Mathematical modelling for determining COVID-19 incidence from testing data

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Joint work with Christian Berrig and Viggo Andreasen

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▶ Different approaches to COVID-19 mitigation

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▶ Different approaches to COVID-19 mitigation

► To compare mitigation-strategies, the impact of

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- ▶ Different approaches to COVID-19 mitigation throughout the world
- ► To compare mitigation-strategies, the impact of differences in data-collection must be understood.
- ► The role of testing: Confirmation of symptoms, required for various activities or entirely voluntary?

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- ► Different approaches to COVID-19 mitigation throughout the world
- ➤ To compare mitigation-strategies, the impact of differences in data-collection must be understood.
- ► 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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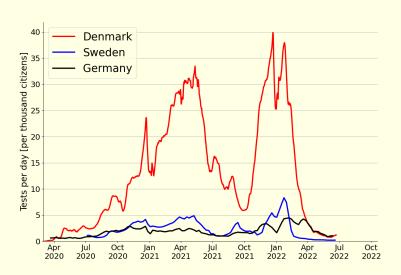
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▶ Different approaches to COVID-19 mitigation throughout the world

- ► To compare mitigation-strategies, the impact of differences in data-collection must be understood.
- ► 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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▶ Overall question: For each reported case of COVID-19, how many unidentified cases?

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▶ Overall question: For each reported case of COVID-19,

▶ We aim to determine a correction factor for observed

how many unidentified cases?

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- ▶ Overall question: For each reported case of COVID-19, how many unidentified cases?
- ▶ We aim to determine a correction factor for observed data.
- ► Approach: Extend the classic SIR-model to include testing.

The conceptual idea

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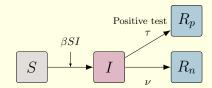
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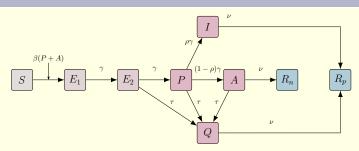
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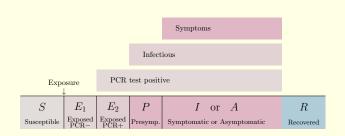
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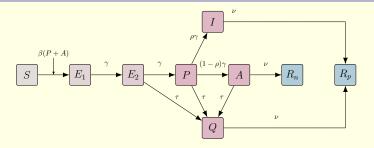
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The model

Determining



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

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 τ : Testing-rate. β : Infectivity.

General model dynamics

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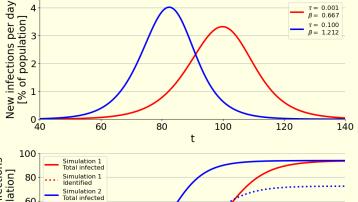
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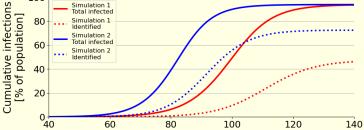
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Other parameters: $\gamma = \nu =$

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We describe the correction factor as ratio between all cases

 $\frac{R_n(t) + R_p(t)}{R_p(t)}$

and cases identified:

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We describe the correction factor as ratio between all cases and cases identified:

$$\frac{R_n(t) + R_p(t)}{R_p(t)} \tag{1}$$

Inspired by previous work on epidemic final size¹ (and after a lot of analysis and calculation), we find that as $t \to \infty$

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

⁽Andreasen, 2018, Bull. Math. Biol.)

Model analysis and correction ratio

We describe the correction factor as ratio between all cases

 $\frac{R_n(t) + R_p(t)}{R_n(t)}$

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

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1 (Andreasen, 2018, Bull. Math. Biol.)

Note that this is independent of β .

and cases identified:

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With parameters: $\gamma = \nu = \frac{1}{3}$ and $\rho = \frac{1}{2}$.

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

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$\frac{R_p}{R_n + R_p} = 1 - \left(1 - \frac{\tau}{\frac{1}{2} + \tau}\right) \left(1 - \frac{\frac{1}{3} \cdot \frac{1}{2} + \tau}{\frac{1}{2} + \tau}\right) \left(\frac{\frac{1}{3}}{\frac{1}{2} + \tau}\right)$

With parameters: $\gamma = \nu = \frac{1}{3}$ and $\rho = \frac{1}{2}$.

Calculating the correction-factor

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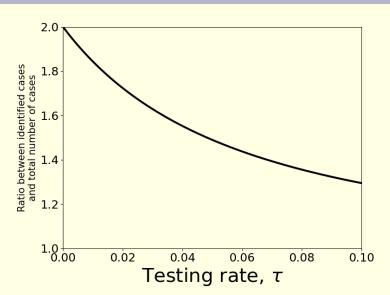
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With parameters: $\gamma = \nu = \frac{1}{3}$ and $\rho = \frac{1}{2}$.

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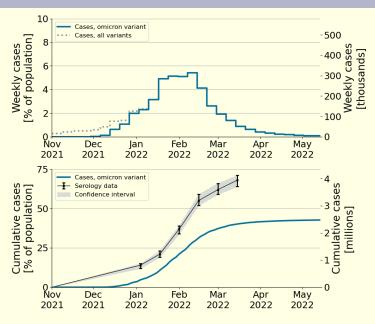
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The Danish data

Cases, omicron variant

Cases, all variants

10 7

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-500

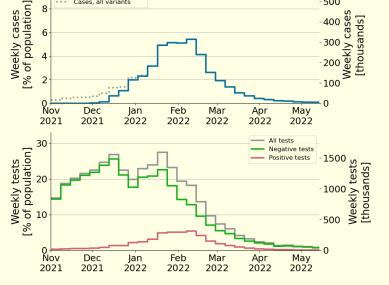
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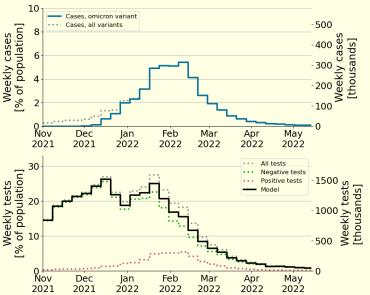
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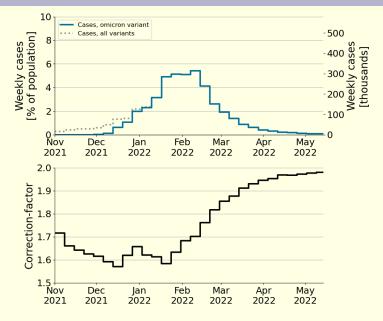
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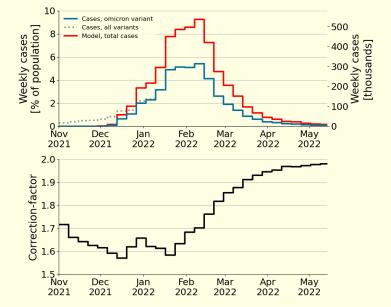
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Cases, omicron variant

Cases, all variants

Model, total cases

10 7

8

6

4

Weekly cases [% of population]





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-300

-200 -100

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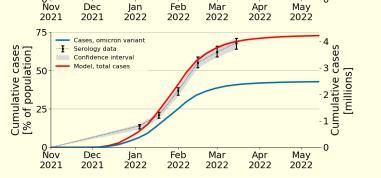
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(7b)

(7d)

(85)

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In general, we consider initial conditions such that the vast majority of the population is initially susceptible, $S_1 \approx 1$, and the initial number of cases is low, $0 < E_{1:n} \ll 1$. In the limit where $S_1 \to 1$, with $E_{1:n} \to 0$, $E_{2:n} \to 0$. $P_0 \rightarrow 0$ and $A_0 \rightarrow 0$, equations (4) become:

 $\log \sigma = -\beta (T_P - T_A)$ $\sigma = 1 - (\gamma + \tau)T\nu$ $\sigma = 1 - (\gamma + \tau)T_{\theta} - \tau T_{\theta}$. $\sigma = 1 - (\nu + \tau)T_{\delta} - (\gamma \rho + \tau)T_{\theta} - \tau T \nu.$ Assuming $T_0 + T_+ \neq 0$, this can be written as:

 $T_P = \frac{1}{1 - \tau} \left(1 - \sigma - \tau T_{E_2}\right)$

 $T_A = \frac{1}{\nu + \tau} \left(1 - \sigma - (\gamma \rho + \tau)T_P - \tau T_{E_2}\right)$

We define $K_F = \frac{r_p}{r_n + r_n}$ and note that at steady state $\sigma = 1 - r_p - r_n$ must hold. This implies that $K_F = \frac{r_F}{r_F}$. Combining equations (8) with equations (5) and (6) under the assumptions $R_{p,0} = 0$ and $R_{\alpha,0} = 0$ and simplifying yields:

> $K_F = \frac{r_p}{r_p + r_n} = \frac{r_p + r_n - r_n}{r_p + r_n} = 1 - \frac{r_n}{r_p + r_n} = 1 - \frac{r_n}{1 - \sigma} = 1 - \frac{\nu}{1 - \sigma} T_A$ $K_F = 1 - \left(\frac{\nu}{\nu + \tau}\right) \left(1 - \frac{\tau}{\nu + \tau}\right) \left(1 - \frac{\gamma \rho + \tau}{\nu + \tau}\right)$

For initial conditions sufficiently close to the case where $S_n = 1$ and all other variables are zero, K_F is an approximation of the final size of K(t) as $t \to \infty$

We note that equation (8a) describes a relation between β and σ . Since T_P and T_A are described in terms

Note that the expression for K_F , equation (10) is independent of σ and β . Furthermore, in the absence of tests, i.e. for $\tau = 0$, we have $K_F = 1 - 1(1 - 0)(1 - \rho) = \rho$. This is expected, as only the symptomatic cases, I, are found in the situation where $\tau = 0$, and the symptomatic cases make up exactly ρ of all cases In the situation where all cases are symptomatic, $\rho = 1$, we obtain $K_F = 1$, that is, all cases are identified of γ , τ , ν and σ , it is possible to use equation (8a) to determine a value of β that yields a particular σ .

(4b)

(40)

$$r_p = R_{p,0} = \nu T_0 + \nu T_I$$
 (f
 $r_n = R_{n,0} = \nu T_A$ (f

As $t \to \infty$, the model system approaches a steady state without any active cases. In this section, we derive an analytic expression for the value that the fraction of cases identified, K(t), approaches as $t \to \infty$. To obtain an expression for K_F , we follow the methodology previously considered by 7. For notational numbers, we define for each variable x, the integral over the full endemic as $T_- = \int_{-\infty}^{\infty} x dt$. From the system of differential equations given in equations (1), we write up the following quantities:

S/S = -B(P + A)

As t approaches infinity, the stability of the systems implies that all variables apart from S, R_0 and R_n are

 $\log \sigma = -\beta (T_P - T_A)$ $\sigma - S_0 - E_{1,0} - E_{2,0} = -(\gamma + \tau)T_{E_1}$

 $\dot{S} + \dot{E_1} + \dot{E_2} = -(\gamma + \tau)E_1$

 $\dot{S} + \dot{E_1} + \dot{E_2} + \dot{P} = -(\gamma + \tau)P - \tau E_2$ $S + E_1 + E_2 + P + A = -(\nu + \tau)A - (\gamma \rho + \tau)P - \tau E_2$

 $\sigma - S_0 - E_{1,0} - E_{2,0} - P_0 = -(\gamma + \tau)T_P - \tau T_{E_1}$

 $\sigma = S_0 - F_1 \circ - F_2 \circ - P_2 - P_3 = -(\nu + \tau)T_4 - (\gamma \sigma + \tau)T_9 - \tau T_9$

Furthermore, observe that the equations for \hat{R}_0 and \hat{R}_0 , equations (1) and (1h) respectively, when integrated

A.3 Final Size Calculations

Integrating equations (3) from t=0 to $t=\infty$ yields:

Where X_0 denote the initial condition for variable X.

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$$\frac{R_p}{R_n + R_p} = 1 - \left(1 - \frac{\tau}{\gamma + \tau}\right) \left(1 - \frac{\gamma \rho + \tau}{\gamma + \tau}\right) \left(\frac{\nu}{\nu + \tau}\right)$$

can be rewritten as:

$$1 - \frac{R_p}{R_n + R_p} = \frac{R_n}{R_n + R_p} = \left(\frac{\gamma}{\gamma + \tau}\right) \left(\frac{(1 - \rho)\gamma}{\gamma + \tau}\right) \left(\frac{\nu}{\nu + \tau}\right)$$

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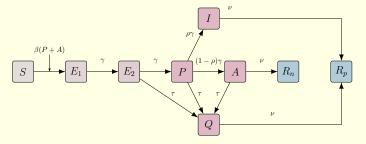
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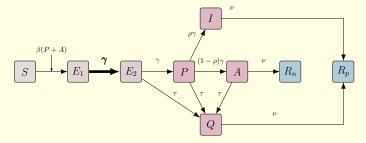
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$\left(\frac{\gamma}{\gamma}\right)$

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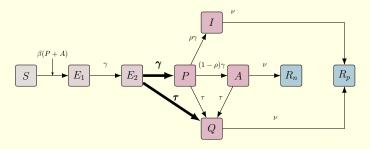
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$\left(\frac{\gamma}{\gamma}\right)\left(\frac{\gamma}{\gamma+\tau}\right)$

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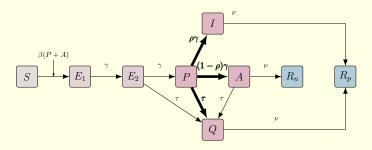
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$$\left(\frac{\gamma}{\gamma}\right)\left(\frac{\gamma}{\gamma+\tau}\right)\left(\frac{(1-\rho)\gamma}{\gamma+\tau}\right)$$

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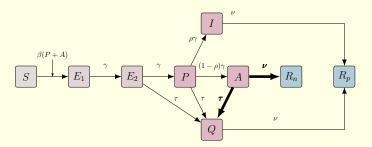
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$$\left(\frac{\gamma}{\gamma}\right)\left(\frac{\gamma}{\gamma+\tau}\right)\left(\frac{(1-\rho)\gamma}{\gamma+\tau}\right)\left(\frac{\nu}{\nu+\tau}\right)$$

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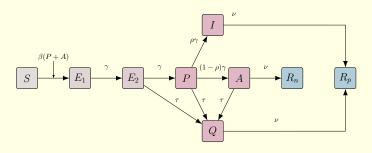
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$$\frac{R_n}{R_n + R_p} = \left(\frac{\gamma}{\gamma + \tau}\right) \left(\frac{\gamma(1 - \rho)}{\gamma + \tau}\right) \left(\frac{\nu}{\nu + \tau}\right)$$

Extension to other models, example 1

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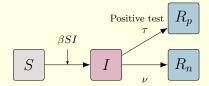
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Flow-considerations:

Extension to other models, example 1

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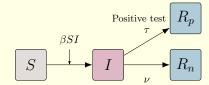
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$$\frac{R_n}{R_n + R_n} = \frac{\nu}{\nu + \tau}$$

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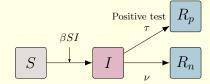
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Flow-considerations:
$$\frac{R_n}{R_n + R_n} = \frac{\nu}{\nu + \tau}$$

Correction factor: $\frac{\nu + \tau}{\tau}$

Simplified method, Matrix-form

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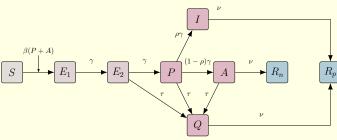
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For SIR-type models², the inverse of a matrix V describing flows in the "infected sub-system" is typically computed to determine the reproduction number \mathcal{R}_0 .

 $^{^{1}}$ See (van den Drische and Watmough, 2002) for definition and derivation.

Simplified method, Matrix-form



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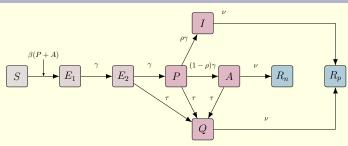
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For SIR-type models², the inverse of a matrix V describing flows in the "infected sub-system" is typically computed to determine the reproduction number \mathcal{R}_0 .

With sub-system $x = (E_1, E_2, P, I, A)$ and matrix V, we consider "inputs" $\alpha = (1, 0, 0, 0, 0)$ and "outputs" $\omega = (0, 0, 0, 0, \nu)$, and find that:

$$\frac{R_n}{R_n + R_p} = \omega V^{-1} \alpha^T$$

 $^{^{1}}$ See (van den Drische and Watmough, 2002) for definition and derivation.

 τ_H

 τ_L

 τ_H

 $\beta(I_L + I_H)$

 $\beta(I_L + I_H)$

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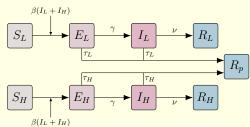
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$$x = (E_H, E_L, I_H, I_L), \quad V = \begin{pmatrix} \gamma + \tau_H & 0 & 0 & 0 \\ 0 & \gamma + \tau_L & 0 & 0 \\ \gamma & 0 & \nu + \tau_H & 0 \\ 0 & \gamma & 0 & \nu + \tau_L \end{pmatrix}$$

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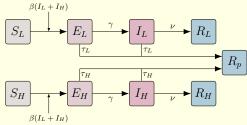
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$$x = (E_H, E_L, I_H, I_L), \quad V = \begin{pmatrix} \gamma + \tau_H & 0 & 0 & 0 \\ 0 & \gamma + \tau_L & 0 & 0 \\ \gamma & 0 & \nu + \tau_H & 0 \\ 0 & \gamma & 0 & \nu + \tau_L \end{pmatrix}$$

$$lpha = \left(rac{S_H}{S_H + S_L}, rac{S_L}{S_H + S_L}, 0, 0
ight)$$
 and $\omega = (0, 0, \nu, \nu)$

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$$x = (E_H, E_L, I_H, I_L), \quad V = \begin{pmatrix} \gamma + \tau_H & 0 & 0 & 0 \\ 0 & \gamma + \tau_L & 0 & 0 \\ \gamma & 0 & \nu + \tau_H & 0 \\ 0 & \gamma & 0 & \nu + \tau_L \end{pmatrix}$$

$$lpha = \left(rac{S_H}{S_H + S_L}, rac{S_L}{S_H + S_L}, 0, 0
ight)$$
 and $\omega = (0, 0,
u,
u)$

Hence:
$$\omega V^{-1} \alpha^T = \frac{\nu \gamma}{S_H + S_L} \left(\frac{S_H}{(\nu + \tau_H)(\gamma + \tau_H)} + \frac{S_L}{(\nu + \tau_L)(\gamma + \tau_L)} \right)$$

► We determine a relation between observed COVID-19 cases and total new cases, as a function of testing-rate.

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Thank you for your attention.



Feel free to email me with questions or comments

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