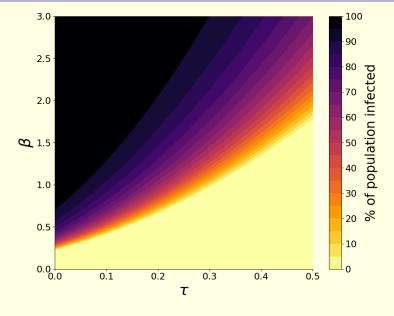
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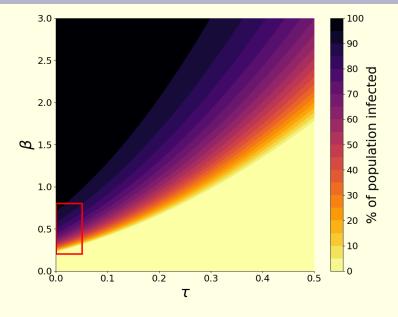
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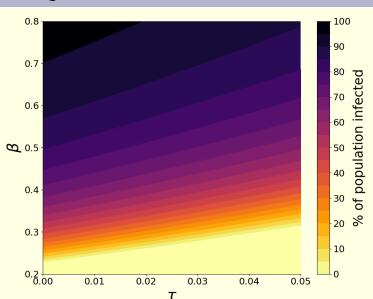
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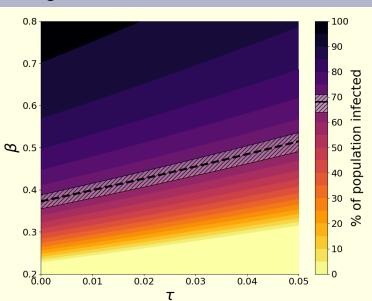
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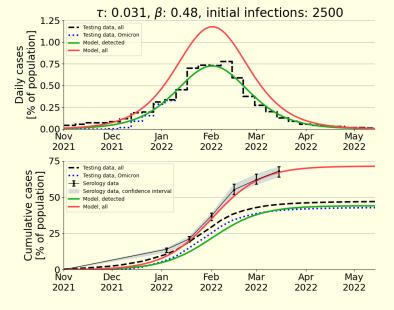
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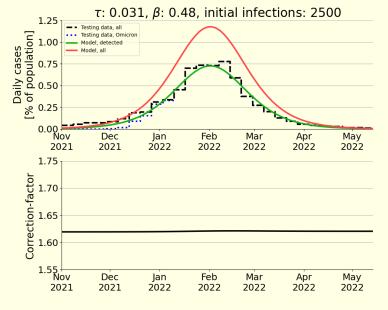
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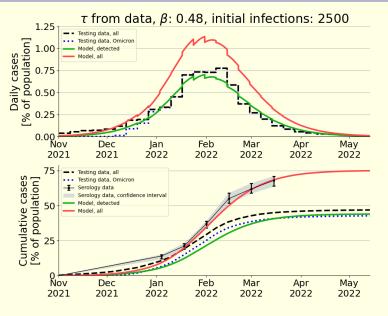
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Testing data, all

Model, all

Testing data, Omicron

1.25

Daily cases



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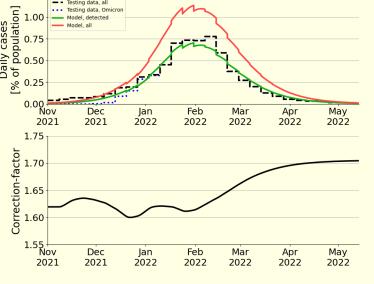
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 τ from data, β : 0.48, initial infections: 2500

Testing data, all

Model, all

Testing data, Omicron

1.25

1.00



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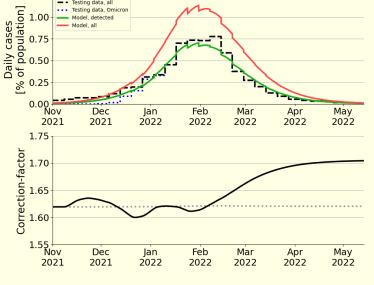
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 τ from data, β : 0.48, initial infections: 2500

► For comparing the impact of COVID-19 between countries, accurate estimates of final size are necessary, particular when evaluating mitigation strategies.

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- ► For comparing the impact of COVID-19 between countries, accurate estimates of final size are necessary, particular when evaluating mitigation strategies.
- ► Using an extended SIR-model, we are able to estimate the fraction of COVID-19 cases identified in the Omicron wave of early 2022 in Denmark.

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► For comparing the impact of COVID-19 between countries, accurate estimates of final size are necessary, particular when evaluating mitigation strategies.

- ▶ Using an extended SIR-model, we are able to estimate the fraction of COVID-19 cases identified in the Omicron wave of early 2022 in Denmark.
- ► The simple model allows for analytical results about the epidemic final size in addition to simulations.

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► For comparing the impact of COVID-19 between countries, accurate estimates of final size are necessary, particular when evaluating mitigation strategies.

- ▶ Using an extended SIR-model, we are able to estimate the fraction of COVID-19 cases identified in the Omicron wave of early 2022 in Denmark.
- ► 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.

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- ► For comparing the impact of COVID-19 between countries, accurate estimates of final size are necessary, particular when evaluating mitigation strategies.
- ▶ Using an extended SIR-model, we are able to estimate the fraction of COVID-19 cases identified in the Omicron wave of early 2022 in Denmark.
- ► 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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