

# Web Material

## Estimating the effect of social distancing interventions on COVID-19 in the United States

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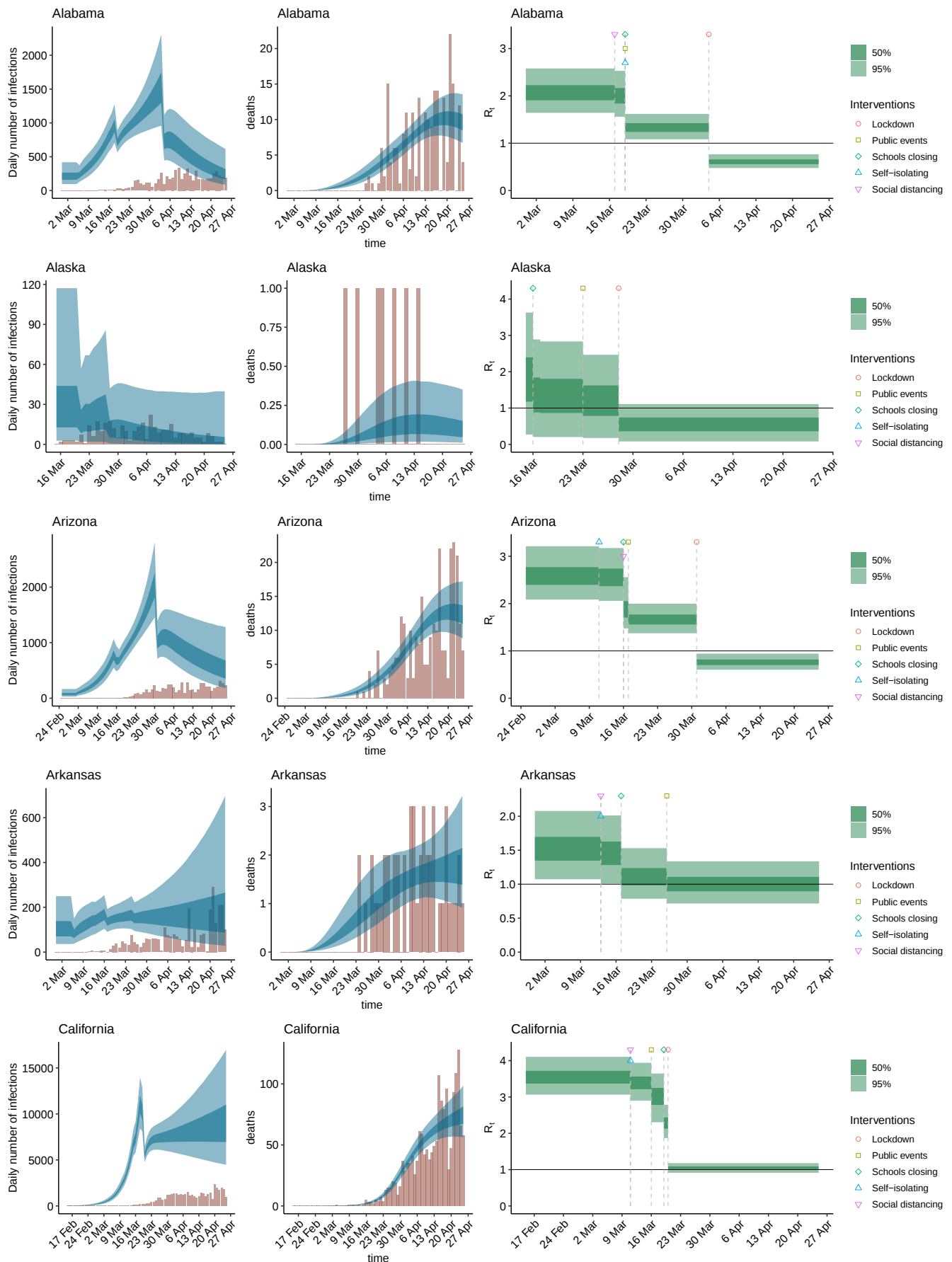
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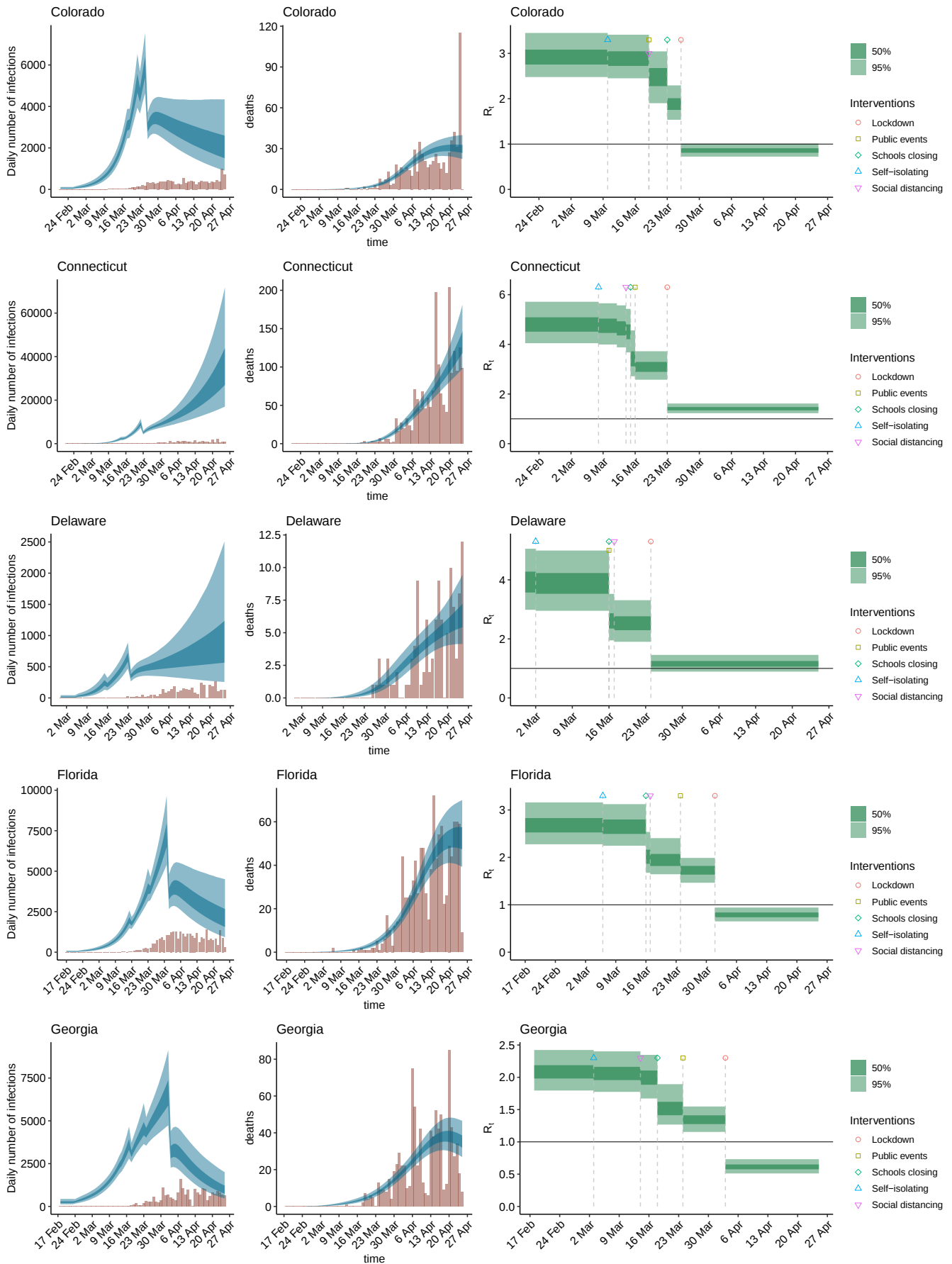
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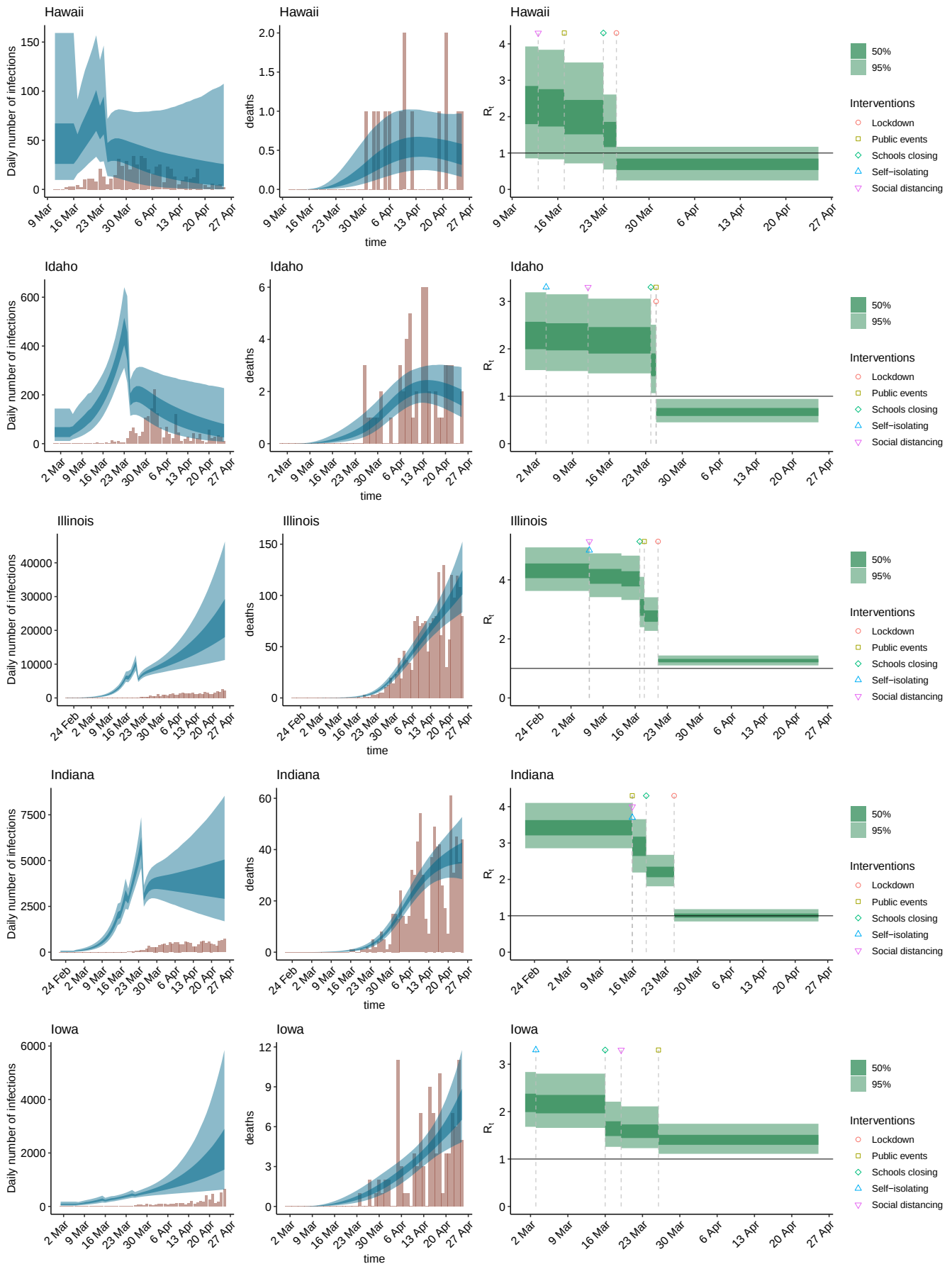
### Web Figure 1: Model Estimates

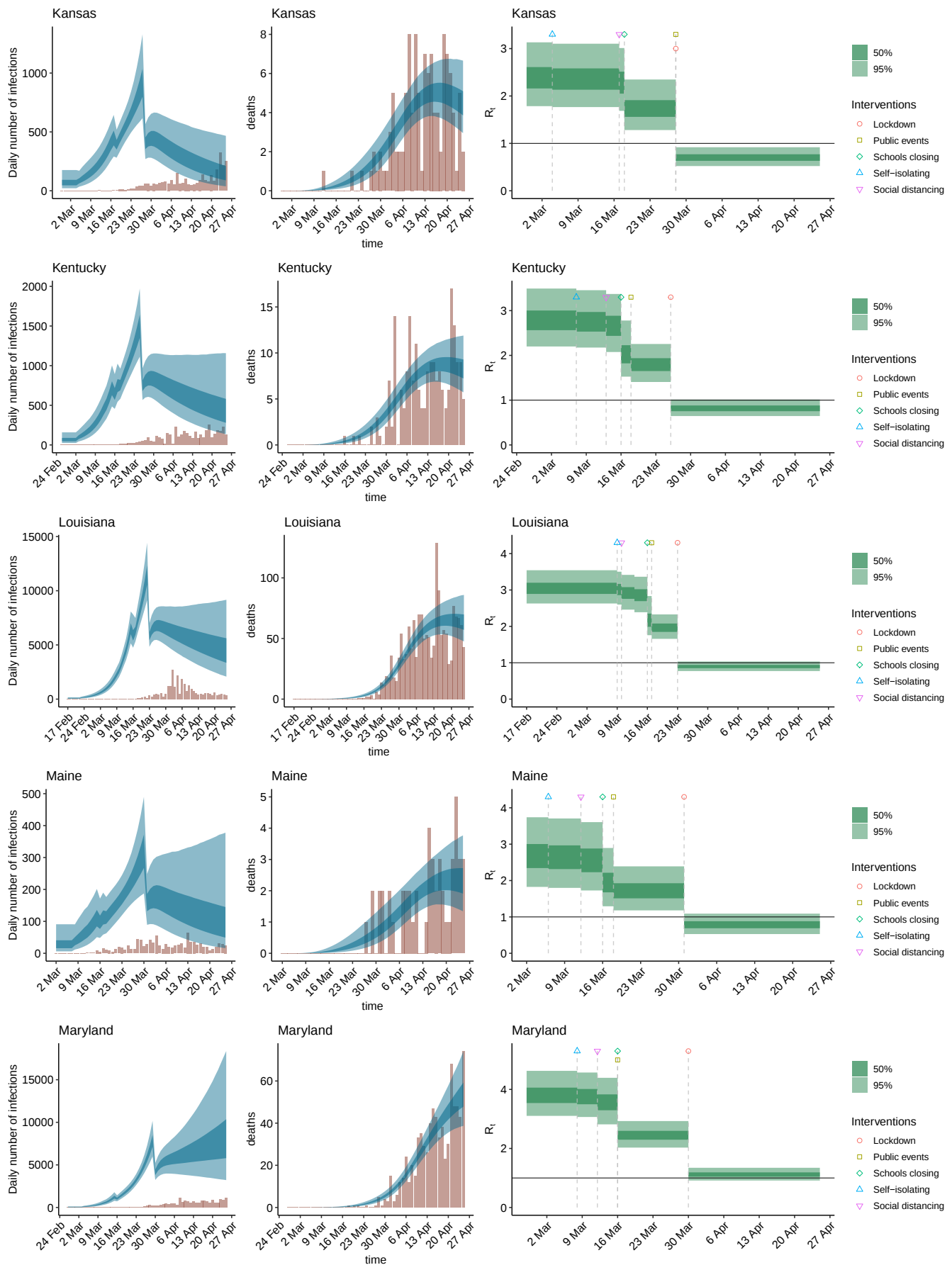
The following three panel graphs show the model fit for each U.S. state for the period modeled (in each state, 30 days before 7 deaths up to April 25, 2020). Note all three panels have the same range of dates on the x-axis. The left panel shows the daily count of infections (red) and the model's estimated infections (dark blue, 50% credible interval; light blue, 95% credible interval). The middle panel shows the daily count of deaths and model estimates using the same annotations as the left panel. The right panel shows the estimated  $R_t$  before and after the social distancing interventions listed in the legend (dark green, 50% credible interval; light green, 95% credible interval). A horizontal line at  $R_t = 1.0$  provides a reference for whether the infections are estimated to grow (above 1.0) or decline (below 1.0).

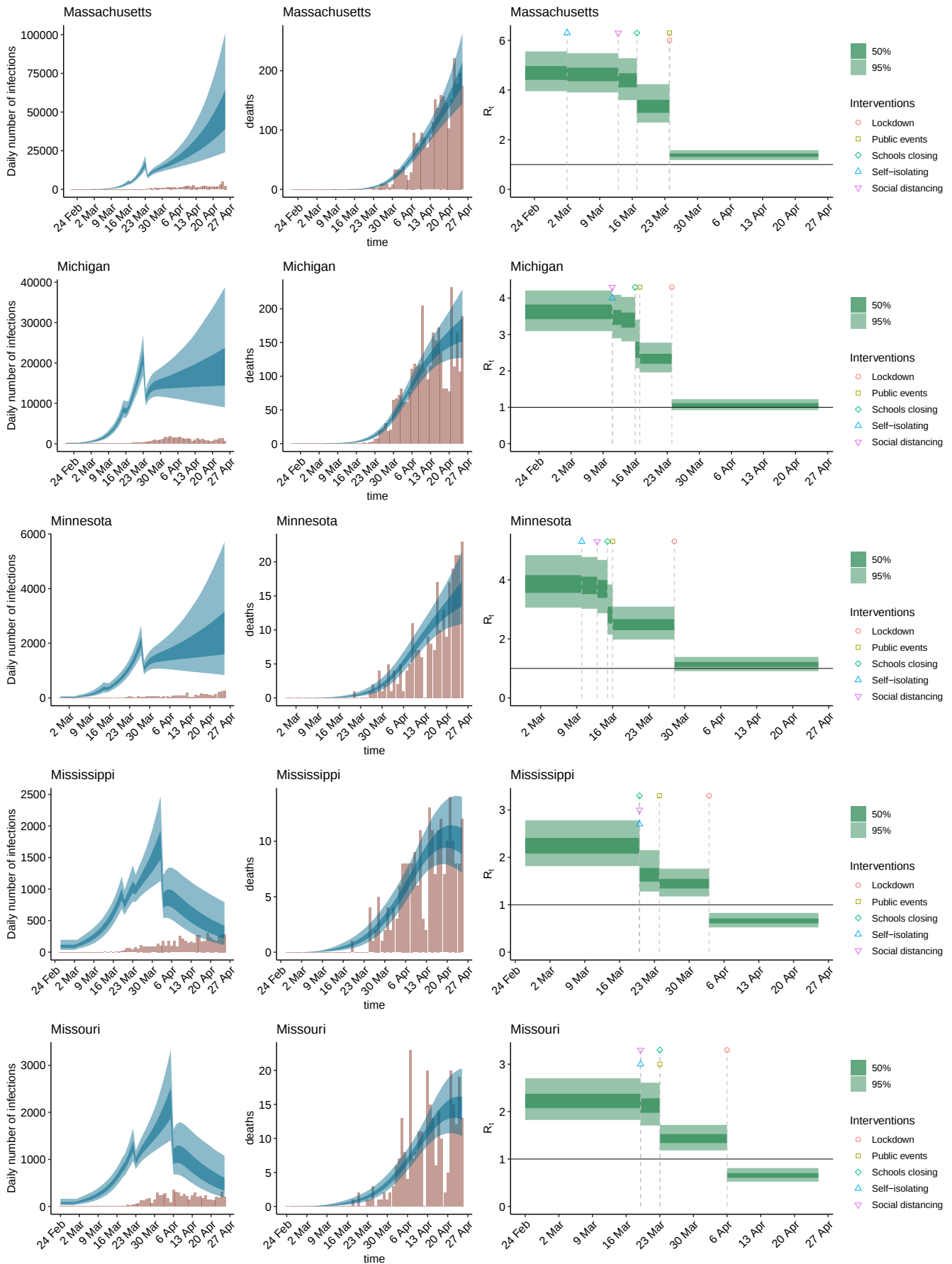
The three panel graphs give a qualitative sense of the model's behavior, as well as the model fit on the left and middle panels. Comparisons between the right panel and the others further illustrates how changes in estimated  $R_t$  are reflected in estimated case and death counts, particularly as  $R_t$  approaches 1.0.

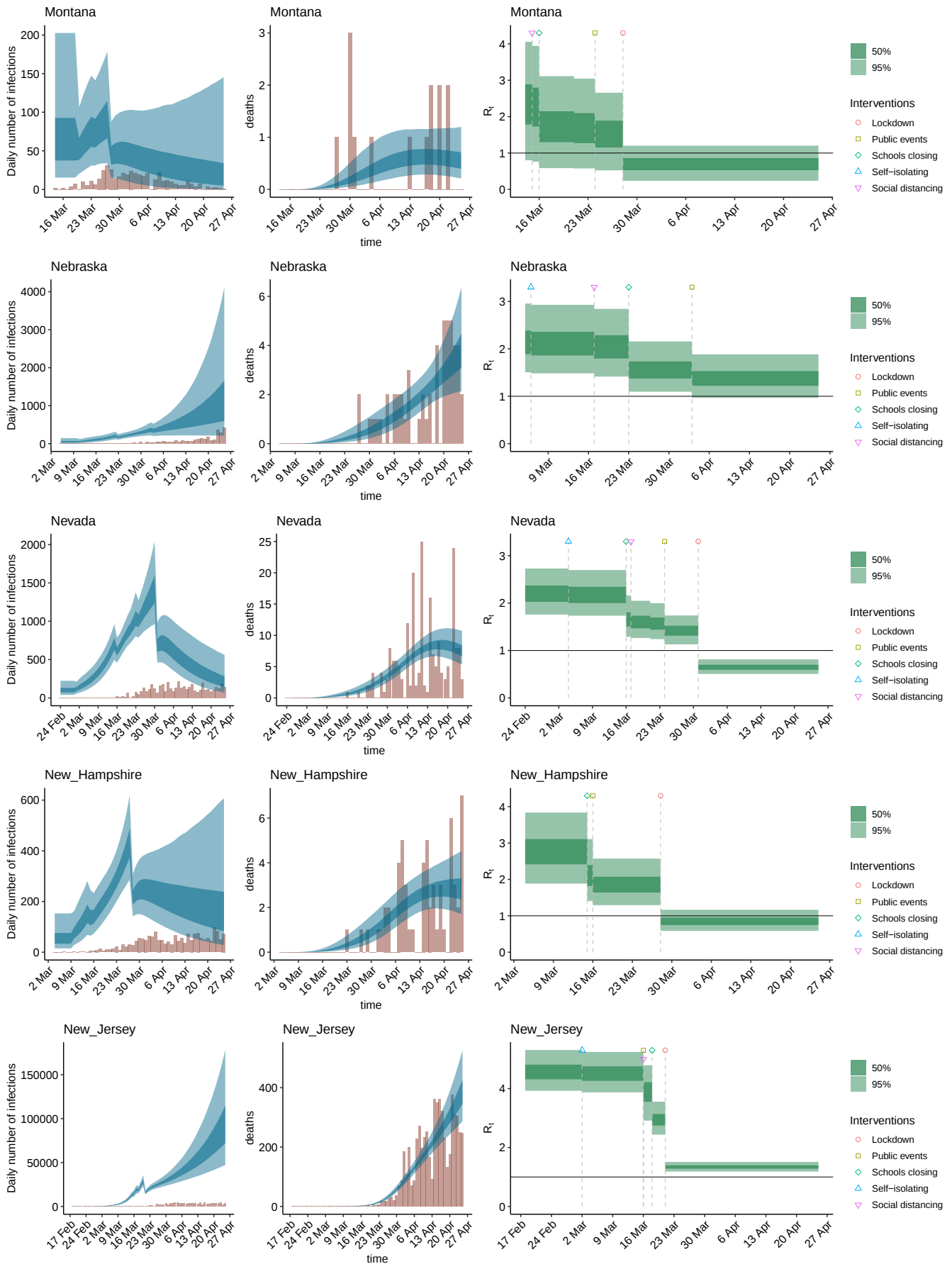


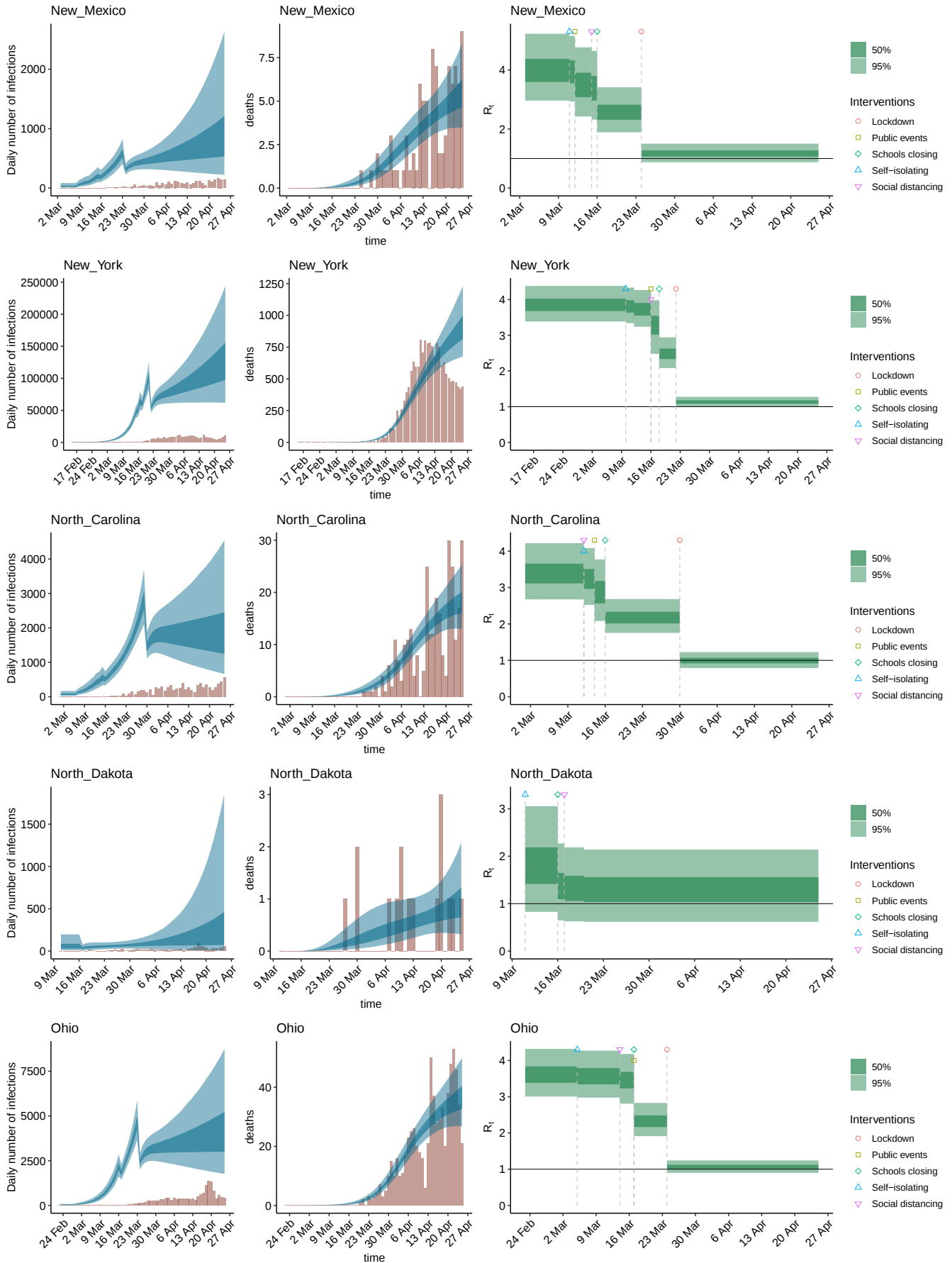


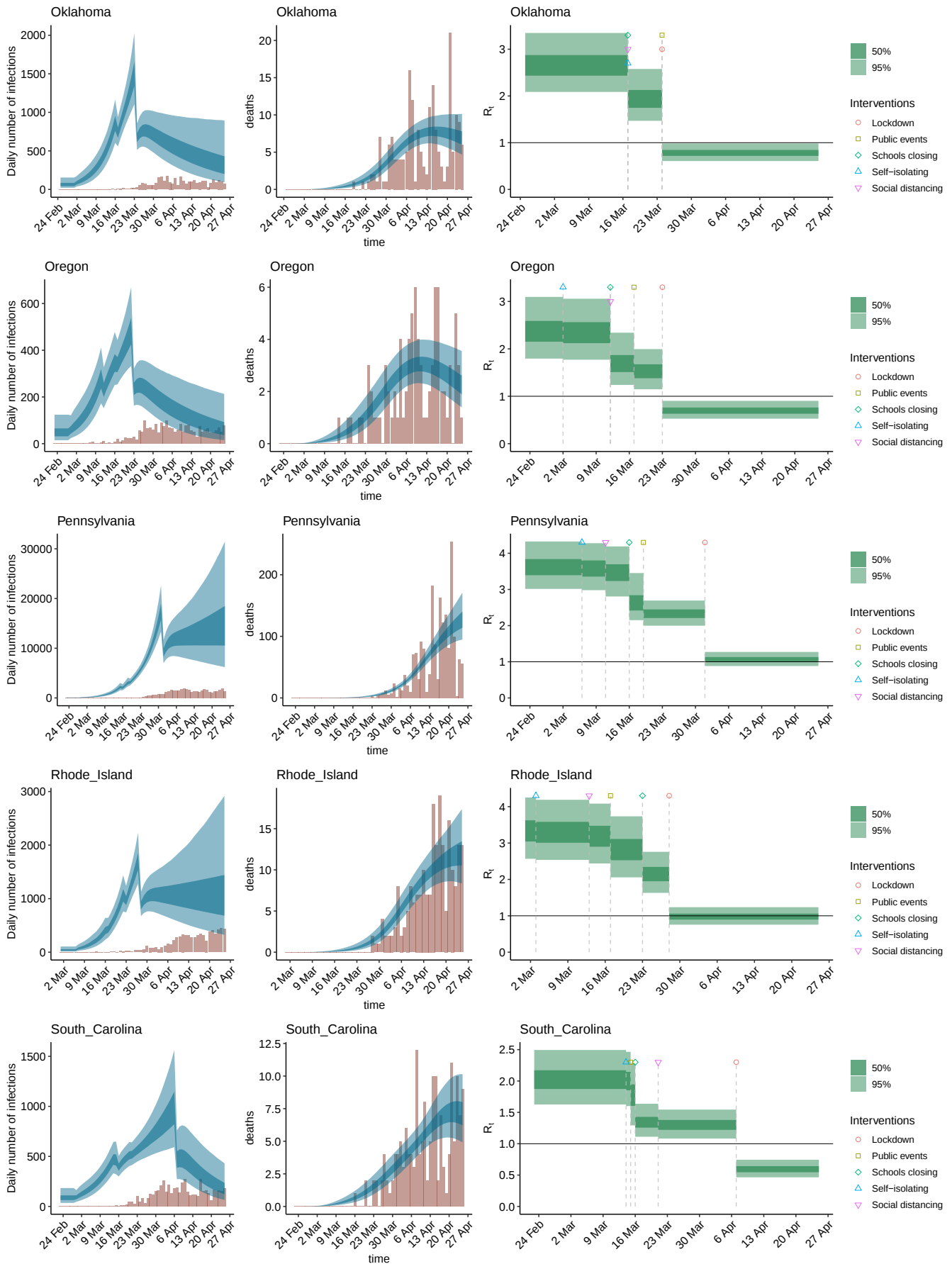


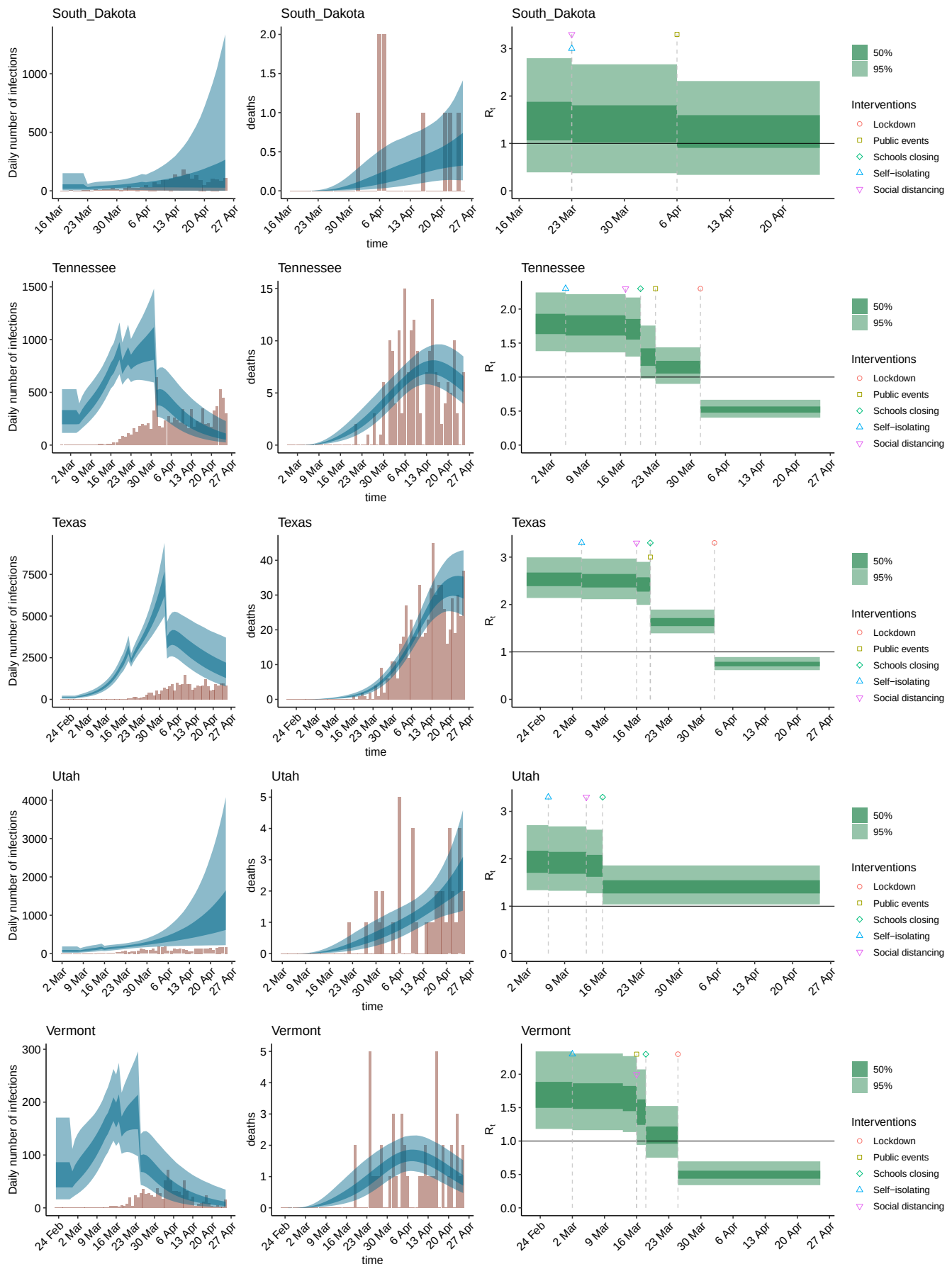


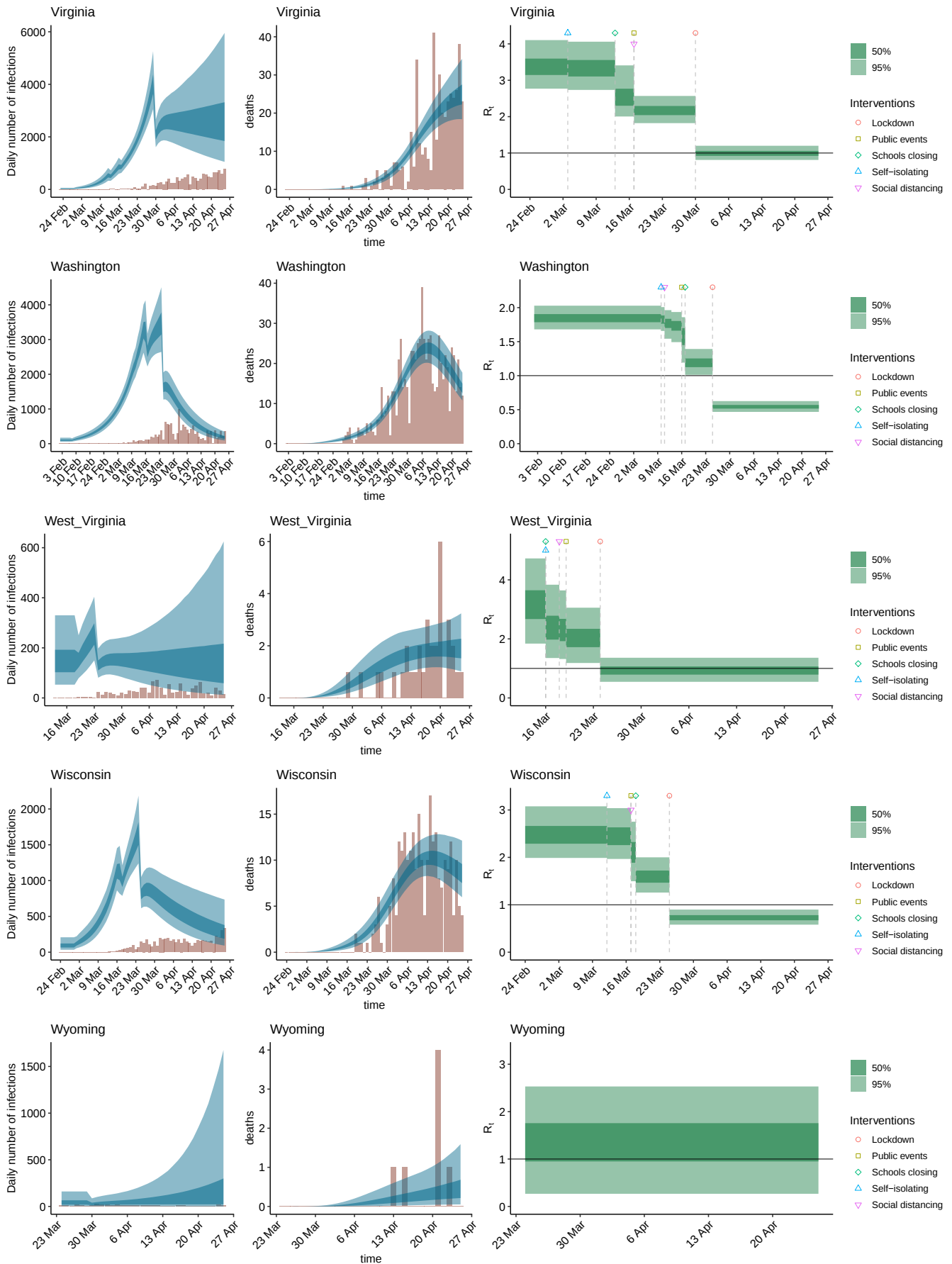








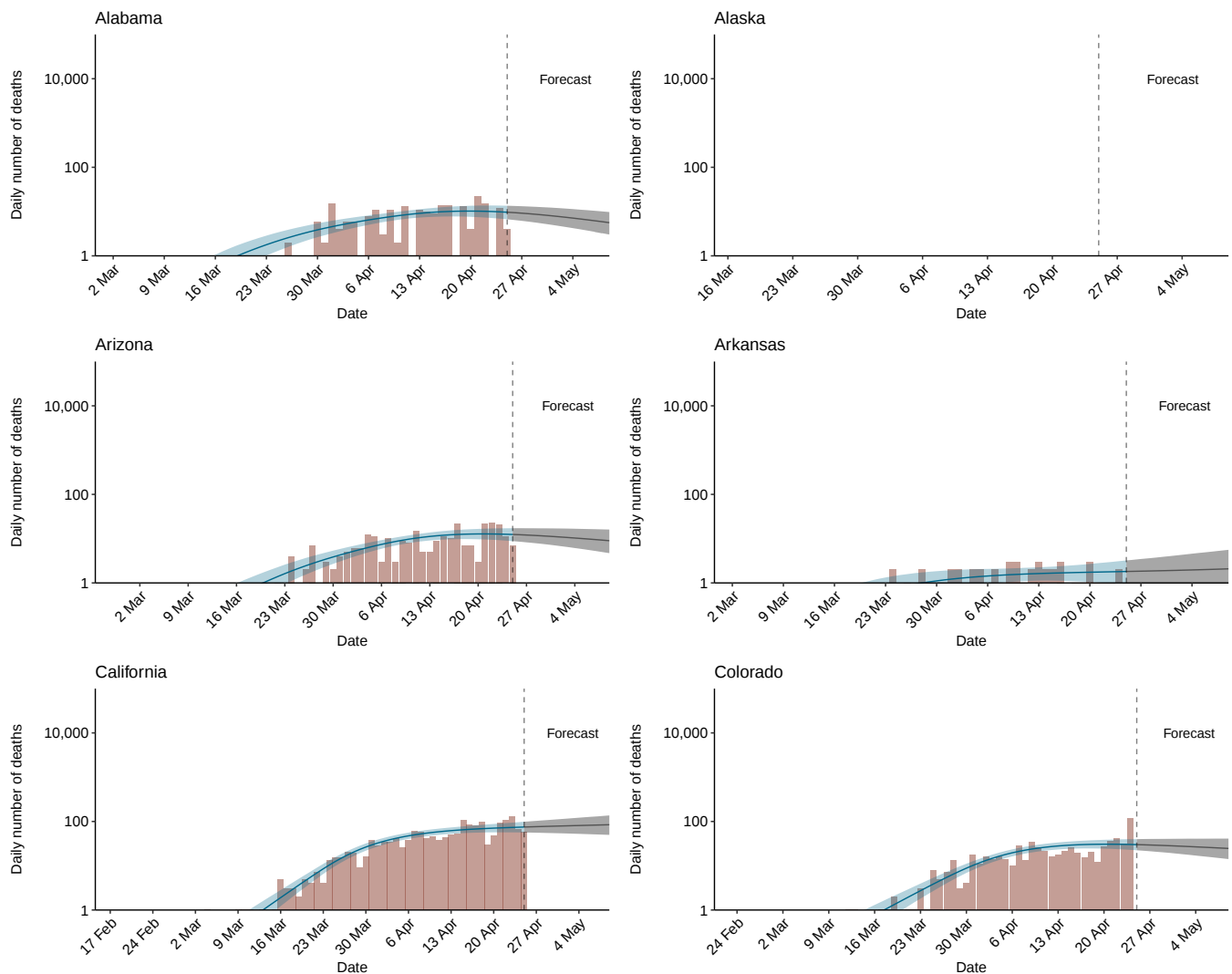


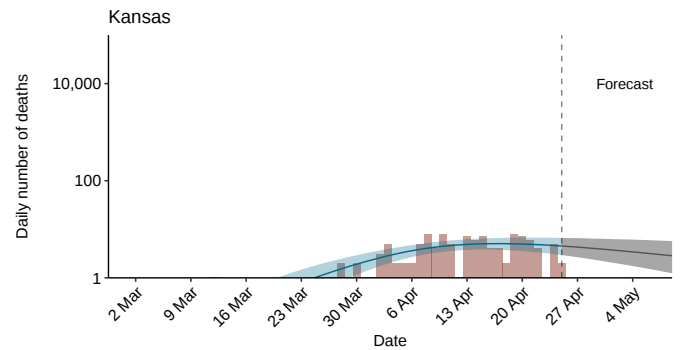
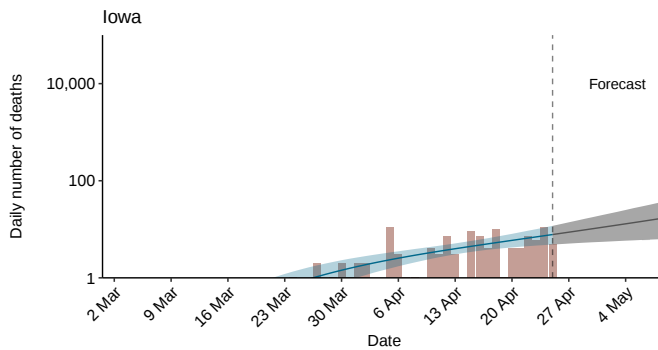
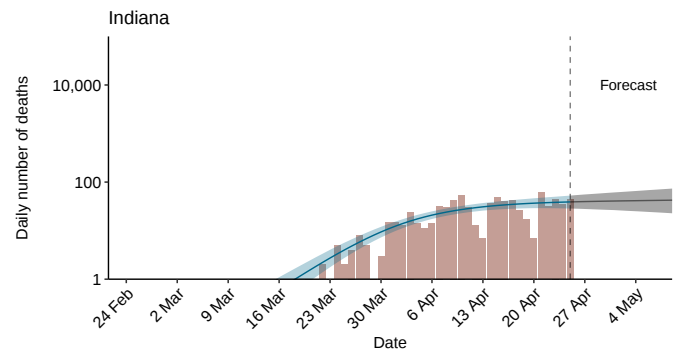
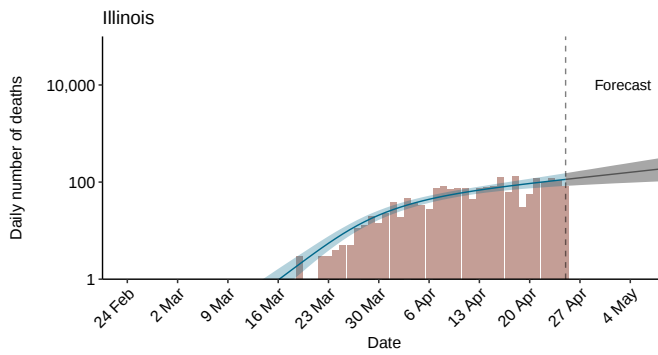
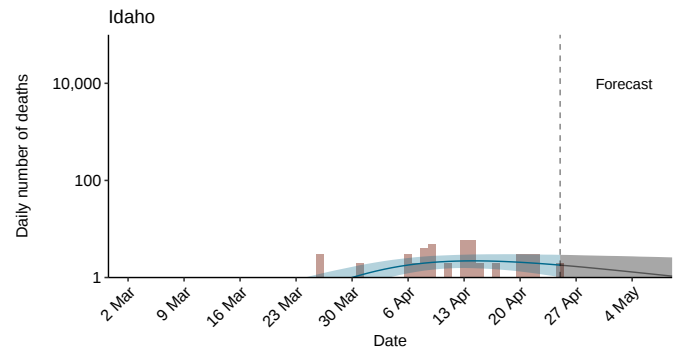
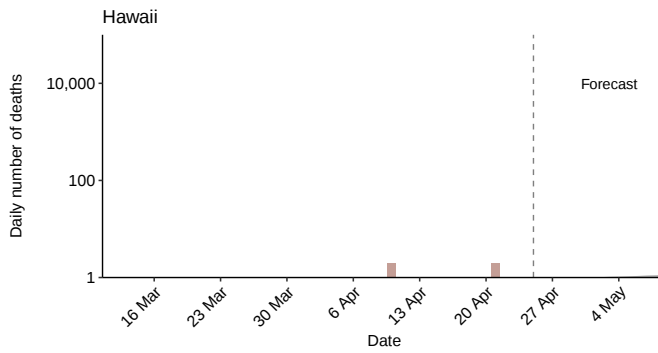
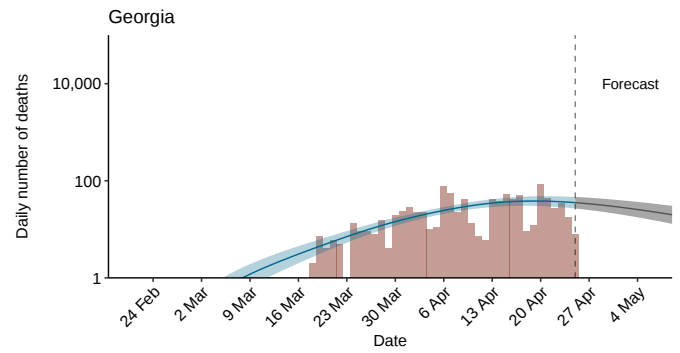
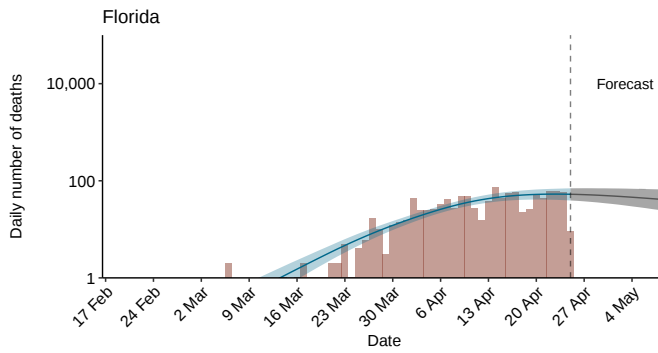
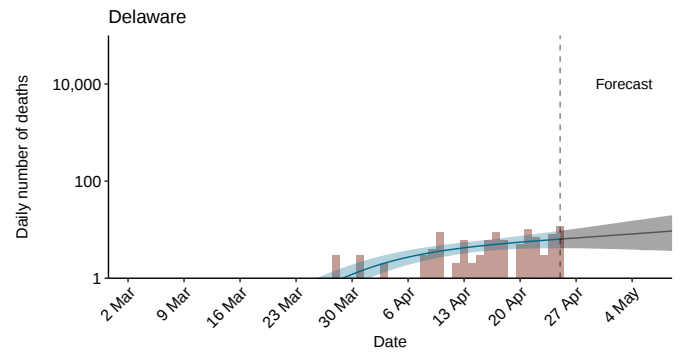
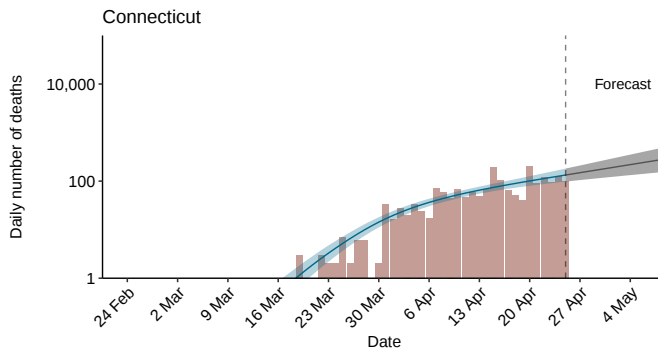


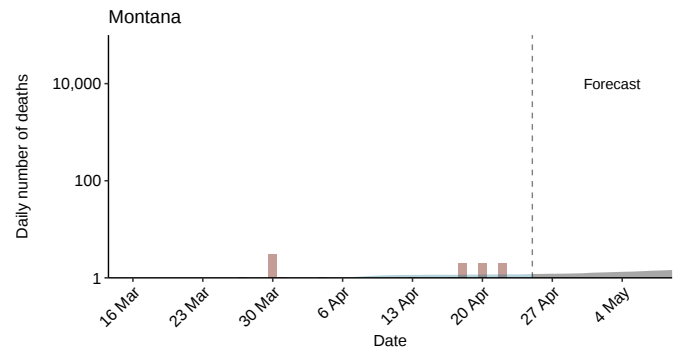
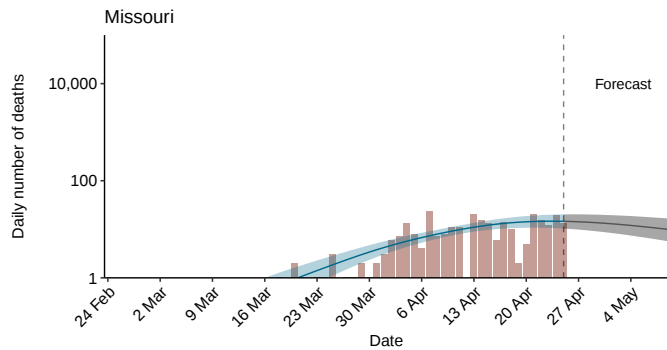
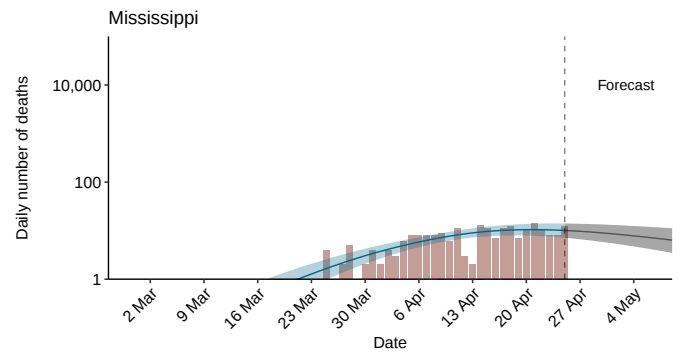
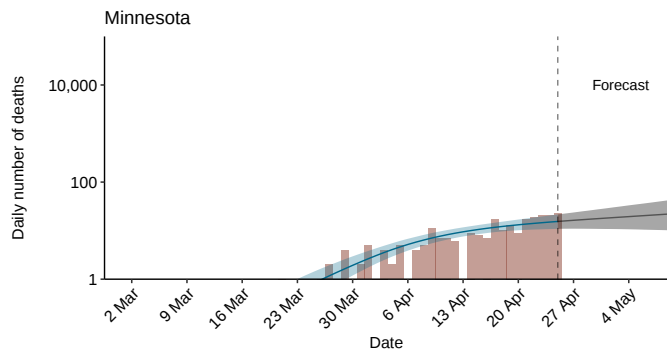
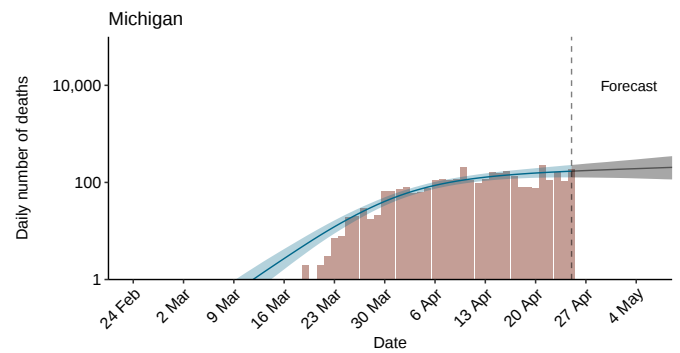
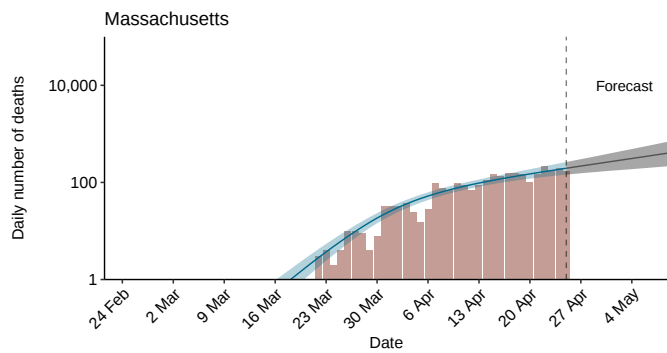
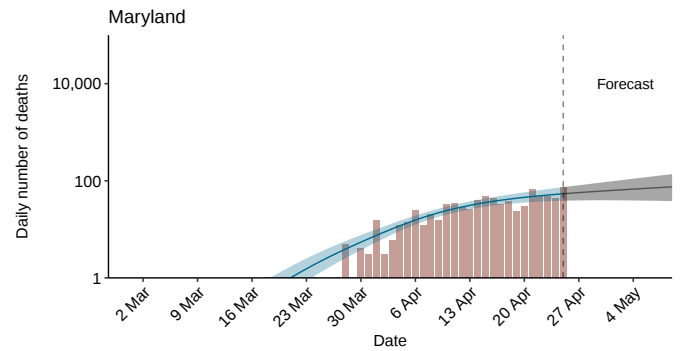
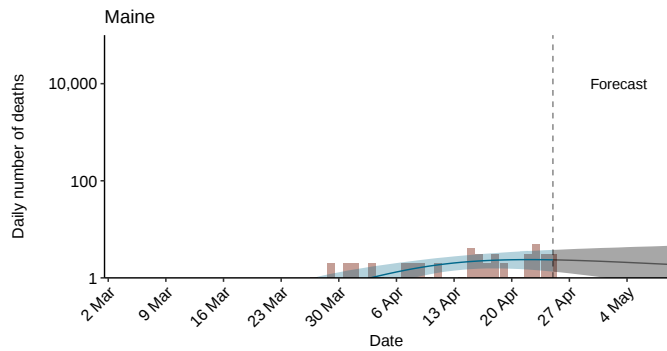
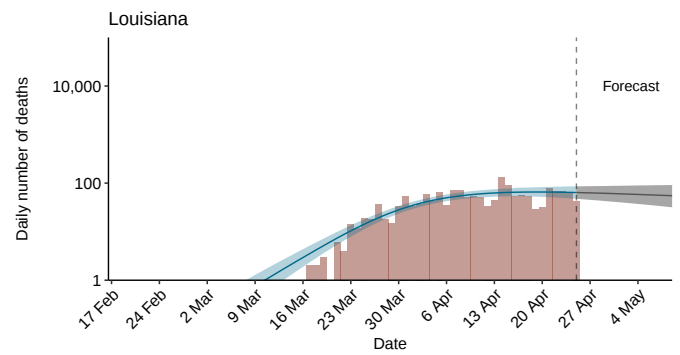
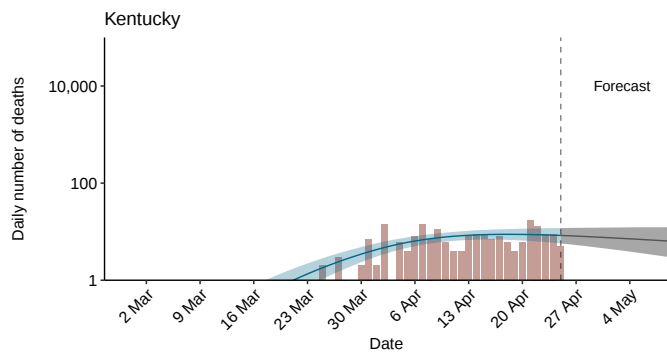
## Web Figure 2: Model Forecasts

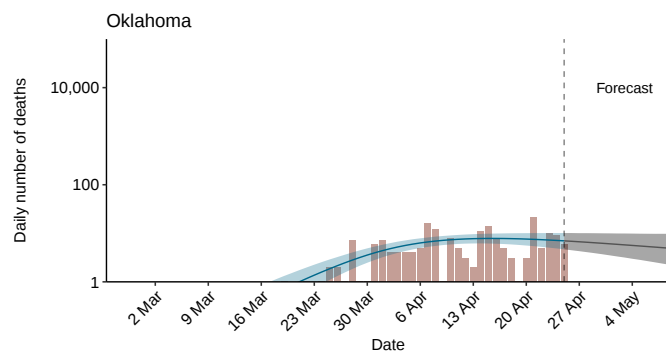
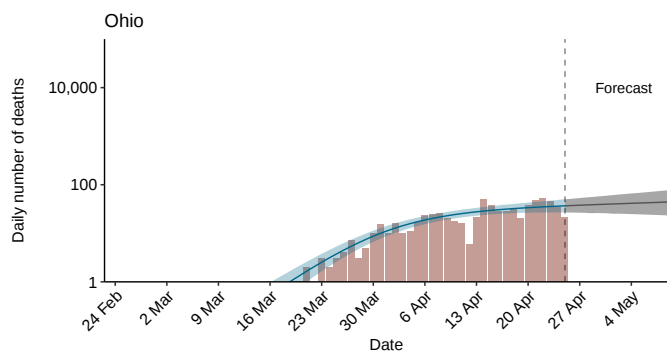
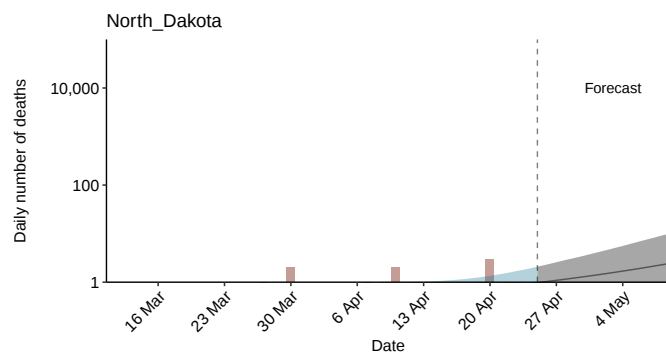
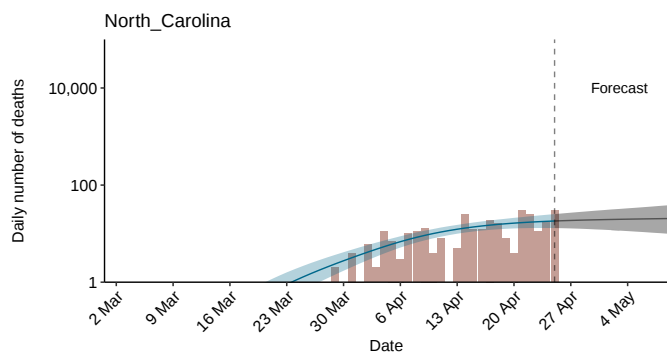
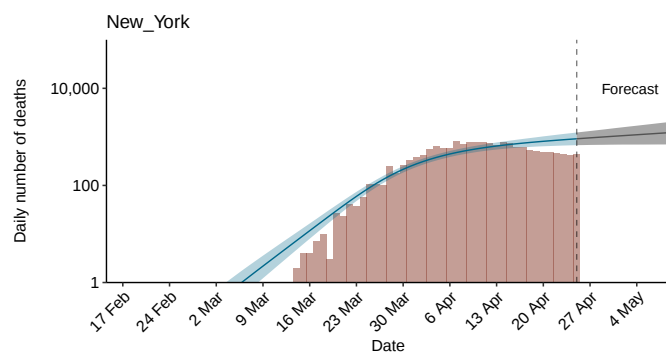
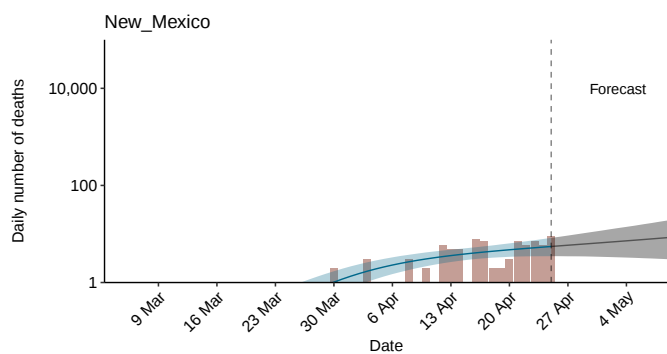
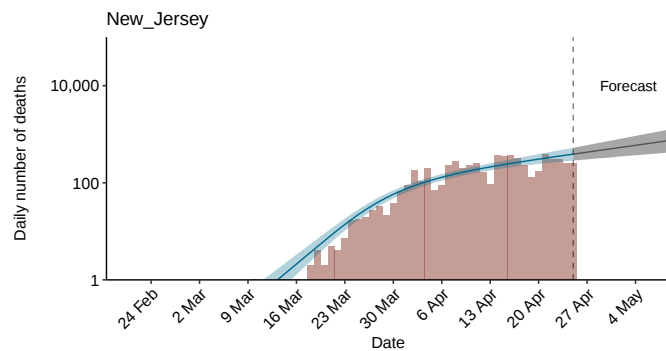
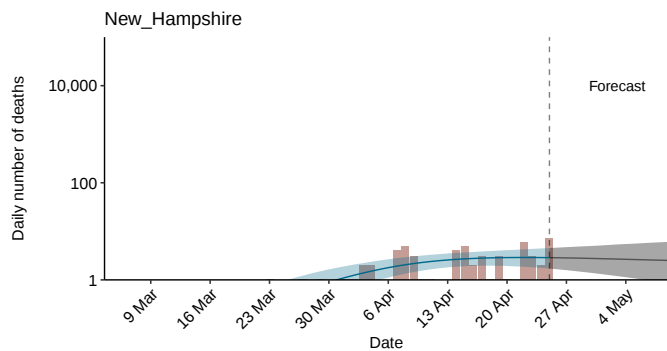
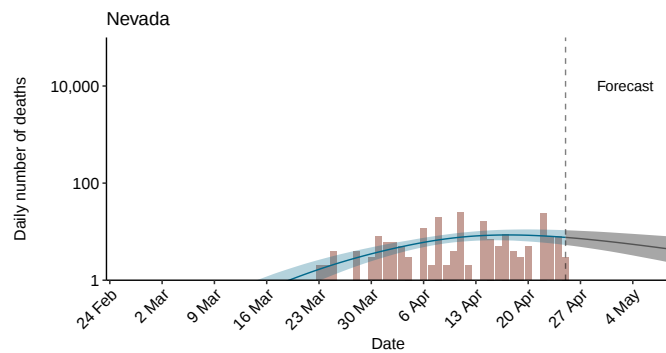
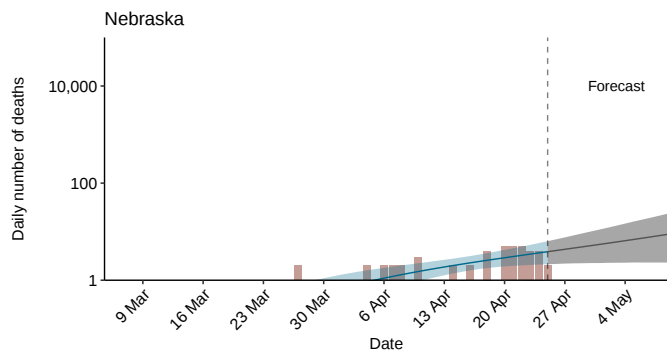
The following graphs show the model estimates of daily deaths for each U.S. state during two periods. Note the y-axis is log scaled. The first period is the period modeled (in each state, 30 days before 7 deaths up to April 25, 2020). During this period, each graph shows the daily count of deaths (red) and the model's estimated deaths (dark blue, 50% credible interval; light blue, 95% credible interval). The second period is a forecast period from April 25th, 2020 to May 9th, 2020 and is demarcated from the first period by a dashed vertical line. During the second period, only the model's estimates are shown (dark gray, 50% credible interval; light gray, 95% credible interval).

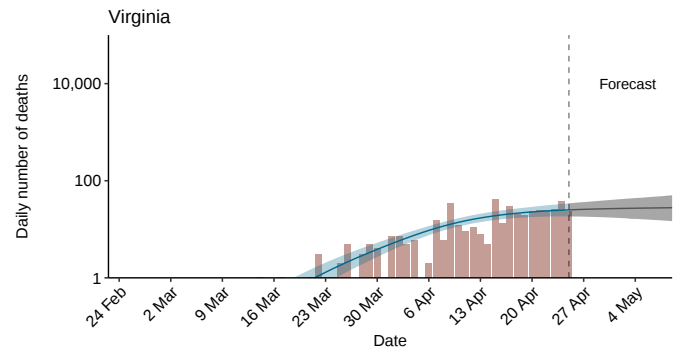
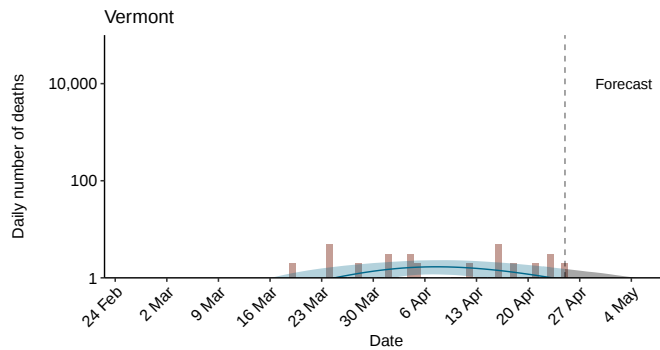
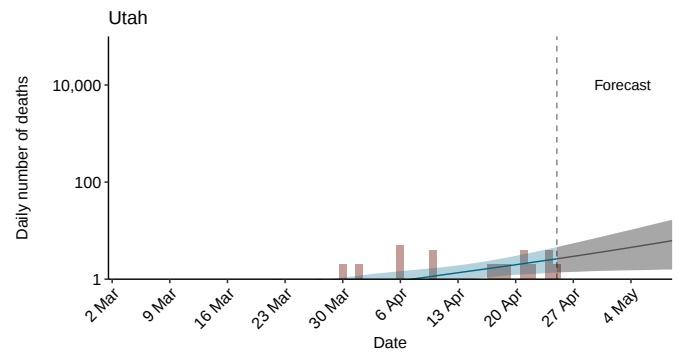
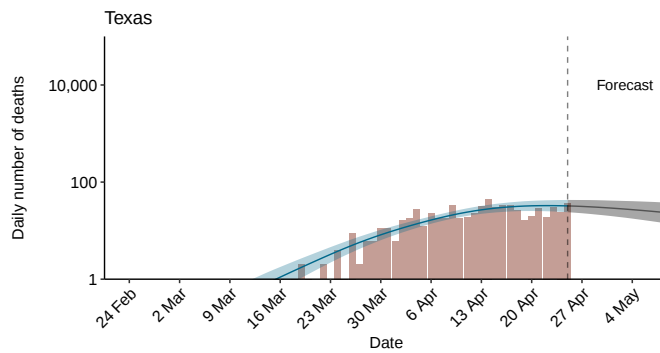
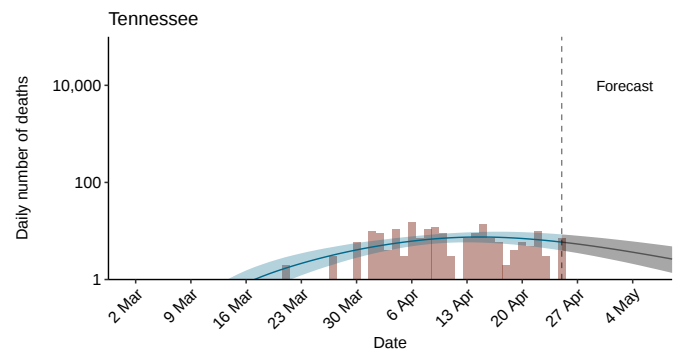
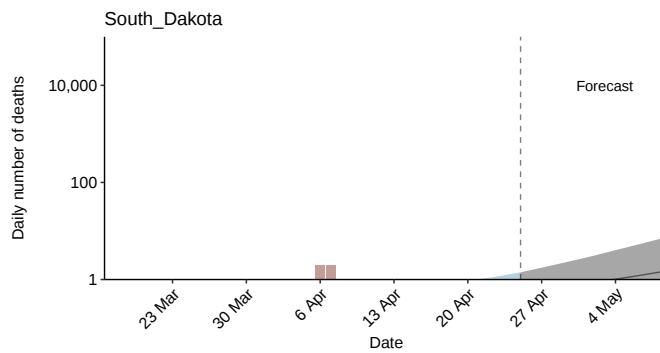
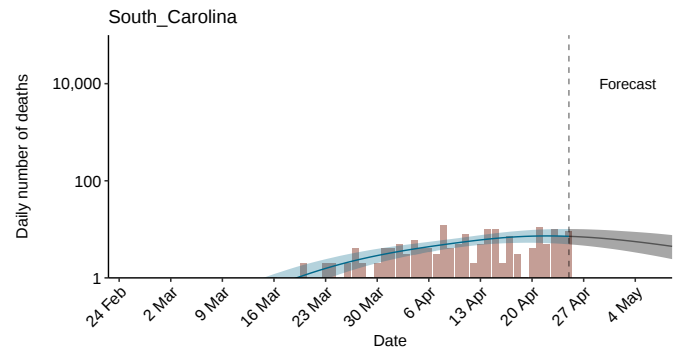
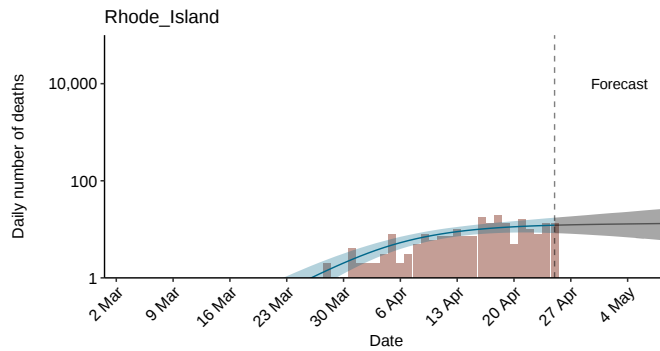
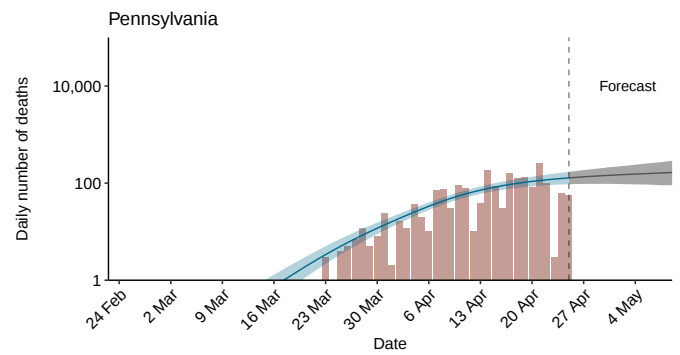
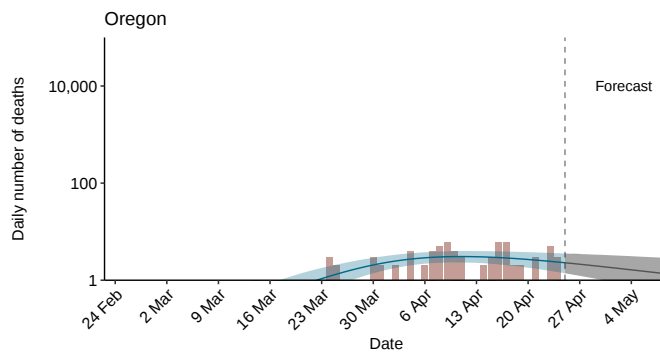
The graphs give a qualitative sense of the model's fit during the period modeled and the forecast period. Because the y-axis is log scale, downward curves (below a straight line) indicate a slowing growth in the number of infections. These graphs further illustrate how the model is altering its behavior to the conditions in each state and forecasting upward, flat, or downward trends as appropriate.

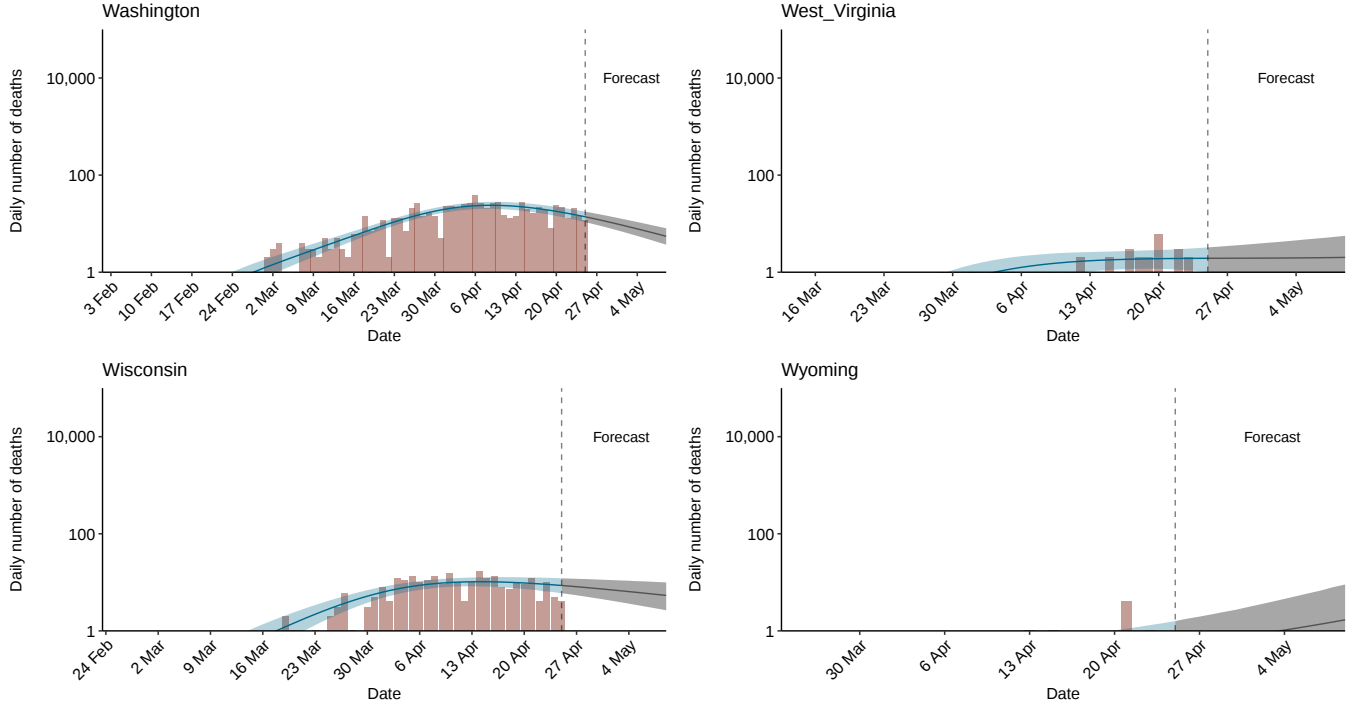












## Web Appendix: Model Details

Informally stated, the model uses an observed sequence of daily death counts to infer an earlier time-lagged unobserved sequence of daily infection counts. A death count on a given day is estimated by previous infections and the probability that an infection will result in death. Probability of death is calculated using the given state's infection fatality ratio as well as the number of days since infection. The number of infections on a given day is estimated by the previous infections, the days since infection, and the reproduction number  $R_t$ .  $R_t$  at any given time is modeled as an exponential reduction of the initial  $R_t$ , where each of the six interventions has a single, positive parameter controlling the reduction:

1. Self-isolating if ill
2. Social distancing encouraged
3. Schools or universities closing
4. Sport
5. Public events
6. Lockdown

With this informal definition in mind, we briefly describe the model in formal terms. The reader should refer to the references cited in the main text for a fuller description.

Let  $R_{t,m}$  be the time-varying reproductive rate for day  $t \in 1, \dots, n$  in state  $m \in 1, \dots, p$ :

$$R_{t,m} = R_{0,m} \exp\left(-\sum_{k=1}^6 \alpha_k I_{k,t,m}\right)$$

where  $\alpha_k$  is the cross-state effect of intervention  $k \in 1, \dots, 6$  and  $I_{k,t,m}$  is an indicator that equals 1 if intervention  $k$  is implemented on day  $t$  in state  $m$  and 0 otherwise. This functional form guarantees that  $R_{t,m}$  will be positive since initial  $R_{0,m}$  is held positive and  $\alpha_k \sim \text{Gamma}(0.5, 1)$ . Furthermore,  $R_{0,m} \sim \mathcal{N}^+(2.4, |\kappa|)$  where  $\kappa \sim \mathcal{N}^+(0, 0.5)$ .

The number of infections  $c_{t,m}$  on day  $t$  in state  $m$  is given by the convolution function:

$$c_{t,m} = R_{t,m} \sum_{\tau=0}^{t-1} c_{\tau,m} g_{t-\tau}$$

where  $c_{\tau,m}$  is the number of new infections on day  $\tau \in 1, \dots, n$  in state  $m$ , and  $g$  is a serial interval distribution with density  $g_\tau$  corresponding to the time between infection and transmission to the next carrier. This serial interval distribution is shared across states and is discretized as  $g_s = \int_{\tau=s-0.5}^{s+0.5} g(\tau) d\tau$  for  $s = 2, 3, \dots$  and  $g_1 = \int_{\tau=0}^{1.5} g(\tau) d\tau$ . Furthermore,  $g \sim \text{Gamma}(6.5, 0.62)$ , i.e. mean 6.5 days infection-to-transmission.

The expected number of deaths  $d_{t,m}$  on day  $t$  in state  $m$  is defined as:

$$d_{t,m} = \sum_{\tau=0}^{t-1} c_{\tau,m} \pi_{t-\tau,m}$$

where  $\pi_m$  is a density corresponding to the time between infection and death and discretized as  $\pi_{s,m} = \int_{\tau=s-0.5}^{s+0.5} \pi_m(\tau) d\tau$  for  $s = 2, 3, \dots$  and  $\pi_{1,m} = \int_{\tau=0}^{1.5} \pi_m(\tau) d\tau$ . Furthermore,  $\pi_m \sim \text{ifrm} \cdot (\text{Gamma}(5.1, 0.86) + \text{Gamma}(18.8, 0.45))$ , where  $\text{ifrm}$  is the infection fatality ratio of state  $m$  and the Gamma distributions represent infection-to-onset (mean 5.1 days) and onset-to-death (mean 18.8 days). See the main text for more details on the calculation of  $\text{ifrm}$ .

Finally, observed deaths  $D_{t,m}$  on day  $t$  in state  $m$  are assumed to be distributed as follows:

$$D_{t,m} \sim \text{Negative Binomial}(d_{t,m}, d_{t,m} + \frac{d_{t,m}^2}{\Psi})$$

$$\Psi \sim \mathcal{N}^+(0, 5).$$

Model parameter estimation was performed using Stan (see main text). We ran 4 chains with 4000 iterations with 2000 warmup iterations, a thinning factor of 1, and an adapt delta parameter of .90 for adaptive Hamiltonian Monte Carlo. We assessed convergence using standard convergence diagnostics.