Novel Estimates Reveal Subnational Heterogeneities in Disease-Relevant Contact Patterns in the United States

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Abstract

Population contact patterns fundamentally determine the spread of directly transmitted airborne pathogens such as SARS-CoV-2 and influenza. Reliable quantitative estimates of contact patterns are therefore critical to modeling and reducing the spread of directly transmitted infectious diseases and to assessing the effectiveness of interventions intended to limit risky contacts. While many countries have used surveys and contact diaries to collect national-level contact data, local-level estimates of age-specific contact patterns remain rare. Yet, these local-level data are critical since disease dynamics and public health policy typically vary by geography. To overcome this challenge, we introduce a flexible model that can estimate age-specific contact patterns at the subnational level by combining national-level interpersonal contact data with other locality-specific data sources using multilevel regression with poststratification (MRP). We estimate daily contact matrices for all 50 US states and Washington DC from April 2020 to May 2021 using national contact data from the US. Our results reveal important state-level heterogeneities in levels and trends of contacts across the US over the course of the COVID-19 pandemic, with implications for the spread of respiratory diseases.

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Author Summary: Reliable quantitative estimates of contact patterns are in high demand because they are a critical input for modeling and reducing the spread of directly transmitted infectious diseases such as COVID-19 and influenza. But, while national-level contact data are available from surveys collected in many countries – including the United States – local-level estimates of age-specific contact patterns are almost never available. Yet these local-level contact patterns are crucial, since disease dynamics and public health policy vary by geography. Here, we introduce a new method for estimating levels and trends in local-level rates of disease-relevant contacts by combining information from national-level contact data and other locality-specific data sources. We illustrate our method by estimating novel state-level estimates of contact patterns in the US over the course of the COVID-19 pandemic. These estimates are an important resource for researchers and policymakers who wish to understand the state-level dynamics of the COVID-19 pandemic in the United States. The new methods we introduce are applicable to any directly transmitted infectious disease and can be applied in many different settings all over the world.

1 Introduction

As of April 2022, the COVID-19 pandemic is estimated to have infected over 505 million people and caused at least 6.2 million deaths around the world (WHO, 2022). Like many other directly transmitted diseases – including influenza, pertussis, and measles – the pathogen that causes COVID-19 is spread through respiratory droplets that can be transmitted during close, person-to-person interactions (Wu and McGoogan, 2020; Yuki, Fujiogi and Koutsoyianni, 2020; Rohani, Zhong and King, 2010; Goeyvaerts et al., 2010; Wallinga, Teunis and Kretzschmar, 2006). For these directly transmitted infectious diseases, reliable quantitative estimates of levels and patterns of interpersonal contact are central to measuring, modeling, and reducing transmission. Contact patterns serve as critical inputs to mathematical disease models, allowing for the direct incorporation of contact heterogeneity by age, geography, and time to more realistically simulate disease transmission dynamics (Mistry et al., 2021; Liu et al., 2022).

While national-level estimates of age-specific contact patterns are available in many countries (Mossong et al., 2008; Zagheni et al., 2008; Feehan and Mahmud, 2021; Wallinga, Teunis and Kretzschmar, 2006; Prem, Cook and Jit, 2017; Prem et al., 2021), local-level estimates are almost never available. Yet these local-level contact patterns are crucial, since disease dynamics and public health policy vary by geography within a country. This need for timely local-level estimates of contact patterns is especially apparent during the COVID-19 pandemic. In the US, for example, state-to-state differences in physical distancing policies, epidemic waves, seasonality, culture, and other factors have led to many heterogeneous COVID-19 outbreaks, rather than one coherent national outbreak. To accurately model these local COVID-19 outbreaks, each state would ideally collect its own periodic contact surveys to quantify changing local patterns of interpersonal interaction over the course of the pandemic. However, repeatedly collecting contact data for each state would require a very large sample, making it prohibitively expensive.

To overcome this challenge, we introduce a novel approach to estimating subnational interpersonal contact patterns by combining information from national-level contact data and other locality-specific data sources – such as census data – using multilevel regression

with poststratification (MRP) (Park, Gelman and Bafumi, 2004; Gelman et al., 2018). Conceptually, our approach proceeds in two steps: first, we fit Bayesian hierarchical models to age-specific contact patterns observed in the national-level contact survey data. The purpose of these models is to predict age-specific contact rates based on geographic and demographic covariates. Second, we poststratify our model-based estimates by aggregating them up to state-level age-stratified contact rates using weights that represent the population composition of each state. Age-stratified contact rates are key because of age-related variation in transmission, mortality, and immunity (O’Driscoll et al., 2021; Davies et al., 2020).

We apply our method to estimate daily age-stratified contact matrices for all 50 US states and Washington DC between April 2020 and May 2021. All estimates are publicly available at https://osf.io/aecwn/?view_only=0de9a7de36b241d1a5f3f7174629e368. Our results reveal substantial state-level heterogeneity in levels and trends of contacts across the US over the course of the COVID-19 pandemic, with overall contact intensity being highest for the Southern and Rocky Mountain states and lowest for states on the West Coast and in New England. Contact patterns generally became increasingly assortative with respect to age over our observation window, with significant state-level differences in these trends. Taken together, our results demonstrate that national-level contact patterns are not a suitable replacement for state-level contact patterns. Our method can be applied in many other settings where national-level contact data is available, but local-level estimates are needed. The resulting age-stratified contact matrices are relevant for a range of infectious diseases, such as COVID-19, influenza, pertussis, and measles.

2 Methods

2.1 Data

We use data from Waves 1-6 of the Berkeley Interpersonal Contact Study (BICS), a nationally-representative study of interpersonal interaction in the US (Feehan and Mahmud, 2021). Respondents were asked to report on the number of household and non-household persons they had *conversational contact* with the day before the survey. Conversational contact was

defined as a two-way conversation with three or more words in the physical presence of the other person. This is the definition used by the POLYMOD project (Mossong et al., 2008). Respondents were asked to provide age and sex information on all household members and detailed information on up to three of their non-household contacts, including demographic profile, length of interaction, and where the conversation took place. These detailed contacts were up-weighted to reflect the total number of contacts, for which detailed information may or may not have been collected (see Appendix, Section 1.1 for details).

Six waves of data were collected from April 2020 to May 2021. Waves were generally conducted over a few weeks. Table 1 shows the number of interviews conducted per month.

Wave	Month	Year	Interviews
1	April	2020	856
1	May	2020	525
2	June	2020	1113
3	September	2020	1486
4	December	2020	1094
5	February	2021	1304
6	May	2021	2412

Table 1: Number of BICS interviews administered monthly.

2.2 New approach to estimating subnational contact patterns

Our paper introduces a new method for estimating levels and trends in state-level rates of disease-relevant contacts in the United States over the course of the COVID-19 pandemic by combining information from national-level contact data and other locality-specific data sources. The methods we introduce are applicable to any directly transmitted infectious disease – including, for example, influenza, pertussis, and measles – and can be applied in many different settings all over the world.

Researchers construct age-structured contact matrices to summarize patterns of interpersonal contact in a population. These age-structured contact matrices describe average rates of contact between age groups and serve as a key input to most mathematical models of directly transmitted infectious diseases. Formally, we assume the population has been

divided into A discrete age groups. Let c_{ij} be the average number of contacts that a person in age group i has with people in age group j over a given time period. Then the contact matrix $C = (c_{ij})$ is the $A \times A$ matrix that is composed of the expected number of contacts between each pair of age groups.

A growing body of methodological work is concerned with how best to estimate the entries c_{ij} of the contact matrix C (Wallinga, Teunis and Kretzschmar, 2006; Zagheni et al., 2008; Dorélien et al., 2021; Iozzi et al., 2010; Mossong et al., 2008; Prem, Cook and Jit, 2017; Prem et al., 2021). A conventional strategy, called indirect estimation, is based on fitting models that back-estimate the entries in the contact matrix C from epidemiological data, such as case-counts or estimates of seroprevalence. Indirect estimation is appealing because these methods do not require special data collection. However, this convenience comes at a cost – indirect estimation requires making several assumptions that are hard to validate or check. More recently, attention has turned to direct estimation methods which involve collecting data to estimate each entry c_{ij} of the contact matrix. Several different types of data can be collected to achieve this goal: previous studies have explored estimating c_{ij} from time-use data (Dorélien et al., 2021; Zagheni et al., 2008), wearable sensors (Barrat et al., 2014; Mastrandrea, Fournet and Barrat, 2015), and surveys, including diary studies (Mossong et al., 2008; Feehan and Mahmud, 2021; Smieszek et al., 2012).

This study focuses on using surveys that ask respondents to report about their face-to-face interactions with other people (Wallinga, Teunis and Kretzschmar, 2006). This direct estimation approach is appealing because it is extremely flexible. Surveys can be used by researchers to: (1) make inferences about contact patterns in a population that is not constrained to a small geographic area, (2) gather information about the interactions most relevant to the spread of directly transmitted pathogens, and (3) collect important information beyond the contacts themselves, including contextual information about interpersonal interactions (e.g., their location and duration) and about the people who interacted (e.g., their age, sex, occupation, and relationship to one another). This contextual information can be very useful when developing policies to limit contacts in the hopes of slowing the spread of a directly transmitted infectious disease.

While surveys or diary studies have now been used to produce national-level estimates

of age-specific contact patterns in many countries around the world (Mosson et al., 2008; Zagheni et al., 2008; Feehan and Mahmud, 2021; Wallinga, Teunis and Kretzschmar, 2006; Hoang et al., 2019; Mousa et al., 2021; Liu et al., 2021), the majority of countries still lack nationally representative contact surveys. One stream of research has developed an approach for extrapolating synthetic national-level contact matrices in countries where no contact data are available at all (Prem, Cook and Jit, 2017; Prem et al., 2021). Principled national-level extrapolations of contact patterns are vastly preferable to no information at all. These principled extrapolation methods can be seen as a complement to the methods we introduce here, which can instead be used when national-level contact data are available but researchers wish to make fine-grained, local-level inferences. Our approach is thus more similar to interpolation, as opposed to extrapolation.

In order to use nationally representative BICS data to estimate contact matrices at the state-level (Efron and Morris, 1975; Fay and Herriot, 1979; Schmertmann et al., 2013; Assunção et al., 2005; Alexander, Zagheni and Barbieri, 2017; Rao and Molina, 2015), we extend a promising approach called multilevel regression with poststratification (MRP). First developed by Gelman and Little 1997, MRP has recently been extended to estimate subnational public opinion (Gelman and Little, 1997; Gelman et al., 2018; Lax and Phillips, 2013; Park, Gelman and Bafumi, 2004), forecast elections (Wang et al., 2015), and estimate small-area population health outcomes (Zhang et al., 2014). This study is the first application of MRP to the estimation of social contact patterns.

MRP consists of two main steps. In the first step (multilevel regression), we fit Bayesian hierarchical models to estimate contact patterns for all poststratification “cells – mutually exclusive groups cross-classified by key covariates. For example, one cell used in our study is Non-Hispanic Black women aged 25-35 living in New York in a household of size 4. In the second step (poststratification), we aggregate the cell-level estimates up to the state-level by weighting each cell by its relative proportion in the state. For our study, we add a third step, which takes state-level estimates and aggregates them up to contact matrices.

MRP has traditionally been used to study static outcomes. However, we needed to estimate contact matrices for each US state over many time periods. One approach is to use a separate MRP model for each time period (e.g., year) and combine these separate MRP

models into a single time-series model. However, combining separate MRP models doesn't make full use of all available information and is less flexible for incorporating time trends into a model. Therefore, we fit a single "dynamic MRP" model explicitly incorporating a time trend (Gelman et al., 2018). This model allows us to produce estimates for all 51 states and 411 different time periods (days). Dynamic MRP allows us to take advantage of all data available when making predictions.

To summarize, we follow three steps to estimate state-level contact matrices from nationally-representative BICS data: (1) we fit Bayesian hierarchical models to the national-level survey data; (2) we poststratify model estimates; (3) we calculate state-level contact matrices from the poststratified estimates. We now describe each of these steps in turn.

2.3 Models

Our hierarchical models overcome the instability of estimates from very finely partitioned cells by estimating cell-level averages from a hierarchical model that allows for "random" or "modeled" effects for some predictors. Random effects allow for partial pooling towards the group mean, with greater pooling for less-populated cells (Fay and Herriot, 1979). When little to no data are available for a cell, estimates are based on data from similar cells; when lots of data are available for a cell, estimates are closer to the original survey responses.

There are fundamental differences between household contacts and non-household contacts; for example, we would expect non-household contacts to change substantially over the course of the pandemic while household contacts remain relatively stable. Therefore, we develop two flexible hierarchical models for the contact data in the BICS survey: one for non-household contacts and one for household contacts. We estimate the total number of contacts by summing the predicted number of household and non-household contacts.

For the non-household contacts models, we include a national-level cubic time trend and state-level hierarchical cubic time trend, which allows for state-level deviations from the national time trend. We chose our final model by fitting a series of models with different specifications and performing model selection using Pareto-smoothed importance sampling leave-one-out cross validation (PSIS LOO-CV) to select the model with the best performance (Vehtari, Gelman and Gabry, 2017). For further details, see Appendix Section 2.3.

We incorporate Google Community Mobility reports on visits to seven different place categories – grocery and pharmacy, parks, transit stations, retail and recreation, residential, and workplaces (Google, 2021; Nouvellet et al., 2021) – into our model. We follow Jewell et al. (2021) by aggregating these seven signals into one predictor, the three-week rolling average of the first principal component. We find this mobility predictor only marginally increases our model’s performance (see Table 2). However, we include the mobility predictor in our model to highlight the model’s ability to incorporate state-level contextual predictors. Highly comparable estimates from a model without the mobility predictor are presented in Appendix Section 3.5, demonstrating this method can be used without mobility data.

For our model, we let y_{ic} be the number of contacts for person i in age category c for $1 \leq c \leq C$. Then $\mathbf{y}_i = (y_{i1}, \dots, y_{iC})^T$ is a vector with the number of contacts person i has with people in each age group. We fit separate models to predict the total number of contacts (calculated by up-weighting detailed contacts) in each of the 7 defined age categories: 0 – 17, 18 – 24, 25 – 34, 35 – 44, 45 – 54, 55 – 64, and 65+. We assume each $y_{i,c}$ follows a negative binomial distribution,

$$y_{i,c} \sim \mathcal{NB}(\mu_{i,c}, \phi), \quad (1)$$

where $\mu_{i,c}$ is the expected number of contacts. We model the log of the expected number of contacts using

$$\begin{aligned} \log(\mu_{i,c})_{non-household} = & \alpha_{0,c} + a_{j[i],c}^{\text{gender}} + a_{j[i],c}^{\text{age category}} + a_{j[i],c}^{\text{household size}} + a_{j[i],c}^{\text{race}} + a_{j[i],c}^{\text{mobility}} + a_{j[i],c}^{\text{gender:agecat}} \\ & + a_{j[i],c}^{(\text{day}+\text{day}^2+\text{day}^3)} + \\ & + b_{j[i],c}^{(1+\text{day}+\text{day}^2+\text{day}^3)|\text{state}} \end{aligned} \quad (2)$$

and

$$\begin{aligned} \log(\mu_{i,c})_{\text{household}} = & \alpha_{0,c} + a_{j[i],c}^{\text{gender}} + a_{j[i],c}^{\text{age category}} + a_{j[i],c}^{\text{household size}} + a_{j[i],c}^{\text{race}} + a_{j[i],c}^{\text{gender:agecat}} \\ & + b_{j[i],c}^{1|\text{state}}, \end{aligned} \quad (3)$$

where $\alpha_{0,c}$ is the fixed intercept term and the terms $a_{j[i],c}^{\text{var}}$ denote the population-level effects (fixed effects) associated with each categorical variable. We use the subscript $j[i]$ to denote the group membership for the i th respondent. For example, the $a_{j[i],c}^{\text{race}}$ variable can take values $\{a_{\text{Black},c}^{\text{race}}, a_{\text{Hispanic},c}^{\text{race}}, a_{\text{White},c}^{\text{race}}, a_{\text{Other Race},c}^{\text{race}}\}$ depending on the racial self-identification of respondent i . The terms $b_{j[i],c}^{\text{var}|\text{state}}$ denote the group effects (random effects or hierarchically modeled effects).

We include group effects because they allow the model to take advantage of partial pooling: when many observations are available, the estimates are closer to the original survey responses, and when few observations are available for a group, the estimates are pulled away from survey responses towards the overall mean. By assuming that the group effects for a given variable (e.g. the $b_{j[i],c}^{1|\text{state}}$ for the 51 states) are exchangeable, we can treat the variance $\sigma^{2,\text{state}}$ of their prior as a free parameter that will affect the degree of partial pooling. Thus, the amount of partial pooling – how much cell estimates are pulled towards the overall mean – is estimated from the data. In the household contact models, we model the state-specific intercepts as $b_{j[i],c}^{1|\text{state}} \sim N(0, \sigma^{2,\text{state}})$. We use a weakly informative hyper-prior for the variance parameters to avoid boundary estimates (i.e., to avoid a group-level variance estimate of 0 where such an estimate is a priori implausible (Chung et al., 2013; Gelman, 2006)). Specifically, we assume a half-t-distribution (truncated from below at 0) with 3 degrees of freedom for the prior of the standard deviation, σ^{state} : $\sigma^{\text{state}} \sim \text{half-}t_3(0, 2.5)$.

In the non-household contact models, we have state-specific cubic time trends, which require estimating a vector of four parameters per state. To benefit from partial pooling, we model these four state-specific parameters hierarchically via

$$b_{j[i],c}^{(1+\text{day}+\text{day}^2+\text{day}^3)|\text{state}} \sim N(0, V), \quad (4)$$

220 where the variance-covariance V is

$$\begin{aligned} V &= \text{diag}(\sigma)\Sigma\text{diag}(\sigma) \\ \Sigma &\sim \text{LKJ}(1) \\ \sigma &\sim \text{half-}t_3(0, 2.5). \end{aligned} \tag{5}$$

221 Here, we employ the strategy of Bürkner (2017), which separately models the marginal
 222 variances σ (a vector with four entries) and the correlation structure between the four
 223 parameters. The LKJ(1) prior implies a uniform prior distribution over correlation matrices.
 224 Similar to the household contacts model, we adopt a weakly informative half-t-distribution
 225 hyperprior for the variances. Specifically, we use a half-t-distribution with 3 degrees of
 226 freedom (truncated from below at 0) for the standard deviation.

227 Finally, we specify relatively uninformative priors for some of the model parameters:

$$\begin{aligned} \phi &\sim \text{Gamma}(\alpha = 0.01, \beta = 0.01) \\ \alpha_{0,c} &\sim t_3(-2.3, 2.5). \end{aligned} \tag{6}$$

228 All other parameters have a flat prior.

229 2.4 Poststratification

230 For our post-stratification step, we aggregate the cell-level estimates up to the state-level
 231 by weighting each cell by its relative share of the state’s population. We define the target
 232 population using the Public Use Micro Data Samples from the American Community Survey
 233 2014-2018 5-year sample (Ruggles et al., 2020). We split the target population into 14,688
 234 cells based on 5 categorical variables: gender (2 categories), state (51 categories), age group
 235 (6 categories), household size (6 categories), and Race / Hispanic origin (4 categories). Note
 236 that, under traditional poststratification, our survey would not be large enough to produce
 237 estimates for these 14,688 cells: we would have little or no data for most cells, and the
 238 resulting estimates would be extremely noisy. However, this number of cells is not a problem
 239 for MRP, which borrows information from similar cells to smooth out estimates for otherwise
 240 noisy cells.

Figure 1 illustrates our method by comparing our MRP-adjusted estimates for April 2020 with the original survey responses for two states: California, where many interviews were conducted ($N = 95$), and Alabama, where fewer interviews were conducted ($N = 9$). While the MRP estimates align closely with the original survey responses for California, they differ significantly for Alabama. This reflects the partial pooling of the hierarchical model: since Alabama has little data available, MRP estimates use information from similar cells to smooth out the noisy raw estimates produced from just 9 interviews. This partial pooling is particularly relevant for months where we collected no data. For example, no interviews were conducted in Alabama in November, but we are still able to use the dynamic MRP model to make predictions for November.

Next, we used the models to predict average age-specific contacts in each cell, and then poststratified the model predictions using the American Community Survey 2014-2018 5-year sample. The resulting estimates of state-level contact patterns for April 2020 to May 2021 were adjusted for reciprocity and arranged into contact matrices. As an illustration, Figure 2 shows the estimated contact matrices for South Dakota and Washington in July 2020. Appendix Section 3.7 shows the estimated contact matrices for all states and all months from April 2020 to May 2021.

For each estimated contact matrix $\hat{C}$, we define the relative contact intensity index to be equal to $\frac{\rho(\hat{C})}{\rho(C^{\text{UK}})}$, where $\rho(\hat{C})$ is the dominant eigenvalue of the estimated contact matrix and $\rho(C^{\text{UK}})$ is the dominant eigenvalue of the contact matrix for the UK POLYMOD study. We follow other studies in using contact patterns from UK participants in the POLYMOD study as a pre-pandemic baseline reference (Mossong et al., 2008; Feehan and Mahmud, 2021). Assuming no age-specific differences in susceptibility or infectiousness, the contact intensity index is directly proportional to the ratio of the R_0 values implied by the two contact matrices (Diekmann, Heesterbeek and Metz, 1990). Additionally, we calculate each age group’s relative contribution to overall transmission. This is proportional to the leading left eigenvector of the contact matrix, assuming no age-specific variation in transmissibility or susceptibility (Hurford, Cownden and Day, 2010). The leading left eigenvector is defined as a row vector $\mathbf{v}_L$ such that $\mathbf{v}_L \hat{C} = \rho(\hat{C}) \mathbf{v}_L$, where $\hat{C}$ is the estimated contact matrix and $\rho(\hat{C})$ is the leading eigenvalue.

Figure 1: Comparison of MRP-adjusted estimates (black) with unweighted BICS estimates for Alabama (panel A) and California (panel B) from April of 2020. MRP estimates are presented with 95% credible intervals. Where more data are available, predictions more closely track original survey estimates.

Finally, to assess the degree of assortative mixing with respect to age (i.e., the tendency for people to have higher contact with others similar to them in age), we estimate the q-index, a common measure of the assortativity of contacts. The q-index gives a measure of departure from perfectly proportionate mixing: a value of 0 indicates perfectly proportionate mixing and a value of 1 indicates a full assortativity. Specifically, the q-index is defined as:

$$\text{q-index} = \frac{|\hat{\lambda}_1|}{|\hat{\lambda}_2|} \quad (7)$$

where $\hat{\lambda}_1$ is the largest eigenvalue and $\hat{\lambda}_2$ is the second largest eigenvalue.

3 Results

We use our model to estimate daily age-stratified contact matrices for all 50 US states and for Washington DC. The model combines information from (1) the Berkeley Interpersonal Contact Study (BICS) waves 1 - 6 (N = 8,920), which collected responses at the US national level from April 2020 to May 2021; and (2) locality-specific data sources, including the American Community Survey and digital estimates of population mobility from Google (“Methods”). Our model produces estimated age-stratified contact rates for each state and each day, but we focus here on monthly average estimates for each state in order to investigate changes over moderate time scales and to smooth predicted values, as recommended in the small-area estimation literature (Mills et al., 2020; Downes et al., 2018).

Figure 2 compares predicted contact matrices for Washington and South Dakota – two states chosen to illustrate an example of a state with low and high contact, respectively – over all days in July 2020. Appendix Section 3.7 shows additional estimated contact matrices for all states and all months from April 2020 to May 2021. Two substantive findings emerge from Figure 2 and Appendix Section 3.7. First, the levels of interpersonal contact differ significantly across states. For example, in July 2020, members of the [18 – 25) age group in South Dakota had on average 11.6 total contacts in the past 24 hours, while members of the [18 – 25) age group in Washington had only 6.4 total contacts in the past 24 hours. Second, estimated state-level contact patterns have high levels of assortative mixing by age for all

Figure 2: MRP estimates of state-level contact matrices for Washington and South Dakota in July, 2020. Each entry i, j in the contact matrix represents the average number of contacts that a person (ego) in age group j has with other people (alter) in age group i in the past 24 hours. Each cell is shaded according to the estimated mean number of total (household and non-household) contacts. The contact matrices have been adjusted for reciprocity; however, this is not necessarily reflected visually in the contact matrices due to the differential size of the population subgroups.

states and across the course of the pandemic: at each month, the leading diagonal stripes visible in both state’s estimated contact matrix in [Figure 2](#) show highest relative rates of contact between members of the same age group at all or nearly all ages. Members of the $[0 - 18)$ age group are also estimated to have high average daily contacts with members of age groups $[25 - 35)$ and $[35 - 45)$ across all states and time periods, suggesting the persistent influence of generational and household structure on interpersonal interaction. These findings are consistent with previous national-level contact studies conducted in countries outside the US both before and during the COVID-19 pandemic ([Mosson et al., 2008](#); [Verelst et al., 2021](#)).

To compare the intensity of interpersonal contact across states and time, we define a quantity called the *relative contact intensity index*. The relative contact intensity index summarizes how high or low age-structured contact rates are in a specific state at a specific time, relative to a baseline. A relative contact intensity value of 1 means that contact intensity is unchanged since baseline; a value less than 1 means that contact intensity has reduced since baseline, and a value greater than 1 means that contact intensity has increased since baseline (for full mathematical details, see “Methods”).

[Figure 3](#) shows how the relative contact intensity index for each state changes from March of 2020 to May of 2021, using UK participants in the POLYMOD study as a pre-pandemic baseline reference ([Mosson et al., 2008](#)). Consistent with the cross-state variation [Figure 2](#) revealed for July 2020, [Figure 3](#) shows significant heterogeneity in total levels of contact across states at all time periods. This heterogeneity suggests that national-level contact rates would be a misleading proxy for the local level: in July 2020, national contact rates would over-estimate contact intensity for Washington by 18%, while under-estimating contact intensity in South Dakota by 34%. All states experienced an upward trend in contacts over time. Relative contact intensity is lowest in March 2020 and increases until August 2020. Beginning in September 2020, some states experience a substantial decline in contact intensity (Iowa, Kansas, and New York), while other states (Florida, Hawaii, and Massachusetts) experienced a modest increase. In January 2021, contact intensity began increasing in almost every state until the end of our observation window in May 2021. The variation in contact intensity was lowest in April 2020, and peaked in August 2020 (see [Figure 9](#) for full analysis).

Figure 3: Monthly state-specific estimates of relative contact intensity index over time. Horizontal black line shows pre-pandemic baseline contact intensity. Vertical dashed line denotes July 2020, the month we present contact matrices for in [Figure 2](#).

Figure 4: Relative contribution of each age-group to overall transmission in California, New York, and Texas assuming no age-specific differences in transmissibility or susceptibility. We pick the youngest age group $[0 - 18)$ as a reference group which all other estimates are rescaled to. Error bars represent 80% credible intervals.

The relative contact intensity index is a useful measure of the overall intensity of inter-personal contact. But, by summarizing the level of contact across all age groups with a single quantity, the relative contact intensity index can mask important age-specific variation over time. For example, because many diseases such as COVID-19 and influenza have strong age-specific patterns of mortality (O’Driscoll et al., 2021), age-specific contact rates are key to understanding underlying transmission dynamics. To demonstrate the implications of age-specific heterogeneity in contact rates, we create an index capturing each age group’s relative contribution to overall transmission, assuming no age-specific differences in susceptibility or infectiousness (Klepac et al., 2020). Figure 4 shows the results for each age group in three large US states with different population and policy dynamics: California, New York, and Texas. For interpretability, we normalize each value by dividing by the value for the $[0 - 18)$ age group within each state and month. The contribution to overall transmission is highest for the $[0 - 18)$ age group and lowest for the $[55 - 65)$ and $[65 - 100)$ age groups. These differences vary across states. For example, in January 2021, the relative contribution for the $[65 - 100]$ age group was 87% larger for Texas than for California.

Finally, to understand how assortativity with respect to age changed over time, we estimate monthly, state-level estimates of the q-index. The q-index takes on values between 0 (proportionate mixing) and 1 (fully assortative mixing) (Zhang et al., 2020); see “meth-

Figure 5: Change in age assortativity, as measured by the q-index, over the course of the pandemic. A higher q-index value corresponds to higher age assortativity.

ods” for full mathematical definition. Figure 5 shows contacts generally became more age-assortative over time, consistent with previous findings in Wuhan, China (Zhang et al., 2020). However, trends vary across states: New Jersey’s age assortativity peaks in January 2021, with a gradual decline until May of 2021. In California, age assortativity remains low until January 2021, when there is a sharp uptick.

Previous work has found that non-pharmaceutical interventions (NPIs), such as state-level social distancing regulations and their enforcement, are associated lower aggregate-level contact intensity (Coletti et al., 2020; Gimma et al., 2022; Liu et al., 2021; Latsuzbaia et al., 2020; Tizzani et al., 2022). As a robustness check, we refit our models adding the Oxford Stringency Score as a covariate (Hale et al., 2021). The Oxford Stringency Score is an NPI that measures the stringency of “lock-down” policies that primarily restrict people’s social behavior. We find no significant improvement the predictive accuracy of the model (see Appendix Table 3). Incorporating data on NPIs in other settings may be very useful in predicting contact rates, and we emphasize that our modeling framework makes this possible.

4 Discussion

In this paper, we introduce a dynamic MRP model for estimating state-level contact patterns from national-level survey data. We apply this model to national-level contact survey data collected from the Berkeley Interpersonal Contact study to produce age-stratified contact matrices for all 50 US states and Washington DC. This method for estimating subnational contact patterns can be easily adopted to other settings in countries that have recently collected national-level contact data and have available poststratification targets from a census or similar data source.

Our results reveal several key substantive insights into social contact patterns in the US during the COVID-19 pandemic. First, there is significant heterogeneity across states in overall levels of contact intensity. Second, while trends varied by state, contact intensity changed dramatically over time, with a low in April 2020, a spike in the summer of 2020 followed by a decline until January of 2021, and a gradual increase between February 2021 and May 2021. Finally, we observe a general increase in age-related contact assortativity over time, again with distinct state-level patterns of change. In sum, our findings demonstrate the crucial importance of state-level contact patterns; we find that during the COVID-19 pandemic in the US, national-level contact patterns mask important state-level variation and are not a suitable proxy for state-level estimates.

We have several methodological recommendations for other studies that may wish to produce subnational contact rate estimates from national contact data. First, we recommend researchers collect data on both household and non-household contacts and model them separately, as predictors for household and non-household contacts may differ in important ways. Second, if the contact data was collected over time, a time trend should be included in the model (Gelman et al., 2018). The cubic time-trend specified in our model may not generalize to other situations. Third, we recommend researchers fit several models with different time trends and use principled model selection techniques to pick the final model. Finally, we echo past advice in the small-area literature: model at the finest level possible and aggregate to the desired geography and time scale (Mills et al., 2020; Downes et al., 2018).

Despite the promise of this approach, our study has important limitations and there are several directions for future work. We employ an ad-hoc approach to enforcing reciprocity in aggregate contacts between age groups (see “Methods”). Future work could explicitly incorporate these reciprocity constraints into the modeling approach. This would allow for a fully Bayesian strategy with credible intervals that may better capture the full uncertainty inherent in our model. The model could be adapted to more directly capture the age structure of reported contacts. This will involve more explicitly modeling the relationship between reported contacts in different age groups (as opposed to fitting parallel negative binomial models, as we did here). Because we have no survey respondents under the age of 18, we use the principle of reciprocity to impute the average daily number of contacts for this age group (Feehan and Mahmud, 2021); future surveys could try to interview children under 18 or obtain proxy reports from children’s parents. The reported contacts by age could be smoothed within the modeling framework, thereby reducing large jumps between neighboring cells in the total number of contacts. The BICS survey did not directly interview respondents under age 18; thus, we follow previous studies in inferring the within-group contact from all (excluding school) contacts from the UK POLYMOD (see Appendix Section 1.2 for details). As some schools in the US were open during this period, our estimate for the relative contribution the $[0 - 18)$ group makes to overall transmission may be an underestimate for some states and time periods. Additionally, we assumed that all household

407 members were contacts, but future research could relax this assumption and model trends in
408 contact among household members over time. Perhaps most importantly, these results could
409 be validated against other estimates from a high-quality state-level contact study, which
410 ideally captures several states during several different time periods. These are important
411 components of future work, which will advance our ability to produce accurate and timely
412 small-area estimates of contact patterns from national-level contact data.

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Data Availability

All code and data used to produce the analyses presented in this manuscript are available from an Open Science Framework Repository: <https://doi.org/10.17605/OSF.IO/AECWN>

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S1 File: File containing additional detail about the data, model, and supplemental tables and figures. **Table S1:** Model selection metrics. A larger ELPD denotes a more predictive model. This table shows that Model 3 is the best model, as Model 3 has the lowest ELPD. **Figure S1:** The R_0 value implied by contact patterns in each state. **Figure S2:** State-specific MRP estimate of total contact (combined household and non-household contacts). **Figure S3:** Illustration of partial pooling. **Table S2:** Model Performance with and without the Oxford Stringency Score. **Figure S4:** Monthly standard deviation of contact intensity across states. **Figure S5:** Model input and output for state of California. **Figure S6** State-level change in relative contact intensity index over time from a model without mobility data predictors. **Figure S7-Figure S20:** Estimated contact matrix for each month between April 2020 and May 2021.

Supplemental Information

A BICS Contact Survey

A.1 Contact-level Weights

Respondents were asked to report the age and sex of all household contact members and to provide detailed information on up to three non-household contacts, including contact age, sex, contact location, and their relation to the contact. In all waves, some respondents reported more than three non-household contacts, but these respondents were prompted to report only on the first three contacts that came to mind. To account for this, within-respondent weights were constructed to provide detailed information on all contacts. Each of the three initial contacts receives the following weight a_i :

$$a_i = \frac{\text{Total number of contacts}}{\text{Total number of contacts for which detailed data was collected}}. \quad (8)$$

To illustrate, if respondent i reports 12 contacts and provides detailed information on 3 contacts, each of the 3 original contacts are assigned a weight $a_i = 4$. Intuitively, the within-respondent weights represent the total number of contacts represented by each of the three contacts who were reported about in detail. This approach assumes that the first three contacts who come to mind are a randomly selected sample of all contacts. For a more detailed explanation, see [Feehan and Cobb \(2019\)](#). We round each respondent's weighted number of contacts in each age category to the closest integer using stochastic rounding:

$$\text{Round}(\text{contacts}) = \begin{cases} \lfloor \text{contacts} \rfloor, & \text{with probability } 1 - (\text{contacts} - \lfloor \text{contacts} \rfloor) \\ \lfloor \text{contacts} \rfloor + 1, & \text{with probability } (\text{contacts} - \lfloor \text{contacts} \rfloor) \end{cases}$$

For example, if the weighted number of alters in a certain age category was 5.3 alters, it would be rounded to 5 with probability 0.7 and to 6 with probability 0.3. Stochastic rounding preserves the expected value of the number of weighted contacts, which might not

671 be the case for conventional rounding.

672 **A.2 Youngest Age Group**

673 For the youngest age group $[0 - 18)$, for which there are no survey respondents, we use
674 the principle of reciprocity to impute the average daily number of connections (Feehan and
675 Mahmud, 2021). Specifically, we assume that the number of contacts for the youngest age
676 group is:

$$\hat{c}_{1j} = \frac{c_{j1}N_j}{N_1} \quad (9)$$

677 where c_{ij} is the unadjusted, average daily contacts respondents in age group i reported to
678 their contacts in age group j , and N_j is the population size of group j . Intuitively, we are
679 using reciprocity principles to infer the number of connections from the $[0 - 18)$ group to
680 other groups using reports from other groups to the $[0 - 18)$ group. However, we cannot use
681 this method to infer the average daily number of contacts the $[0 - 18)$ group has to other
682 members of the $[0 - 18)$ group. To do this, we calculate the leading eigenvalue of each of our
683 contact matrices and compare it to the leading eigenvalue of the contact matrix from the
684 UK POLYMOD. We then scale the number of contacts in the UK POLYMOD $[0 - 18)$ by
685 the ratio of the leading eigenvalues; we use this imputed value for the average daily contacts
686 from members of the $[0 - 18)$ group to contacts in the $[0 - 18)$ group.

687 While we must make several assumptions to estimate contact matrices for the $(0-18]$ age
688 class, these assumptions do not affect our estimates of contact patterns among adults.

689 **B Methodological Details**

690 **B.1 Reciprocity Constraints**

691 We aggregated our poststratified estimates of contact rates by state and time into crude
692 contact matrices and then adjusted these crude contact matrices to enforce reciprocity, an
693 important feature of contact matrices. To simply motivate why contact matrices should be
694 reciprocal: if person A had conversational contact with person B, person B must have also
695 had conversational contact with person A. Therefore, a contact matrix should have the same

total number of contacts from age-group i to age-group j as from age group j to age group i . In practice, estimated contact patterns from survey data (and poststratified estimates) are not necessarily reciprocal. To ensure reciprocity (Mossong et al., 2008), we use the following formula to estimate adjusted mean contacts $\hat{c}_{ij}$, the average number of contacts that a member of group i has with people in group j :

$$\hat{c}_{ij} = \frac{1}{2N_i} \times (c_{ij}N_i + c_{ji}N_j) \quad (10)$$

where

- N_i = size of age-group i from ACS
- N_j = size of age-group j from ACS
- c_{ij} = estimated average number of contacts that a member of group i has with people in group j
- c_{ji} = estimated average number of contacts that a member of group j has with people in group i

B.2 Poststratification

Survey-based estimates are commonly adjusted using poststratification, a technique that incorporates auxiliary information about the population of interest to improve estimates from a sample. The traditional poststratification approach first assigns respondents to mutually exclusive “cells” – groups cross-classified by key covariates. For example, one cell might be women aged 25-35 living in New York. Next, the cell-level estimates are generated by taking the mean sample response within each cell. Finally, the cell-level estimates are aggregated by weighting each cell relative to its proportion in the population.

This classic poststratification approach works well when the assumptions it relies upon are satisfied. In particular, classic poststratification assumes that each person within a cell has the same chance of being sampled. This assumption is generally violated in practice unless cells have been very finely partitioned. However, once cells have been finely partitioned, the number of interviews per cell typically becomes very small, resulting in unstable cell-level averages. Thus, under classic poststratification there is a tension between how finely cells

	Mobility	Time Trend	ELPD (Diff)	SE Diff
Model 3	Yes	national cubic + state-specific cubic random effect	0.0	0.0
Model 2	No	national cubic + state-specific cubic random effect	-1.2	6.89
Model 1	No	state-specific cubic random effect	-60.9	17.9

Table 2: A larger ELPD denotes a more predictive model. This table shows that Model 3 is the best model, as Model 3 has the lowest ELPD. For the full model specifications, see `brms` syntax in the Appendix Section 6.10.

are partitioned and how stable cell-level average estimates are.

Hierarchical models like the one proposed here have the potential to help resolve this tension. The idea is to overcome the instability of estimates from very finely partitioned cells by estimating cell-level averages from a hierarchical model that allows for “random” or “modeled” effects for some predictors. Random effects allow for partial pooling towards the group mean, with greater pooling for less-populated cells (Fay and Herriot, 1979): when little to no data are available for a cell, estimates are based on data from similar cells; when lots of data are available for a cell, estimates are closer to the original survey responses.

B.3 Model Selection

We fit a series of models with different levels of complexity to identify a model that is as flexible as possible without overfitting. To perform model selection, we use Pareto-smoothed importance sampling leave-one-out cross validation (PSIS LOO-CV) (Vehtari, Gelman and Gabry, 2017). Conventional LOO-CV requires omitting a single observation and refitting the model. However, for complex models or larger datasets, this can be computationally expensive (e.g., for our model, LOO-CV would require repeating estimation 8,920 times). PSIS LOO-CV is a computationally efficient method for estimating the pointwise out-of-sample predictive accuracy of a model using the Pareto-smoothed importance sampling. PSIS LOO-CV calculates importance weights which come from evaluating the ratio of a set of draws from the full posterior distribution to a set of draws from the leave-one-out posterior distribution. PSIS LOO-CV then fits a Pareto distribution to the upper tail of importance weights to smooth out extreme values. The results are then combined into a single measure, the expected log pointwise predictive density (ELPD). The ELPD is a summary of out-

Model	ELPD (Diff)	SE Diff
Model 3	0.0	0.0
Model 3 + Oxford Stringency Index	-8.4	6.7

Table 3: Incorporating the Oxford Stringency Score into our best-performing model (model 3) decreased our models performance, as measured by the expected log predictive density (ELPD). A larger ELPD denotes a more predictive model.

of-sample predictive accuracy using posterior simulations, and can be used both to assess the (out-of-sample) predictive accuracy of the model and for model comparison. Table 2 summarizes the ELPD predictive density for four different model fits. Based on these results, we chose Model 3 for our analysis: it had the best performance as measured by its LOO-CV ELPD.

Fits shown here were obtained using the `brms` package (Bürkner, 2017). Models were run with 1,000 warm-up iterations and 1,000 sampling iterations. Each model was run on four different sampling chains; the R-Hat statistics were between 1 and 1.01, suggesting that the chains had mixed successfully.

Table 3 shows that incorporating the Oxford Stringency Score (Hale et al., 2021)—an NPI that measures the stringency of “lock-down” policies that primarily restrict people’s social behavior—as a covariate into our model led to a slight decrease in model performance. Understanding why incorporating NPIs into our model did not improve its predictive accuracy is a potential avenue for future research.

B.4 Summarizing contact intensity

While a contact matrix contains valuable detail about age-specific transmission rates, a single summary measure of total level of social contact can facilitate comparisons across time and place. We use the leading eigenvalue of the contact matrix C as a summary measure of the overall levels of contact implied by a contact matrix.

To motivate this choice, we briefly review the link between the contact matrix C and the next generation matrix N , which is useful in modeling the early stages of a disease outbreak; see Diekmann, Heesterbeek and Metz (1990) and Diekmann, Heesterbeek and Britton (2013) for a full account. The next generation matrix $N = (n_{ij})$ is an $A \times A$ matrix that maps a

vector with counts of infected individuals in each age group at generation g , ϕ_g , to a vector of counts of infected individuals in each age group in the subsequent generation, $\phi_{g+1} = N\phi_g$. The dominant eigenvalue of the next generation matrix, $\rho(N)$, is the basic reproductive number, R_0 (Diekmann, Heesterbeek and Metz, 1990). R_0 is a critical quantity in infectious disease epidemiology: it summarizes the number of secondary infections expected to result from one infected individual in an entirely susceptible population.

The social contact hypothesis says that the next generation matrix is proportional to the contact matrix, i.e., $N = \alpha C$ where $\alpha > 0$ is a proportionality constant that depends on the pathogen and other factors, assuming that there is no age-specific heterogeneity in susceptibility and transmissibility (Wallinga, Teunis and Kretzschmar, 2006; Hens et al., 2012; Diekmann, Heesterbeek and Britton, 2013). Under this hypothesis, the dominant eigenvalue of the social contact matrix is $\rho(C) = \rho(\alpha N) = \alpha R_0$. Thus, the dominant eigenvalue of a social contact matrix can be a useful summary of the aggregate level of contact.

The social contact hypothesis can also help compare contact matrices across place or time. Given two contact matrices C_1 and C_2 , there will be R_0 values associated with each one, say R_0^1 and R_0^2 . Assume that the pathogen of interest is the same and that factors other than contact are held constant, so that the proportionality constant α is the same for both matrices. Then under the social contact hypothesis, $\frac{\rho(C_1)}{\rho(C_2)} = \frac{\alpha R_0^1}{\alpha R_0^2} = \frac{R_0^1}{R_0^2}$. Thus, if the dominant eigenvalue of C_2 is twice the dominant eigenvalue of C_1 , then the R_0 value associated with C_2 is twice as big as the R_0 value associated with C_1 . Under the social contact hypothesis, this ratio can be identified even if the proportionality constant α is not known.

B.5 Alternative Contact Intensity Measures

In the main body of our paper, we quantify contact rates using the relative contact intensity. Here, we present two alternative measures of contact intensity: (1) the average number of total daily contacts and (2) a measure of R_0 for a respiratory pathogen such as COVID-19 (with age-specific differences in the probability of transmission given contact with an infectious individual). We calculate R_0 using a deterministic, age-stratified compartmental model that has been used previously to study COVID-19 dynamics (Davies et al., 2020). The

model assumes that all people are initially susceptible, and then can become exposed through a contact with an infected person. After exposure, there is a latent period before individuals become infected either clinically or sub-clinically. Sub-clinical infections are assumed to be less infectious compared with clinical infections. After the infectious state, individuals then move to the recovered state. To calculate R_0 , we take the absolute value of the leading eigenvalue of the next-generation matrix (NGM), which is defined as [Davies et al. \(2020\)](#):

$$NGM = D_u C D_y D_x \quad (11)$$

where

- D_u is a diagonal matrix with elements u_i , the probability of transmission given contact with an infected person for an individual in age-class i (i.e. the relative susceptibility of individuals in age-class i)
- C is the state-specific age-structured contact matrix
- D_y is a diagonal matrix with elements y corresponding to the mean infectious period
- D_x is a diagonal matrix with elements $\rho_j + (1 - \alpha)\rho_j$; ρ_j is the probability of having clinical symptoms in age-class j and α is the relative infectiousness of sub-clinical cases

The probability of transmission given contact with an infected person in a given age-class (u_i) and the probability of having clinical symptoms per age group (ρ_j) were drawn from the literature ([Davies et al., 2020](#)). We assume a relative infectiousness of clinical vs. subclinical individuals (α) of 0.5 ([McEvoy et al., 2020](#)) and a mean infectious period of 6 days ([Holmdahl et al., 2020](#)). We re-scale these u_i values such that a model fit to a baseline contact matrix from UK participants in the POLYMOD study ([Mossong et al., 2008](#); [Feehan and Mahmud, 2021](#); [Chin et al., 2021](#)) produces the R_0 value of 2.5 ([Viceconte and Petrosillo, 2020](#)). We then fit this model with the rescaled u_i values on all estimated contact matrix; estimates are shown in [Figure 6](#).

Figure 6: The R_0 value implied by contact patterns in each state. R_0 was estimated using an age-stratified deterministic compartmental model.

Figure 7: State-specific MRP estimate of total contact (combined household and non-household contacts).

C Additional Analyses

C.1 Internal validation check

To assess the internal validity of our method, we re-estimate our models on two subsamples. These subsamples are intended to illustrate the effects of having less data in two states: Florida and Washington. We chose these two states to illustrate partial pooling because they deviated from the overall mean in distinct ways. Florida deviates from the overall mean because there is no noticeable decline in contacts over the period between November 2020 and March 2021. Washington broadly shares similar trends over time to the overall mean, but has a lower contact rate. For the first subsample, we randomly drop all but 20% of the responses for each wave from Florida and Washington; we do not drop any data from other states. For the second subsample, we randomly drop all but 60% of the responses for each wave from Florida and Washington; again, we do not drop any data from other states. [Figure 8](#) plots the the estimated contact intensity from models fit to these two subsamples and to the full sample. The figure demonstrates how partial pooling works: when there is less data available (60% subsample), the estimates are pulled towards the overall mean. When more data is available (20% subsample), the estimates more closely resemble the raw survey data. This is clearly illustrated in Florida and Washington, as estimates from the 60% subsample and full sample are pulled away from the overall mean. Additionally, this provides some internal validation check for this method, as the estimates are fairly reasonable even when there is little data.

C.2 Variation in Contact Intensity

[Figure 9](#) shows the standard deviation of the relative contact intensity index across states by month. This measure of how variable contact intensity was across states reveals several interesting patterns. The state-level similarity in contact intensity changed dramatically over the course of the COVID-19 pandemic. Contact intensity was most similar across states during April 2020, when social contact was lowest. When contact intensity spiked during July and August of 2020, state-to-state variation in contact intensity was highest.

Figure 8: Illustration of partial pooling. The black dashed line shows the average estimated relative contact intensity across all states.

Figure 9: Monthly standard deviation of contact intensity across states.

C.3 Mobility data illustration for CA

Figure 10 shows model input and predictions for California to give intuition about the relationship between model input and ultimate predictions of contact intensity. Specifically, panel (a) shows the first principal component of the Google mobility data and panel (b) shows the rolling three-week average of first principal component of mobility data. We used the rolling-three week average of the first principal component to smooth the data. A higher value of the first principal component indicates higher levels of mobility. Panel (c) shows the average monthly reported number of contacts in California. Panel (d) shows the implied R_0 value and panel (e) shows daily predictions of the relative contact intensity index. The cubic trend – observed in both BICS unadjusted survey data and mobility data – is also reflected in both the predicted relative contact intensity index and the monthly estimate of implied R_0 .

C.4 Model without mobility predictors

While we find mobility data is only marginally predictive (see Table 2), we include it in our model to highlight the model’s flexible ability to incorporate state-level contextual predictors.

Figure 10: Model input and output for state of California. Panel a shows the first principle component of seven different Google mobility signals. Panel b shows the three-week rolling average of the first principle component of seven different Google mobility signals. Panel c shows the unadjusted estimates of contact from BICS survey. Panel d shows the change in R_0 over time. Panel e shows the daily MRP model predictions.

861 In Figure 11, we show the estimated state-level relative contact intensity index over time
862 from a model fit *without* the mobility predictor. The estimates from our model without the

Figure 11: State-level change in relative contact intensity index over time from a model without mobility data predictors.

863 mobility predictor closely track our estimates from the model with the mobility predictor,
 864 demonstrating that mobility data is not a prerequisite for this approach.

C.5 Model Code

All models were fit using the `brms` package in R. Full `brms` syntax below:

```
## non-household model
nonhh_model <- brm(
  formula = mvbind(alter_age_0_18, alter_age_18_25, alter_age_25_35,
    alter_age_35_45, alter_age_45_55, alter_age_55_65, alter_age_65_100) ~
    agecat +
    gender +
    hhsize +
    race +
    weekday +
    agecat:gender +
    rolling_pca_3wks + ## mobility data
    poly(day_std, 3) + ## national polynomial trend
    (poly(day_std, 3) | estimated_state), ## state level hierarchical polynomial trend
  family = 'negbinomial',
  inits = 0,
  data = df_formodel_topcode,
  chains = 4,
  cores = 16,
  backend = "cmdstanr",
  threads = threading(4),
  # control = list(adapt_delta = 0.9),
  iter = 4000)

## household model
hh_model <- brm(
  formula = mvbind(alter_age_0_18_hh, alter_age_18_25_hh, alter_age_25_35_hh,
    alter_age_35_45_hh, alter_age_45_55_hh, alter_age_55_65_hh, alter_age_65_100_hh) ~
    agecat +
    gender +
    hhsize +
    race +
    agecat:gender +
    (1 | state),
  family = 'negbinomial',
  inits = 0,
  data = df_formodel_topcode_household,
  chains = 4,
  cores = 16,
  iter = 4000)
```

C.6 Contact Matrices by month

State-Level Contact Matrices (2020-04)

State-Level Contact Matrices (2020-05)

State-Level Contact Matrices (2020-06)

871

State-Level Contact Matrices (2020-07)

State-Level Contact Matrices (2020-08)

State-Level Contact Matrices (2020-09)

State-Level Contact Matrices (2020-10)

State-Level Contact Matrices (2020-11)

876

State-Level Contact Matrices (2020-12)

877

State-Level Contact Matrices (2021-01)

State-Level Contact Matrices (2021-02)

State-Level Contact Matrices (2021-03)

State-Level Contact Matrices (2021-04)

881

State-Level Contact Matrices (2021-05)

882