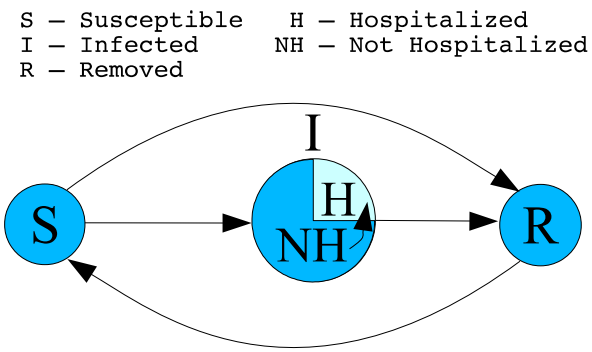
Supplementary Material

Description of the Bayesian SIR model.

The Mayo Clinic Bayes SIR model and incorporation of vaccines into the model is described in detail elsewhere (Storlie et al., 2021); however, we give an overview here for convenience. Figure A provides a depiction of the state space for the Bayes SIR model. Individuals in each county start as susceptible, and then transition into infected or directly to removed (via vaccination). The latest version of the model also allows for the transition from removed to susceptible again to allow for the impact of waning immunity and new strains. The infected pool can transition to hospitalization or to recovered (i.e., removed). Hospitalization is broken into general care (floor) and intensive care unit (ICU). Transitions between these sub-states of the infected state are allowed as well as direct admission to the ICU. Finally, infected

Figure A: Model State Space



individuals, hospitalized or not, eventually transition into the removed state.

The number of test positive reported cases in a given US county on a given day is assumed to be distributed as Binomial, with number of trials equal to the number of actual new infections and the proportion of successes is a function of the amount of testing per capita being performed in that county. The number of actual new daily infections at the county level are not observed

directly, but rather modeled as a latent variable with Poisson distribution, proportional to the number of currently infected, the proportion of the county in the susceptible state, and an infection rate that varies over county and day as a spatio-temporal stochastic process. Infected individuals can become hospitalized according to a Geometric waiting time model, with a rate that also varies smoothly over county and day as a stochastic process. For some individuals, the waiting time to hospital admission is shorter than the transition time into the removed state producing a hospitalization event. Transitions within a hospital admission from ICU to Floor beds also occur as competing Geometric waiting times (competing with discharge) in this model with a static rate. All parameters in the model are estimated in a hierarchical Bayesian framework via Markov chain Monte Carlo (see Kruschke 2014, for example).

Incorporation of vaccinations into the Bayesian SIR model

Let the number of currently infected (or infectious) in county i at time t be $I_{i,t}$ and the number in the removed state as $R_{i,t}$. Finally, N_i is the number of people in residing in county i and the number in the susceptible state is determined by the constraint that $S_{i,t} = N_i - I_{i,t} - R_{i,t}$, imposed by the assumption that there is no migration across counties.

The $R_{i,t}$ are governed by the relationship

$$R_{i,t} = R_{i,t-1} - D_{i,t} + C_{i,t} + E_{i,t},$$

where (i) $D_{i,t}$ are the number in the removed class that transition back to susceptible, assumed to be geometric waiting time with prior distribution having mean of 1 year (2 years as a 95% upper bound), (ii) $C_{i,t}$ is the number of infected that transitioned into the removed class on day t (again assumed Geometric with posterior rate estimated to be ~13 days, and (iii) $E_{i,t}$ is the number of

effective vaccinations that occurred in county i on day $t - 14$. That is, vaccinations are assumed to not produce a transition into the removed state until two weeks after receiving it based on the biological science underlying the vaccines (Polack FP, et.al., 2020; Baden LR, et.al., 2021). It is also assumed that not all vaccinations will transition into the removed class. Specifically, the number of effective vaccinations $E_{i,t}$ has a Binomial distribution with number of trials being the total number of vaccinations each day $\tilde{E}_{i,t}$ and success (i.e., efficacy) proportion π. The vaccination efficacy π is given a prior distribution with mean 80% allowing for the possibility that it is somewhere between 75 to 85% based on results in several studies (Tande et al., 2021; Baden et al., 2021; Polack et al., 2020; Voysey et al., 2021). This is slightly conservative as the clinical trials had reported higher efficacy at > 90%, but it is still a bit less clear how effective vaccines are at preventing asymptomatic infection and against newer variants. Tande et al., 2021 report this to be ~80% in a recent study of a limited population in the state of Minnesota. Thus, roughly 80% of those that are vaccinated are assumed to move directly into the removed state after 2 weeks. In this model, the two-week clock starts after the first dose regardless of vaccine type as even the two-dose Pfizer and Moderna vaccines have shown reasonable efficacy after even just a single dose (Hunter et al., 2021; Chagla et al., 2021).

Predicting the number vaccinated in the future is done in the following manner. Assume that the number of total vaccinations each day $\tilde{E}_{i,t}$ are Poisson with mean $\lambda_{i,t}$, where $\log(\lambda_{i,t})$ is a stationary Markov process in space and time with mean ν_i. The mean ν_i is assumed to have been a constant since March 14 for estimation purposes. That is, future $\tilde{E}_{i,t}$ are assumed to look a lot like they did the past few weeks, with some potential for slow down or speed up. The vaccinations are assumed to continue in this fashion until we reach a point of "saturation" where

there is no longer demand for vaccine. This is currently assumed to happen at some point between 50 and 75% of the population vaccinated, a priori, with a mean of 60%.

Note that while the model does allow a transition back to susceptible once vaccinated, this transition is assumed to be relatively slow (~1 year), so this will have little impact on the four-month projections. However, the role of novel variants to SARS-Cov-2 could alter this rate. Further study is needed to estimate this transition probability in the coming months. Making effective predictions beyond four months will also require a reasonable model for re-vaccination in late 2021 and subsequent years.

