

for each of the 3,014 counties. These coefficients then serve as the dependent variables in the second stage of our cross-sectional analysis, taking into account the uncertainty associated with the estimation of the first-stage coefficients. In the second stage, we evaluate cross-sectional measures, including socioeconomic, demographic, health, epidemiological, climate, pollution, and political characteristics, for each county, after employing the novel OCMT variable selection procedure to identify the most relevant factors. The second-stage models are estimated by wave, using a weighted seemingly unrelated regression (SUR) system estimator, allowing for the importance of explanatory factors to vary during the course of the pandemic.

4.1 First-stage county-level daily panel analysis

In the first stage, we estimated two linear mixed models utilizing county-level daily panel data on confirmed cases, deaths, and vaccination rates from March 2020 through March 2022. These data are generated according to the methodology outlined in Appendix A. Following [Rabe-Hesketh and Skrondal \(2022\)](#), we used random coefficient models¹⁵ to accommodate the observed heterogeneity across waves and counties. We estimated the models separately by wave to allow for variations over those episodes in the transmissibility of the virus, the impact of vaccinations, and improvements in treatment regimes. The models employed an unstructured covariance matrix, providing flexibility for the county-level random effects.

The confirmed cases and deaths series were differenced based on the unweighted average of the seven prior days' cumulative count series adjusted for population (see Appendix A). The first model explains the county-level confirmed case rate as a function of the same variable lagged $j = 14$ days. The second model explains the county-level death rate as a function of the confirmed case rate lagged $j = 14$ days. Thus, both models are autoregressive with a single regressor: the county-level confirmed cases 14 days prior, capturing transmissibility of the disease.¹⁶ When vaccination rates of

¹⁵We assessed the appropriateness of the mixed models using a conservative likelihood-ratio test. We