

**SUPPLEMENTARY MATERIALS: DISCRETE INVERSE METHOD
FOR EXTRACTING DISEASE TRANSMISSION RATES FROM
ACCESSIBLE INFECTION DATA***

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THEOREM SM0.1. *For the SIS model 2.1, given a smooth positive function $f(t)$ generated from prevalence data, $\gamma > 0$, $N > 0$, $\beta_0 > 0$, and $T > 0$, there exists $K > 0$ such that if $\beta_0 < K$ there is a solution $\beta(t)$ with $\beta(0) = \beta_0$ such that $I(t) = f(t)$ for $0 \leq t \leq T$ if and only if $\frac{f'(t)}{f(t)} > -\gamma$ for $0 \leq t \leq T$.*

Proof. Since $I(t) = f(t)$, from the second equation of system (2.1) we have

$$(SM0.1) \quad S(t) = \frac{N(f'(t) + \gamma f(t))}{\beta(t)f(t)}.$$

Substituting (SM0.1) into the first equation of system (2.1) and calculating $S'(t)$ we get

$$(SM0.2) \quad \frac{d}{dt} \left(\frac{N(f'(t) + \gamma f(t))}{\beta(t)f(t)} \right) = -\beta(t) \frac{N(f'(t) + \gamma f(t))}{\beta(t)f(t)} \frac{f(t)}{N} + \gamma f(t).$$

Simplifying equation (SM0.2) yields the following Bernoulli differential equation for $\beta(t)$:

$$(SM0.3) \quad \beta'(t) - p(t)\beta(t) - q(t)\beta(t)^2 = 0,$$

where

$$p(t) = \frac{f(t)f''(t) - (f'(t))^2}{f(t)(f'(t) + \gamma f(t))}, \quad q(t) = \frac{f(t)f'(t)}{f'(t) + \gamma f(t)}.$$

Let $x(t) = \frac{1}{\beta(t)}$. Then equation (SM0.3) can be transformed into the following linear equation:

$$(SM0.4) \quad x'(t) + p(t)x(t) + q(t) = 0, \quad \square$$

Solving equation (SM0.4) by the method of integrating factors we get

$$\frac{1}{\beta(t)} = x(t) = x(0)e^{-\int_0^t p(\tau)d\tau} - e^{-\int_0^t p(\tau)d\tau} \int_0^t e^{\int_0^s p(\tau)d\tau} q(s)ds.$$

We need the condition $f'(t) + \gamma f(t) > 0$ to ensure that the denominator of $p(t)$ and $q(t)$ be nonzero so that a singular solution is prevented.

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To ensure that $\beta(t)$ is positive, $\beta(0)$ must satisfy

$$\frac{1}{\beta(0)} > \int_0^T e^{\int_0^s p(\tau) d\tau} q(s) ds.$$

A discrete SIS model based on centered Euler discretization is given by the following system:

$$(SM0.5) \quad \begin{aligned} S_{n+1} &= S_{n-1} - \frac{2\beta_n S_n I_n \Delta t}{N} + 2\gamma I_n \Delta t, \\ I_{n+1} &= I_{n-1} + \frac{2\beta_n S_n I_n \Delta t}{N} - 2\gamma I_n \Delta t. \end{aligned}$$

THEOREM SM0.2. *For the model system (SM0.5), suppose that the initial disease prevalence data I_0, I_1 are available and the time series of incidence data $y_n, n = 0, 1, \dots, K$ are given at equally spaced time step Δt , then the transmission rates can be estimated by the following iteration process:*

$$\begin{aligned} I_{n+1} &= 2y_n \Delta t - 2\gamma I_n \Delta t + I_{n-1}, \\ S_{n+1} &= N - I_{n+1}, \\ \beta_n &= \frac{N(S_{n-1} - S_{n+1})}{2S_n I_n \Delta t} + \frac{N\gamma}{S_n}, \\ n &= 1, 2, \dots, K-1, \end{aligned}$$

and β_0 and β_K can be approximated by β_1 and β_{K-1} , respectively, if the obtained time series of susceptible and infected compartments as well as transmission rates are all non-negative, which can be tested numerically.

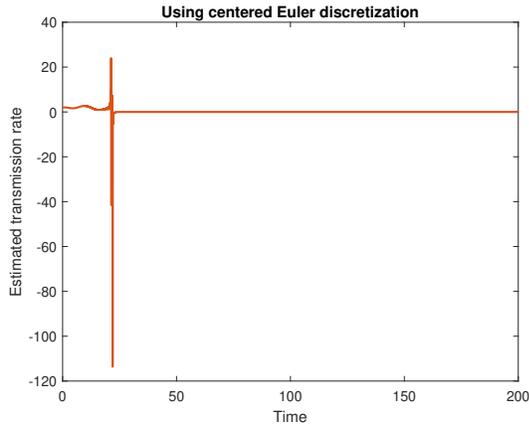


FIG. SM0.1. *The estimated transmission rates by discrete inverse method based on centered Euler discretization.*

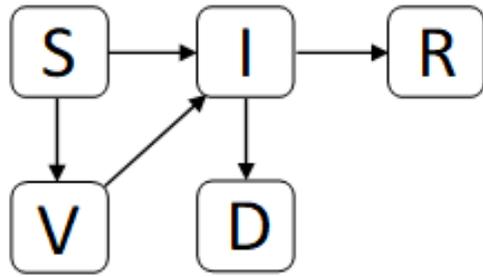


FIG. SM0.2. *Diagram of the flu model (3.1)*

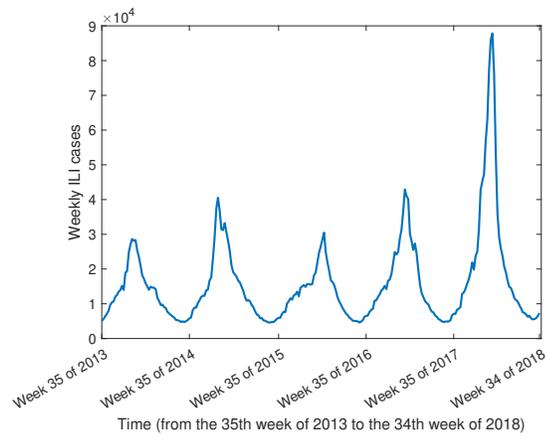


FIG. SM0.3. *Weekly reported ILI cases in the US from the 35th week of 2013 to the 34th week of 2018.*

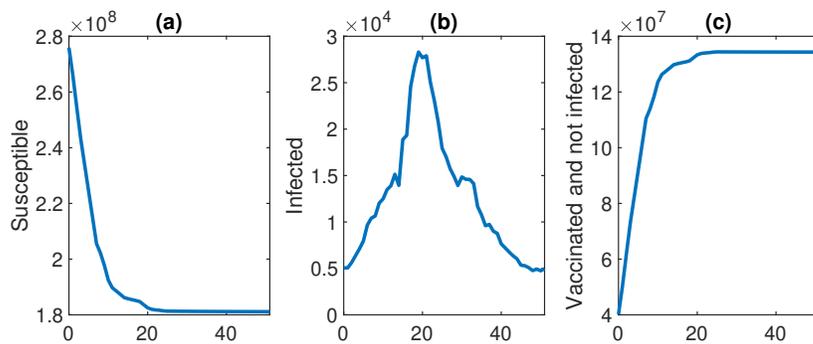


FIG. SM0.4. *Weekly time series of the susceptible, infected, vaccinated and not infected populations from week 35 of 2013 to week 34 of 2014.*

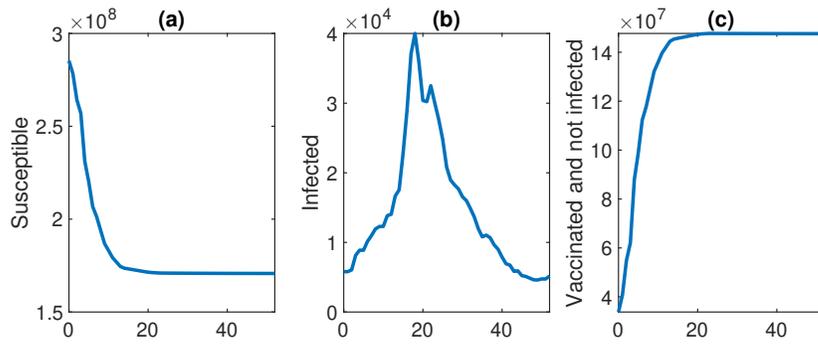


FIG. SM0.5. Weekly time series of the susceptible, infected, vaccinated and not infected populations from week 35 of 2014 to week 34 of 2015.

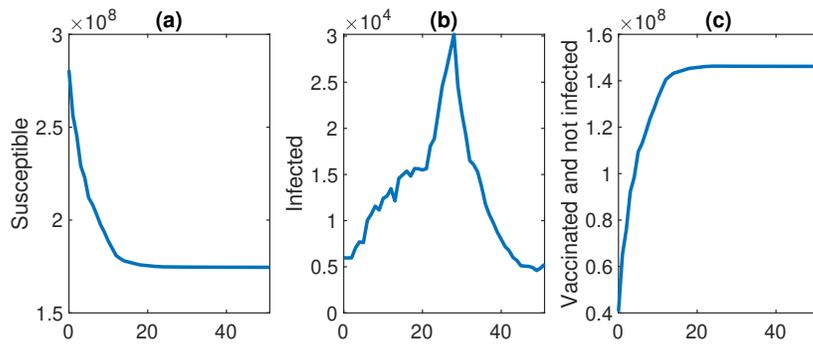


FIG. SM0.6. Weekly time series of the susceptible, infected, vaccinated and not infected populations from week 35 of 2015 to week 34 of 2016.

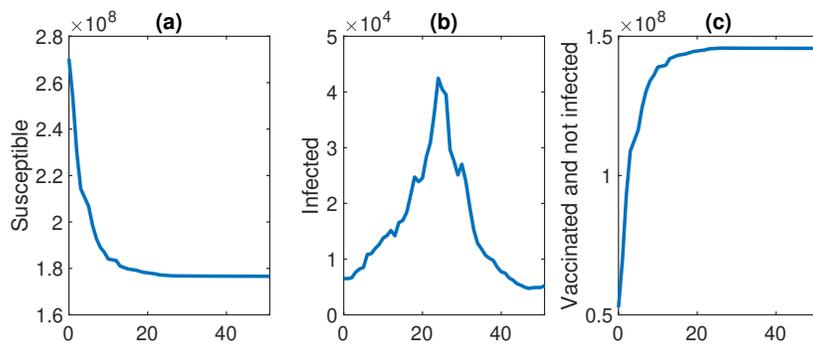


FIG. SM0.7. Weekly time series of the susceptible, infected, vaccinated and not infected populations from week 35 of 2016 to week 34 of 2017.

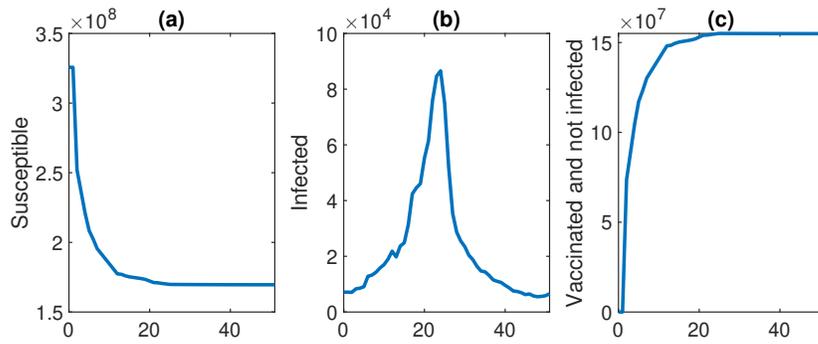


FIG. SM0.8. Weekly time series of the susceptible, infected, vaccinated and not infected populations from week 35 of 2017 to week 34 of 2018.

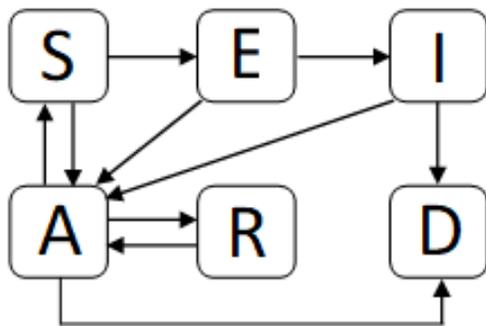


FIG. SM0.9. Diagram of the measles model (4.1)

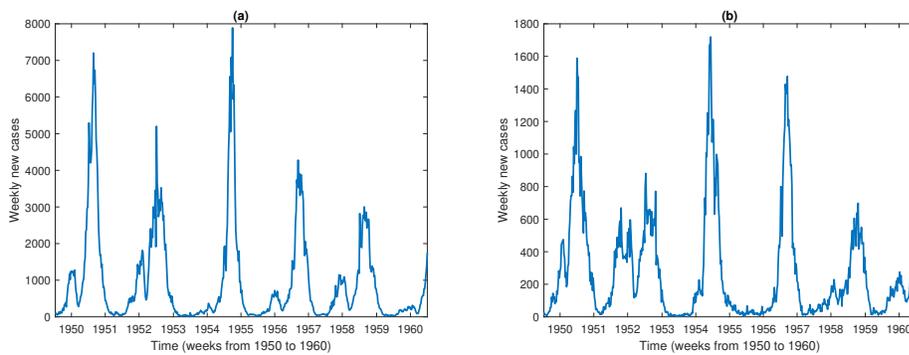


FIG. SM0.10. (a) Weekly new cases of measles in **London** from 1950 to 1960. (b) Weekly new cases of measles in **Manchester** from 1950 to 1960.

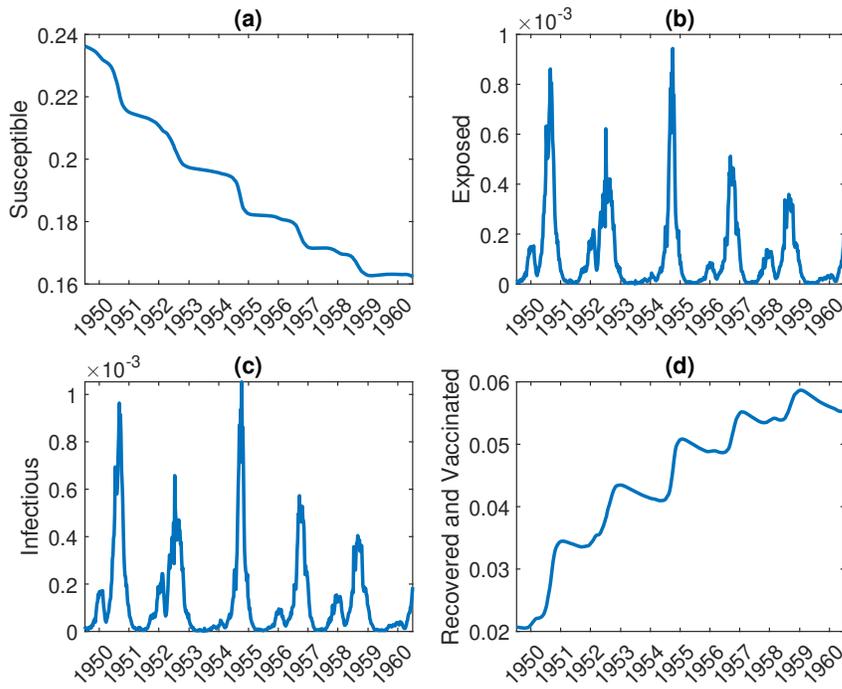


FIG. SM0.11. Weekly time series of the measles model variables in **London** from 1950 to 1960: (a) Susceptible juvenile compartment; (b) Exposed juvenile compartment; (c) Infectious juvenile compartment; (d) Recovered and vaccinated juvenile compartment.

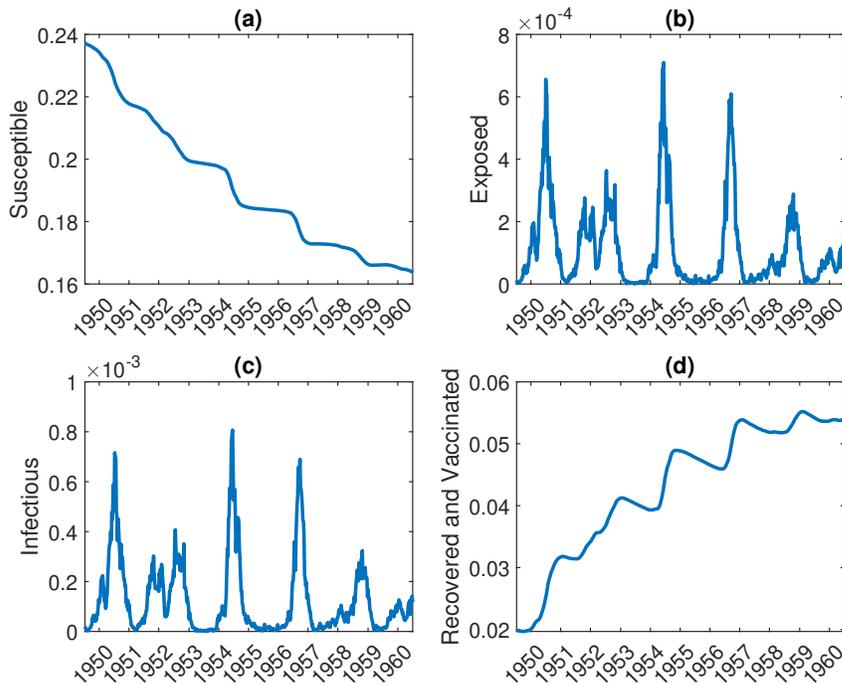


FIG. SM0.12. Weekly time series of the measles model variables in **Manchester** from 1950 to 1960: (a) Susceptible juvenile compartment; (b) Exposed juvenile compartment; (c) Infectious juvenile compartment; (d) Recovered and vaccinated juvenile compartment.

REMARK SM0.3. Suppose that the disease incidence data (i.e., the number of weekly new infections) are known for the measles model (4.1). In order to use the continuous inverse method to derive the transmission rates of measles from system (4.1), we can go with the following procedure:

- Step 1. Interpolate incidence data with a spline to generate a continuous function $\omega(t)$.
- Step 2. Let $aE(t) = \omega(t)$. Then $E(t) = \frac{\omega(t)}{a}$.
- Step 3. Replace the term $aE(t)$ with $\omega(t)$ in the equation for compartment “I” (i.e., the third equation of system (4.1)), and solve for $I(t)$ from the resulting equation. Here we denote the solution as $I(t) = f_I(\omega(t))$ since it depends on $\omega(t)$.
- Step 4. Substitute $E(t) = \frac{\omega(t)}{a}$ and $I(t) = f_I(\omega(t))$ into the equation for compartment “E” (i.e., the second equation of system (4.1)), and solve for $S(t)$. Here we denote the solution as $S(t) = f_S(\beta(t), \omega(t), \omega'(t))$.
- Step 5. Substitute $S(t) = f_S(\beta(t), \omega(t), \omega'(t))$ and $I(t) = f_I(\omega(t))$ into the equation for compartment “S” (i.e., the first equation of system (4.1)) and solve for $A(t)$. Here we denote the solution as $A(t) = f_A(\beta(t), \beta'(t), \omega(t), \omega'(t))$.

$\omega''(t)$.

Step 6. Substitute $A(t) = f_A(\beta(t), \beta'(t), \omega(t), \omega'(t), \omega''(t))$ and $I(t) = f_I(\omega(t))$ into the equation for compartment “R” (i.e., the fourth equation of system (4.1)) and solve for $R(t)$. Here we denote the solution as $R(t) = f_R(\beta(t), \beta'(t), \omega(t), \omega'(t), \omega''(t))$.

Step 7. Substitute $A(t) = f_A(\beta(t), \beta'(t), \omega(t), \omega'(t), \omega''(t))$, $S(t) = f_S(\beta(t), \omega(t), \omega'(t))$, $E(t) = \frac{\omega(t)}{a}$, $I(t) = f_I(\omega(t))$ and $R(t) = f_R(\beta(t), \beta'(t), \omega(t), \omega'(t), \omega''(t))$ into the equation for compartment “A” (i.e., the last equation of system (4.1)). Then we will get an equation about $\beta(t)$, $\beta'(t)$ and $\beta''(t)$, whose coefficients involve the known functions $\omega(t)$, $\omega'(t)$, $\omega''(t)$ and $\omega'''(t)$. Thus, we can solve for $\beta(t)$.

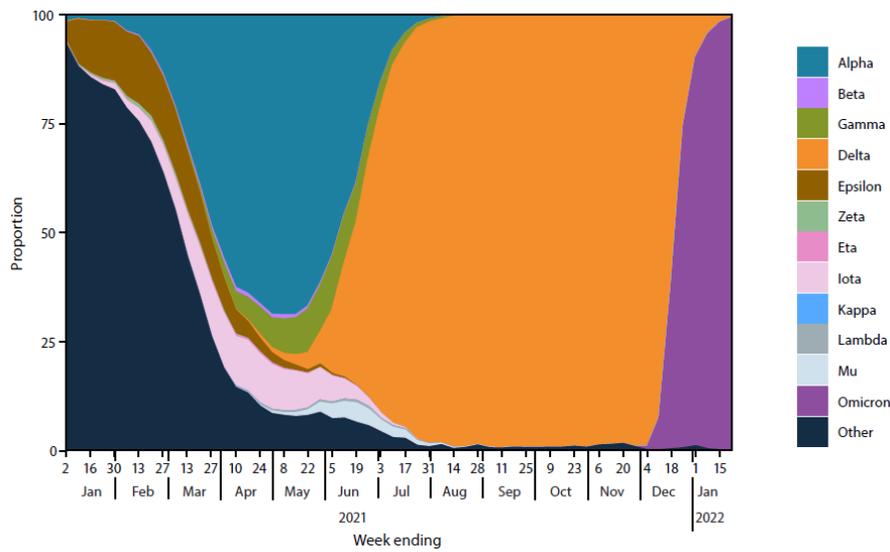


FIG. SM0.13. National weekly proportion estimates of SARS-CoV-2 variants—United States, January 2, 2021–January 22, 2022. Adapted from [SM1].

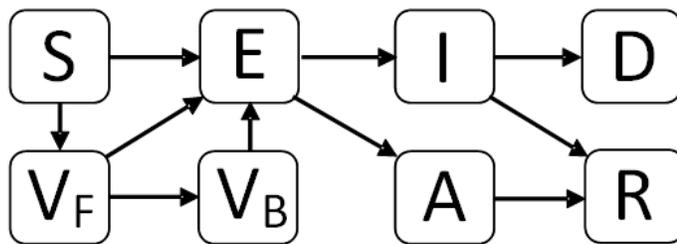


FIG. SM0.14. Diagram of the COVID-19 model (5.1).

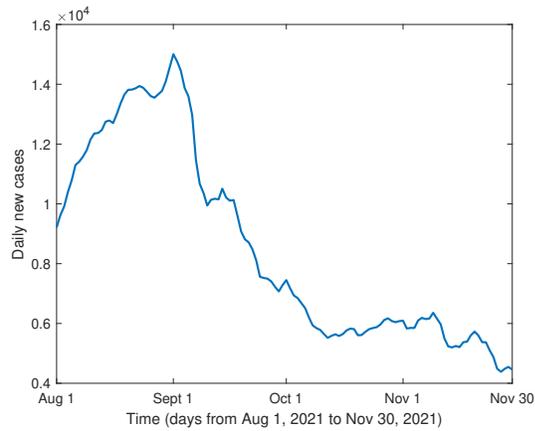


FIG. SM0.15. *Daily confirmed cases of COVID-19 in California from August 1, 2021 to November 30, 2021.*

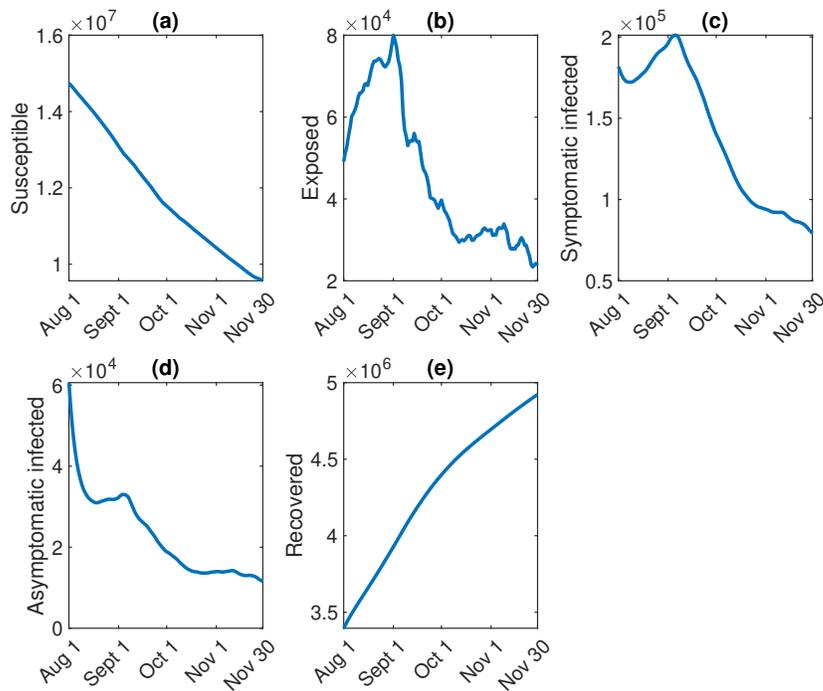


FIG. SM0.16. *Daily time series of the COVID-19 model variables in California from August 1, 2021 to November 30, 2021: (a) Susceptible compartment; (b) Exposed compartment; (c) Symptomatic infected compartment; (d) Asymptomatic infected compartment; (e) Recovered compartment.*

REMARK SM0.4. *Suppose that the disease incidence data (i.e., the number of daily new infections) are known for the COVID-19 model (5.1). In order to use the*

continuous inverse method to derive the transmission rates of COVID-19 from system (5.1), we can go with the following procedure:

Step 1. Interpolate incidence data with a spline to generate a continuous function $\omega(t)$.

Step 2. Let $(1-p)\delta E(t) = \omega(t)$. Then $E(t) = \frac{\omega(t)}{(1-p)\delta}$.

Step 3. Replace the term $(1-p)\delta E(t)$ by $\omega(t)$ in the equation for compartment “I” (i.e., the third equation of system (5.1)), and solve for $I(t)$. Here we denote the solution as $I(t) = f_I(\omega(t))$ since it depends on $\omega(t)$.

Step 4. Substitute $E(t) = \frac{\omega(t)}{(1-p)\delta}$ into the equation for compartment “A” (i.e., the fourth equation of system (5.1)), and solve for $A(t)$. Here we denote the solution as $A(t) = f_A(\omega(t))$.

Step 5. Substitute $I(t) = f_I(\omega(t))$, $E(t) = \frac{\omega(t)}{(1-p)\delta}$ and $A(t) = f_A(\omega(t))$ into the equation for compartment “S” (i.e., the first equation of system (5.1)), and solve for $S(t)$. Here we denote the solution as $S(t) = f_S(\beta(t), \omega(t))$.

Step 6. Substitute $S(t) = f_S(\beta(t), \omega(t))$, $I(t) = f_I(\omega(t))$, $E(t) = \frac{\omega(t)}{(1-p)\delta}$ and $A(t) = f_A(\omega(t))$ into the equation for compartment “ V_F ” (i.e., the fifth equation of system (5.1)), and solve for V_F . Here we denote the solution as $V_F(t) = f_F(\beta(t), \omega(t))$.

Step 7. Substitute $V_F(t) = f_F(\beta(t), \omega(t))$, $I(t) = f_I(\omega(t))$, $E(t) = \frac{\omega(t)}{(1-p)\delta}$ and $A(t) = f_A(\omega(t))$ into the equation for compartment “ V_B ” (i.e., the sixth equation of system (5.1)), and solve for V_B . Here we denote the solution as $V_B(t) = f_B(\beta(t), \omega(t))$.

Step 8. Substitute $S = f_S(\beta(t), \omega(t))$, $V_F = f_F(\beta(t), \omega(t))$, $V_B = f_B(\beta(t), \omega(t))$, $I = f_I(\omega(t))$, $E = \frac{\omega(t)}{(1-p)\delta}$ and $A = f_A(\omega(t))$ into the equation for compartment “E” (i.e., the second equation of system (5.1)). Then we will get an equation about $\beta(t)$, whose coefficients involve $\omega(t)$ and $\omega'(t)$. Thus, we can solve for $\beta(t)$.

REFERENCES

- [SM1] A. S. LAMBROU, P. SHIRK, AND M. K. STEELE, *Genomic surveillance for SARS-CoV-2 variants: Predominance of the Delta (B.1.617.2) and Omicron (B.1.1.529) variants-United States, June 2021-January 2022*, MMWR Morb Mortal Wkly Rep, 71 (2022), pp. 206–211, <https://doi.org/10.15585/mmwr.mm7106a4externalicon>.