Hierarchical Bayes estimation of small area proportions using statistical linkage of disparate data sources

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Abstract

We propose a Bayesian approach to estimate finite population proportions for small areas. The proposed methodology improves on the traditional sample survey methods because, unlike the traditional methods, our proposed method borrows strength from multiple data sources. Our approach is fundamentally different from the existing small area Bayesian approach to the finite population sampling, which typically assumes a hierarchical model for all units of the finite population. We assume such model only for the units of the finite population in which the outcome variable observed; because for these units, the assumed model can be checked using existing statistical tools. Modeling unobserved units of the finite population is challenging because the assumed model cannot be checked in the absence of data on the outcome variable. To make reasonable modeling assumptions, we propose to form a large number of cells for each small area using factors that potentially influence the binary outcome variable of interest. This strategy is expected to bring some degree of homogeneity within a given cell and also among cells from different small areas that are constructed with the same factor level combination. Instead of modeling true probabilities for unobserved individual units, we assume that population means of cells with the same combination of factor levels are identical across small areas and the population mean of true probabilities for a cell is identical to the mean of true values for the observed units in that cell. We apply our proposed methodology to a real-life COVID-19 survey, linking information from multiple disparate data sources to estimate vaccine-hesitancy rates (proportions) for 50 US states and Washington, D.C. (small areas). We also provide practical ways of model selection that can be applied to a wider class of models under similar setting but for a diverse range of scientific problems.

Keywords: Administrative Data, Finite Population sampling, Informative sampling, MCMC, Multiple surveys, Multi-level Modeling, Nonprobability surveys, Synthetic estimation, Robust estimation.

1 Introduction

Ericson (1969) laid a foundation of subjective Bayesian approach to finite population sampling. In this approach, the entire matrix of characteristics for all units of the finite population can be viewed as the finite population parameter matrix. In practice, a function (e.g., finite population mean or proportion of a characteristic of interest) or a vector of functions (e.g., finite population means or proportions of several characteristics) of this finite population parameter matrix is considered for inference. Using a subjective prior on the finite population parameter matrix, inferences on the finite population
parameter(s) of interest can be drawn using the posterior predictive distribution of the unobserved units of the finite population given the observed sample.

Using this basic idea of Ericson (1969), several papers were written on the estimation of finite population parameters. The methodology developed can be used to solve problems in small area estimation, repeated surveys, and other important applications. The papers can be broadly classified as Empirical Bayesian or EB (e.g., Ghosh and Meeden (1986), Ghosh and Lahiri (1987), Ghosh et al. (1989), Nandram and Sedransk (1993), Arora et al. (1997), among others) and Hierarchical Bayesian or HB (e.g., Ghosh and Lahiri (1992), Datta and Ghosh (1995), Ghosh and Meeden (1997), Malec et al. (1997), Little (2004), Chen et al. (2012), Ghosh (2009), Liu and Lahiri (2017), Nandram et al. (2018), Ha and Sedransk (2019), and others). In an empirical Bayesian approach, hyperparameters are estimated using a classical method (e.g., maximum likelihood). In contrast, in the hierarchical Bayesian approach, priors – usually noninformative or weakly informative – are put on the hyperparameters.

The greater accessibility of administrative and Big Data and advances in technology are now providing new opportunities for researchers to solve a wide range of problems that would not be possible using a single data source. However, these databases are often unstructured and are available in disparate forms, making inferences using data linkages quite challenging. There is, therefore, a growing need to develop innovative statistical data linkage tools to link such complex multiple datasets. Using only one primary survey to answer scientific questions about the whole population or large geographical areas or subpopulations may be effective and reliable, but using them for smaller domains or small areas can often lead to unreliable estimation and unrealistic measures of uncertainty. Using an appropriate statistical model to combine information from multiple data sources, one can often obtain reliable estimates for small areas. A good review of different approaches to small area estimation can be found in Jiang (2007), Datta (2009), Pfeffermann (2013), Rao and Molina (2015), Ghosh (2020), among others.

Scott (1977), Pfeffermann and Sverchkov (1999), Bonnery et al. (2012), and others discussed the concept of informative sampling under which the distribution of the sample could be markedly different from the one assumed for the finite population even after conditioning on related auxiliary variables. Most of the papers cited in the preceding paragraphs assume non-informative sampling, so the distribution of the sample is assumed to be identical to the distribution assumed on the finite population. This could be a strong assumption in many applications. The informative sampling approach suggested by Pfeffermann and Sverchkov (1999) and Pfeffermann and Sverchkov (2007) is one possible solution, but this approach requires additional modeling of survey weights. Rubin (1983) suggested modeling the finite population given the inclusion probabilities (or, equivalently, basic weights) for making inferences about the finite population parameters of interest. However, in practice, inclusion probabilities for all finite population units or detailed design information may not be available. Also, survey data may contain information only on the final weights for the respondents that incorporate nonresponse and calibration. Verret et al. (2015) proposed an alternative approach in which inclusion probabilities are used to augment the sample model. Unlike Rubin (1983), their approach needs weights only for the sample. Both Pfeffermann and Sverchkov (2007) and Verret et al. (2015) considered empirical best linear unbiased prediction (EBLUP) of small area means.

In this paper, we propose a hierarchical Bayesian approach to estimate finite population proportions for small areas. Our proposed method combines information from
multiple disparate data sources such as probability surveys, non-probability surveys, administrative data, census records, social media big data and/or any sources of available relevant information. We propose to reduce the degree of informativeness in sampling by incorporating important auxiliary variables that potentially affect the outcome variable of interest. Following Verret et al. (2015), we also add the survey weights in our model. Our approach differs inherently from the existing small area Bayesian approach to the finite population sampling, which typically assumes a hierarchical model for all units of the finite population. We assume such an elaborate model only for the units of the finite population in which the outcome variable was observed. The reason is intuitive; for these units, the model can be checked using existing statistical tools.

Modeling unobserved units of the finite population is challenging because the assumed model cannot be checked in the absence of data on the outcome variable. To make reasonable modeling assumptions, we propose to form numerous cells for each of the small areas using factors that potentially influence our binary outcome variable of interest. This strategy is expected to bring some degree of homogeneity within a given cell and also among cells from different small areas that are constructed with the same factor level combination. In contrast to the usual modeling approaches under similar scenarios, we do not model true probabilities for unobserved individual units. Instead, drawing inspiration from synthetic methods for small areas, we assume that population means of cells with the same combination of factor levels are identical across small areas and the population mean of true probabilities for a cell is identical to the mean of true values for the observed units in that cell. Since the sample size in a given area is small, many such cells are unrepresented in the sample. If a sample for that cell can be found from other areas, the assumed model is used to produce a hierarchical Bayes synthetic estimate of the finite population mean of that cell for the area. This assumes that the observations within a given cell and area are similar to those for the cell from other areas. If the cell is unrepresented in all areas, the cell mean can be predicted from the population model, but to simplify the methodology and to induce a greater degree of robustness, we can simply ignore that cell when the contribution from that cell is negligible as in our illustrative example. The basic idea is to make the proposed methodology robust against possible violation of the assumed model.

As an application of the proposed methodology, we use a real life example, using a COVID-19 probability survey representing the entire US adult population, a non-probability survey representing only active US adult Facebook users, and Census Bureau estimates of adult population counts at granular levels along with data from an independent COVID-19 data reporting website, to estimate the vaccine hesitancy rates (proportions) for the US states and the District of Columbia (small areas). Through this example and application, we will demonstrate the problems with regular design based estimates when used for small areas and how our methodology may be employed to get more robust estimates along with stable measures of uncertainty.

We now give an outline for the rest of the paper. In section 2, we describe our methodology in detail. In section 3, we describe an application of our method to a real life survey. In section 4, we show the results we obtained with this real life application along with model evaluation. Finally, in section 5, we summarize and conclude our paper by giving future research directions of our methodology.
2 Methodology

For each small area \( i = (i = \cdots, m) \), we partition the finite population into \( G \) cells using factors available in the survey data that potentially influence the outcome variable of interest. We assume that population sizes for these cells are known from the census data. Let \( N_{ig} \) be the known population size of the \( g^{th} \) cell in the \( i^{th} \) area, \( i = 1, \cdots, m; g = 1, \cdots, G \).

Let \( y_{igk} \) denote our binary variable of interest (pertaining to our population proportion estimation problem) for the \( k^{th} \) unit belonging to the \( g^{th} \) cell belonging to the \( i^{th} \) small area \( (i = 1, \cdots, m; g = 1, \cdots, G, k = 1, \cdots, N_{ig}) \). We assume that we have access to different types of known auxiliary variables to model our outcome variable. Let \( x_{i(1)} \) be a vector of indicator variables corresponding to cell \( g \), \( x_{i(2)} \) be a vector of known auxiliary variables specific to area \( i \) and \( x_{igk(3)} \) be a vector of individual level auxiliary variables \( (i = 1, \cdots, m; g = 1, \cdots, G, k = 1, \cdots, N_{ig}) \).

Suppose we have a sample of size \( n \) from the finite population. It is possible to have some or all cells in area \( i \) unrepresented in the sample of responding units; let \( G_i \) be the number of cells represented in the sample for area \( i \) \((i = 1, \cdots, m) \). Let \( n_i \) and \( n_{ig} \) be the sample sizes for area \( i \) and for cell \( g \) within area \( i \), respectively, so that \( \sum_{g=1}^{G_i} n_{ig} = n_i \) and \( \sum_{i=1}^{m} n_i = n \). It is possible to have \( n_i = 0 \) for some area \( i \) or \( n_{ig} = 0 \) for some cell \( g \) within some area \( i \) \((i = 1, \cdots, m; g = 1, \cdots, n_{ig}) \). Let \( w_{igk} \) denote the survey weight for \( k^{th} \) sampled respondent belonging to the \( g^{th} \) cell residing in the \( i^{th} \) small area \( (i = 1, \cdots, m; g = 1, \cdots, G_i, k = 1, \cdots, n_{ig}) \).

2.1 Proposed hierarchical models for sampled respondents and the finite population

Our approach calls for specification of an explicit model for the outcome variable \( y \) for all the \( N \) units of the finite population. Since \( y \) is a binary variable, we assume

\[
\text{Level 1: } y_{igk} \mid \theta_{igk} \overset{\text{ind}}{\sim} B(\theta_{igk}),
\]

where \( B(\theta_{igk}) \) is the Bernoulli distribution with parameter \( \theta_{igk} i = 1, \cdots, m; g = 1, \cdots, G, k = 1, \cdots, N_{ig} \).

We will assume an elaborate model for all respondents because we can evaluate such a model through careful model building steps in the actual data analysis. For \( i = 1, \cdots, m; g = 1, \cdots, G_i, k = 1, \cdots, n_{ig} \), we propose the following model for the sampled respondents:

\[
\text{Level 2: } \phi(\theta_{igk}) = x_{i(1)}^t \alpha + x_{i(2)}^t \beta + x_{igk(3)}^t \xi_c + v_i + \lambda h(w_{igk}),
\]

\[
\text{Level 3: } v_i \overset{iid}{\sim} N(0, \sigma^2_v)
\]

where \( \phi() \) is a suitable known link function (e.g., logit link); \( \alpha, \beta, \) and \( \xi_c \) are fixed unknown coefficients (the suffix \( c \) in \( \xi_c \) allows dependence of the regression coefficient on some combination of the factors that form the demographic cells – \( c \) will be determined through the model selection step); \( v_i \) is a random effect specific to area \( i \); \( h() \) is a known function of survey weights to be determined by a model selection step and \( \lambda \) is a fixed unknown coefficient. Verret et al. (2015) considered multiple choices of \( h() \). If the data analysis suggests \( \lambda = 0 \), we can assume non-informative sampling and carry out the analysis without this additional term. In Level 2 we added the survey weights as an additional auxiliary variable in order to reduce the extent of informativeness.
We now discuss our modeling assumptions for the remaining \( N - n \) unobserved units of the finite population. To this end, for the small areas \( i = 1, \cdots, m \), define:

\( \mathcal{G}_{1i} \): the set of cells represented by the sample in the area \( i \),

\( \mathcal{G}_{2i} \): the set of cells not represented by the sample in the area \( i \) but represented by one or more other areas,

\( \mathcal{G}_{3i} \): the set of cells not represented by the sample.

Define the population proportion for the set of cells \( \mathcal{G}_{1i} \) as,

\[
\bar{\Theta}_{1i} = \frac{\sum_{g \in \mathcal{G}_{1i}} N_{ig} \theta_{igk}}{\sum_{g \in \mathcal{G}_{1i}} N_{ig}} = \sum_{g \in \mathcal{G}_{1i}} b_{ig;1} \bar{\Theta}_{ig}, \quad \text{where} \quad b_{ig;1} = \frac{N_{ig}}{\sum_{g \in \mathcal{G}_{1i}} N_{ig}},
\]

and \( \bar{\Theta}_{ig} = \frac{\sum_{k=1}^{N_{ig}} \theta_{igk}}{N_{ig}} \).

Similarly, we define

\[
\bar{\Theta}_{2i} = \frac{\sum_{g \in \mathcal{G}_{2i}} N_{ig} \theta_{igk}}{\sum_{g \in \mathcal{G}_{2i}} N_{ig}} = \sum_{g \in \mathcal{G}_{2i}} b_{ig;2} \bar{\Theta}_{ig}, \quad \text{where} \quad b_{ig;2} = \frac{N_{ig}}{\sum_{g \in \mathcal{G}_{2i}} N_{ig}},
\]

and

\[
\bar{\Theta}_{3i} = \frac{\sum_{g \in \mathcal{G}_{3i}} N_{ig} \theta_{igk}}{\sum_{g \in \mathcal{G}_{3i}} N_{ig}} = \sum_{g \in \mathcal{G}_{3i}} b_{ig;3} \bar{\Theta}_{ig}, \quad \text{where} \quad b_{ig;3} = \frac{N_{ig}}{\sum_{g \in \mathcal{G}_{3i}} N_{ig}},
\]

as the population proportions for the set of cells \( \mathcal{G}_{2i} \) and the set of cells \( \mathcal{G}_{3i} \), respectively.

We make a synthetic assumption that

\[
\bar{\Theta}_{2i} \approx \sum_{g \in \mathcal{G}_{2i}} b_{ig;2} \bar{\Theta}_{ig;\text{syn}},
\]

where

\[
\bar{\Theta}_{ig;\text{syn}} = \frac{\sum_{j \neq i} \sum_{k} \theta_{jgk}}{\sum_{j \neq i} \sum_{k} N_{jg}},
\]

i.e., \( \bar{\Theta}_{2i} \) is identical to the overall proportion of the cells in \( \mathcal{G}_{2i} \) obtainable from one or more areas (other than area \( i \)). We make no assumption on the rest of the finite population units.

2.2 Parameter of interest

We are interested in estimating finite population proportions for all areas, i.e.,

\[
\bar{Y}_i = N_i^{-1} \sum_{g=1}^{G} \sum_{k=1}^{N_{ig}} y_{igk} = \sum_{g=1}^{G} \frac{N_{ig}}{N_i} \bar{Y}_{ig}, \quad (1)
\]

where \( N_i = \sum_{g} N_{ig} \), population size for the \( i \)th area \( (i = 1, \cdots, m) \). Since population sizes \( N_{ig} \) are in general large, appealing to the law of large numbers as in [Jiang and Lahiri (2006)], we can approximate the finite population means to the following functions of parameters of the assumed finite population model.

\[
\bar{Y}_i \approx \bar{\Theta}_i = \sum_{g=1}^{G} \frac{N_{ig}}{N_i} \bar{\Theta}_{ig} = a_{1i} \bar{\Theta}_{1i} + a_{2i} \bar{\Theta}_{2i} + (1 - a_{1i} - a_{2i}) \bar{\Theta}_{3i}, \quad (2)
\]

\[
\approx a_{1i} \bar{\Theta}_{1i} + a_{2i} \bar{\Theta}_{2i}, \quad (3)
\]

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where, 
\(a_{1i}\): population proportion of units belonging to the set of cells \(G_{1i}\),
\(a_{2i}\): population proportion of units belonging to the set of cells \(G_{2i}\).
The approximation in equation (2) will only be reasonable when \((1 - a_{1i} - a_{2i}) \approx 0\).

### 2.3 A Bayesian implementation of the hierarchical model

As is the common practice with most implementation of HB methodology, the model parameters will be estimated using Monte Carlo Markov Chain (MCMC) method of sampling from posterior distributions. Assume weakly informative priors on the hyper-parameters: \(\beta\), and \(\sigma_v\). At each MCMC iteration \((r = 1, \ldots, R)\) step, the following is generated for the area \(i\):

\[
\bar{\theta}^{(r)}_i = a_{1i}\bar{\theta}^{(r)}_{1i} + a_{2i}\bar{\theta}^{(r)}_{2i} + (1 - a_{1i} - a_{2i})\bar{\theta}^{(r)}_{3i} \approx a_{1i}\bar{\theta}^{(r)}_{1i} + a_{2i}\bar{\theta}^{(r)}_{2i}, \quad r = 1, ..., R,
\]

where

\[
\bar{\theta}^{(r)}_{1i} = \sum_{g \in \bar{G}_{1i}} b_{ig;1}\bar{\theta}^{(r)}_{ig}, \quad \text{with} \quad \bar{\theta}^{(r)}_{ig} = \frac{\sum_k w_{igk}\theta^{(r)}_{igk}}{\sum_k w_{igk}},
\]

\[
\bar{\theta}^{(r)}_{2i} = \sum_{g \in \bar{G}_{2i}} b_{ig;2}\bar{\theta}^{(r)}_{ig;\text{syn}}, \quad \text{with} \quad \bar{\theta}^{(r)}_{ig;\text{syn}} = \frac{\sum_{j \neq i} \sum_k w_{jgk}\theta^{(r)}_{jgk}}{\sum_{j \neq i} \sum_k w_{jgk}},
\]

\[
\theta^{(r)}_{igk} = \phi^{-1}\left(x'_{g(1)}\alpha^{(r)} + x'_{i(2)}\beta^{(r)} + x'_{igk(3)}\xi^{(r)} + \nu^{(r)}_i + \lambda^{(r)}h(w_{igk})\right).
\]

To justify, note that

\[
\bar{\Theta}_{1i} = \sum_{g \in \bar{G}_{1i}} b_{ig;1}\bar{\theta}_{ig} \approx \sum_{g \in \bar{G}_{1i}} b_{ig;1}\bar{\theta}_{ig} = \bar{\theta}_{1i}, \text{ say},
\]

where \(\bar{\theta}_{ig} = \frac{\sum_k w_{igk}\theta_{uk}}{\sum_k w_{igk}}\); see [Jiang and Lahiri (2006)] and [Lahiri and Suntornchost (2020)] for similar justifications in empirical best prediction and hierarchical Bayes approaches, respectively. Also,

\[
\bar{\Theta}_{2i} \approx \sum_{g \in \bar{G}_{2i}} b_{ig;2}\bar{\theta}_{ig;\text{syn}} \approx \sum_{g \in \bar{G}_{2i}} b_{ig;2}\bar{\theta}_{ig;\text{syn}} = \bar{\theta}_{2i}, \text{ say},
\]

where \(\bar{\theta}_{ig;\text{syn}} = \frac{\sum_{j \neq i} \sum_k w_{jgk}\theta_{jk}}{\sum_{j \neq i} \sum_k w_{jgk}}\).

The set of \(R\) MCMC replicates for the \(i^{th}\) area, i.e., \(\{\bar{\theta}^{(r)}_i, r = 1, ..., R\}\), will be used for inferences about \(\bar{\theta}_i\).

### 3 A real-life application

As an illustration of our proposed methodology, we consider a problem of current research interest. Specifically, we aim at providing relatively stable state-wise (our small areas of consideration) estimates of proportions of people who are “hesitant” to get vaccinated for COVID-19. In this section, we first provide an outline of disparate data sources that we have considered in this application.
3.1 Primary source of data: Understanding America Study (UAS)

The Understanding America Study (UAS), conducted by the University of Southern California (USC), consists of approximately 9,000 respondents representing the entire United States. The study is an ‘Internet Panel’, which means that respondents answer surveys via the internet on a computer, tablet, or smart-phone, wherever they are and whenever they wish to participate. Households are broadly defined as anyone living together with the person who signed up for participating and answering survey questions in the UAS study. To get useful and insightful information on attitudes, behaviors, including mental health, health care avoidance behavior, economic crisis around the time of the COVID-19 pandemic etc., USC’s Center for Economic and Social Research (CESR) launched the Understanding Coronavirus in America tracking survey on March 10, 2020, using the list of the members of the whole US population representative UAS panel. The collection of this survey data is supported in part by the Bill & Melinda Gates Foundation and a grant by the National Institute on Aging (grant number: U01AG054580).

Initial requests were sent out to the members of the UAS panel to determine their willingness to participate in an ongoing COVID-related survey; 8,547 members were found eligible out of the 9,603 UAS panel members who responded to the initial request. Since its launch on March 2020, data is being collected on many different waves. Our study in this paper focuses only on wave 16 (October 14 - November 11, 2020). Wave 16 survey containing various questions about the impact of coronavirus pandemic on the respondents’ lives were made available to 7,832 UAS participants. Of those 7,832 participants, 6081 completed the survey and are counted as respondents. Of those who are not counted as respondents, 100 started the survey without completing and 1651 did not initiate responding to the survey. The overall response rate was about 78%. As with the other waves, respondents in this wave also had 14 days to complete the survey and were compensated with $15 for completing the survey.

3.2 Direct UAS estimates

For the “hesitancy towards vaccination” problem, we selected responses from the following question: ‘How likely are you to get vaccinated for coronavirus once a vaccine is available to the public?’ The question has the following 5 response options: very unlikely, somewhat unlikely, somewhat likely, very likely and unsure. We encoded the answer to this question into a binary response variable, taking on the value 1 if the respondent answered anything other than ‘very likely’ and 0 otherwise. We use this variable and the associated survey weight to obtain estimates of proportions of people who are not ‘very likely’ to get vaccinated for the 50 states and the District of Columbia. Naturally, these estimates provide us with the “hesitancy” measures that we are interested in this work. While national estimates meet good quality standard (e.g., margin of errors less than 3%), estimates derived from the data for small geographical areas are unreliable.

Table I provides direct survey estimates of proportions of vaccine hesitant people for the 50 states and the District of Columbia, along with their standard errors. We observe an unrealistic estimate of 1 with associated estimated standard error of 0 for the state of Delaware. This is because out of the few samples from Delaware, no one answered ‘very likely’ to the survey question of interest. But this surely does not mean that everyone in Delaware is hesitant to take the vaccine. The estimate for the state of
Alaska is 0.21 with associated estimated standard error of 0.19, which is considered high as the acceptable range for standard error is usually within 0.02. We observe similar results for Vermont, Rhode Island, District of Columbia, and other states.

3.3 Supplementary data descriptions

In the following subsections, we describe different supplementary data sources that we have considered as an application of our methodology.

3.3.1 The COVID-19 Symptom Survey

The COVID-19 Symptom Survey is a joint initiative by public health scholars and the Facebook. The US survey is hosted by the Carnegie Mellon Delphi Research Center and the international one is hosted by the University of Maryland Joint Program in Survey Methodology. Both universities collaborated with the broader public health community in designing the surveys. The goal is to inform public health decisions by providing an accurate representation of self-reported symptoms in the global adult population. The COVID-19 symptom surveys are designed to help researchers better monitor and forecast the spread of COVID-19. In partnership with the University of Maryland and Carnegie Mellon University, Facebook users are invited to take surveys conducted by these two partner universities to self-report COVID-19-related symptoms. The surveys may be used to generate new insights on how to respond to the crisis, including heat maps of self-reported symptoms. This information may help health systems plan where resources are needed and potentially when, where, and how to reopen parts of the society.

This Facebook survey collects data daily. For this research, we needed some reliable state-level covariates, which can be used in our model. We also decided to take static variables – the variables whose values are not expected to change much over time – from the Facebook survey. We decided to take the responses to the following two questions:

- ‘Have you ever been told by a doctor, nurse, or other health professional that you have any of the following medical conditions?’ This question has the following options: diabetes, cancer (other than skin cancer), heart disease, high blood pressure, asthma, chronic lung disease such as COPD or emphysema, kidney disease, autoimmune disorder such as rheumatoid arthritis or Crohn’s disease and none of the above. We encoded the response to this question as 1 if the respondent answered with any or all of the following ailments – diabetes, asthma and chronic lung disease such as COPD or emphysema, or 0 otherwise.
- ‘Have you had a flu shot in the last 12 months?’ This question has the following options: yes or no. We encoded the response to this question as 1 if the respondent answered yes and 0 otherwise.

We combined all the survey responses for the following 29 days: August 5, 2020, to September 9, 2020. We produce state-wise estimates of proportions of people ‘having at least one of the 3 above-mentioned diseases’ and ‘people who took a flu shot in the last 12 months’. These estimates are simply weighted means of our binary encoded variables with the weights being the survey weights provided. We use these state-wise estimates of proportions as continuous covariates in our model.
Table 1: Direct hesitancy estimates and associated standard error estimates based on the UAS survey.

| State                | Direct Estimate | Standard Error Estimate |
|----------------------|-----------------|-------------------------|
| Alabama              | 0.7184          | 0.0004                  |
| Alaska               | 0.2671          | 0.1867                  |
| Arizona              | 0.6138          | 0.0716                  |
| Arkansas             | 0.8201          | 0.0458                  |
| California           | 0.6295          | 0.0163                  |
| Colorado             | 0.6375          | 0.0740                  |
| Connecticut          | 0.5526          | 0.0884                  |
| Delaware             | 1               | 0                       |
| District of Columbia | 0.4968          | 0.2183                  |
| Florida              | 0.7015          | 0.0352                  |
| Georgia              | 0.7738          | 0.0381                  |
| Hawaii               | 0.4161          | 0.2030                  |
| Idaho                | 0.3927          | 0.1176                  |
| Illinois             | 0.7265          | 0.0455                  |
| Indiana              | 0.7315          | 0.0476                  |
| Iowa                 | 0.5652          | 0.0705                  |
| Kansas               | 0.7768          | 0.0496                  |
| Kentucky             | 0.7738          | 0.0488                  |
| Louisiana            | 0.8272          | 0.0712                  |
| Maine                | 0.7450          | 0.0756                  |
| Maryland             | 0.6710          | 0.0961                  |
| Massachusetts        | 0.5035          | 0.0770                  |
| Michigan             | 0.6847          | 0.0435                  |
| Minnesota            | 0.6675          | 0.0652                  |
| Mississippi          | 0.9078          | 0.0306                  |
| Missouri             | 0.6174          | 0.0572                  |
| Montana              | 0.7615          | 0.0634                  |
| Nebraska             | 0.7851          | 0.0781                  |
| Nevada               | 0.7374          | 0.0847                  |
| New Hampshire        | 0.7651          | 0.1307                  |
| New Jersey           | 0.5491          | 0.0668                  |
| New Mexico           | 0.7602          | 0.0558                  |
| New York             | 0.6696          | 0.0417                  |
| North Carolina       | 0.7844          | 0.0368                  |
| North Dakota         | 0.8311          | 0.0857                  |
| Ohio                 | 0.6584          | 0.0359                  |
| Oklahoma             | 0.5508          | 0.0887                  |
| Oregon               | 0.6210          | 0.0785                  |
| Pennsylvania         | 0.7556          | 0.0301                  |
| Rhode Island         | 0.4737          | 0.3206                  |
| South Carolina       | 0.7213          | 0.0583                  |
| South Dakota         | 0.4395          | 0.1220                  |
| Tennessee            | 0.6049          | 0.0551                  |
| Texas                | 0.6558          | 0.0366                  |
| Utah                 | 0.6382          | 0.0899                  |
| Vermont              | 0.3849          | 0.2036                  |
| Virginia             | 0.6066          | 0.0482                  |
| Washington           | 0.6539          | 0.0530                  |
| West Virginia        | 0.6865          | 0.0640                  |
| Wisconsin            | 0.7413          | 0.0411                  |
| Wyoming              | 0.7950          | 0.1839                  |
3.3.2 Census Bureau’s Population Estimates Program

The Census Bureau’s Population Estimates Program (PEP) produces estimates of the population for the United States, its states, counties, cities, and towns, as well as for the Commonwealth of Puerto Rico and its municipios. Demographic components of population change (births, deaths, and migration) are produced at the national, state, and county levels of geography. Additionally, housing unit estimates are produced for the nation, states, and counties.

PEP annually utilizes current data on births, deaths, and migration to calculate population change since the most recent decennial census and produce time series estimates of population, demographic components of change, and housing units. The annual time series estimates begin with the most recent decennial census data and extend to the vintage year.

We use the PEP data to produce state-wise and demographic cell-wise population counts. The demographic cell we focus here is the following: ‘race x ethnicity x gender x age category’. We have considered 4 levels of race – White, Black, Asian and Others, 2 levels of ethnicity – Hispanic and Non-Hispanic, 2 levels of gender – Male and Female and 7 levels of age category – 18−24, 25−34, 35−44, 45−54, 55−64, 65−74 & 75+.

We use the following PEP data for ‘Annual State Resident Population Estimates for 5 race groups (5 race alone or in combination groups) by age, sex, and Hispanic origin: April 1, 2010, to July 1, 2019’. With the data, we had to do some pre-processing to obtain counts for the specific demographic cells that we just described. This mainly involved grouping the entire data as per our defined demographics and collapsing the counts for each of the demographic cells.

3.3.3 The COVID Tracking project

The website https://covidtracking.com collects, cross-checks and publishes COVID-19 data. These data can be freely downloaded from the website. We use this data source to obtain state-specific (50 states and District of Columbia) covariates (continuous) for our model. We created the following two variables:

• Testing rate: Total number of tests with confirmed outcome – positive or negative – divided by the total test counts in the state. Note that these proportions may exceed the value of 1 since a person might have gotten tested more than one time within a certain time interval.

• Positivity rate: Total positive test outcomes divided by the total tests with confirmatory outcomes (positive or negative).

4 Data analysis and evaluation

We consider several covariates for our analysis. As previously discussed in subsection 3.3.2, we refer to ‘RACE’ by a having 4 levels – White, Black, Asian and Others, ‘ETHNICITY’ by b having 2 levels – Hispanic or Non-Hispanic and ‘GENDER’ by c having 2 levels – Male and Female. For the variable, ‘AGE’ we have divided the whole adult population into 7 cells, e.g., 18 − 24, 25 − 34, ..., 65 − 74 & 75+; denoted by d.
Table 2: A list of competing models

| Model | Race x Ethnicity specific intercept | Gender specific slope of Age (Facebook) | Comorbity Rate (Facebook) | Flu Shot Rate (Facebook) | Test Rate (CovidTrack) | Positivity Rate (CovidTrack) | Percent Republican Survey Weight |
|-------|-------------------------------------|----------------------------------------|---------------------------|--------------------------|------------------------|-----------------------------|-------------------------------|
| M1    | ✓                                   | ✓                                      | ✓                         | ✓                        | ✓                      | ✓                           | ✓                             |
| M2    | ✓                                   | ✓                                      | ✓                         | ✓                        | ✓                      | ✓                           | ✓                             |
| M3    | ✓                                   | ✓                                      | ✓                         | ✓                        | ✓                      | ✓                           | ✓                             |
| M4    | ✓                                   | ✓                                      | ✓                         | ✓                        | ✓                      | ✓                           | ✓                             |

We consider fixed effect intercepts by ‘RACE’ x ‘ETHNICITY’ – so, in total, 8 fixed effect intercepts for all the models we considered. A list of competing models is described in Table 2. Recall that this was referred to as $x_g(1)$ in subsections 2.1 and 2.3.

As for the state level covariates $x_i(2)$ (refer to subsection 2.1 for reference to this notation), we use Facebook survey data (refer to subsection 3.3.1) and data from the COVID tracking project (refer to subsection 3.3.3). Facebook COVID symptom survey data is used to calculate two state-level summary variables – survey-weighted proportions of people having one of three pre-existing conditions or co-morbidity rates and survey-weighted proportions of people who took a flu shot in the last 12 months or Flu-Shot rates (as discussed in subsection 3.3.1). We use logit-transforms of these two rates as the covariates in our models described in Table 2. Other state level covariates we have used came from the COVID Tracking project, e.g., testing rates and positivity rates as defined previously in subsection 3.3.3. Finally, we have also used the state level percentage of republican votes that were cast in the 2020 United States presidential election as a state level covariate in our model.

For the first respondent level covariate $x_{igk}(3)$ (again, we refer to subsection 2.1 for reference to this notation), we used the respondents’ 7 age-levels and converted them into numbers 1, …, 7 and used them as a continuous-scale covariate in all our models. We use gender-specific slopes – one for male and the other for female – for the age covariate in our model. For the second respondent level covariate, we use the survey weights associated with every respondent from the UAS-survey data.

4.1 Model fit

Recall, the approximation we did to the population (here, 50 states and DC) parameter of interest $\bar{Y}$ in subsection 2.2 would only hold when the quantity $(1 - a_{i1} - a_{i2}) \approx 0$. Table 3 summarizes the quantity $(1 - a_{i1} - a_{i2})$ for 50 states and Washington, DC. We can reasonably justify our approximation to the equation 2 in subsection 2.2 since both the maximum value (0.0120) and the 3rd quartile (0.0031) are negligible.

Table 3: Summary statistics of $(1 - a_{i1} - a_{i2})$ for 50 states and DC.

| Min. | 1st.Qu. | Median | Mean | 3rd.Qu. | Max. |
|------|---------|--------|------|---------|------|
| $1 - a_{i1} - a_{i2}$ | 0.0004 | 0.0010 | 0.0016 | 0.0026 | 0.0031 | 0.0120 |

Now we discuss the model fits. To fit the models in Table 2 we used the probabilistic programming language Stan [Carpenter et al.] with the Statistical software R [R Core Team (2020)]. The R-package rstan [Stan Development Team (2020)] provides
the R interface to Stan. We restrict all prior choices to the default Weakly Informative Priors (WIP). This means that all the model parameters at Level 2 of the described hierarchical model in subsection 2.1, i.e., \( \alpha, \beta, \xi_c \) and \( \lambda \), and the model parameter at Level 3, i.e., \( \sigma_v \) were assigned the default WIPs in Stan. We ran each model for 4,000 iterations, and the first 2,000 were discarded as burn-in samples. Thus, all the posterior analyses were based on 2,000 post-warm-up MCMC draws.

### 4.2 Model selection

After fitting all the 4 models, we have used a Model Selection criterion to select one ‘best’ working model. The R-package loo was used for this purpose; see Vehtari et al. (2020). This package allows computations of efficient approximate leave-one-out cross-validation for fitted Bayesian models via rstan Vehtari et al. (2017). From existing posterior simulation draws, loo computes approximate Leave-One-Out Cross-Validation (LOO-CV) using Pareto smoothed importance sampling (PSIS), a relatively new procedure for regularizing importance weights. As a byproduct of the calculations, loo can also obtain approximate standard errors for estimated predictive errors and for comparing predictive errors between two models. We have also used PSIS-LOO-CV instead of WAIC, because PSIS provides useful diagnostics and effective sample size and Monte Carlo standard error estimates; see Vehtari et al. (2017). The following Table 4 provides the LOO-CV comparison results for the 4 models.

|     | elpd_diff | se_diff |
|-----|-----------|---------|
| M3  | 0         | 0       |
| M2  | -1.057    | 0.840   |
| M1  | -1.839    | 1.031   |
| M4  | -2.990    | 2.579   |

The ELPD is the theoretical expected log pointwise predictive density for a new dataset, which can be estimated, e.g., using cross-validation. elpd_loo is the Bayesian Leave-One-Out estimate of the expected log pointwise predictive density. elpd_diff is the difference in elpd_loo for two models. For large enough sample sizes (used to fit the data) this difference is an approximate standard normal distribution. From Table 4 we see that LOO criterion selects the Model 3 as the best model and it is better than the Model 2 as seen by the elpd_diff which is significant at ~68%.

Note that the survey weights enter linearly in the model M3. Following Verret et al. (2015), we wanted to see how M3 would perform when the survey weights are entered in the model non-linearly, keeping everything else unchanged, viz., \( \lambda \ln(w_{igk}) \) and \( \lambda w_{igk}^{-1} \) instead of \( \lambda w_{igk} \). Naturally, to check the performance of these two new competing models, we again employed the LOO-criterion. From Table 5 we observe that neither log-transformed survey weights nor the inverse of the survey weights bring about any improvement to the already existing M3. So, we keep M3 as our best working model and follow-up with subsequent analyses with the Model 3 (M3).

Looking at the posterior analyses from the Model 3, outlined in Table 7, we see that the variable co-morbidity from the Facebook survey seem to be insignificant at 70%. That is why we decided to run another model comparison between our chosen Model
Table 5: loo-cv comparison of Model 3 varying weight functions

|                | elpd_diff | se_diff |
|----------------|-----------|---------|
| M3             | 0         | 0       |
| M3 (ln(w^k))   | -1.402    | 1.503   |
| M3 (w^{-1})    | -3.294    | 2.432   |

Table 6 suggests that LOO criterion selects Model 3 with the co-morbidity variable as the better model and it is better than the Model without it significantly at ~68%. So we decided to leave the variable in our model.

Table 6: loo-cv comparison of Model 3 and Model 3 without the co-morbidity rate from Facebook-CMU-Delphi COVID-19 Trends and Impact Survey

|                | elpd_diff | se_diff |
|----------------|-----------|---------|
| M3             | 0         | 0       |
| M3 (without co-morb from FB) | -0.977    | 0.889   |

4.3 Findings from the selected model

In the last subsection, we decided on one model that best fits our data with the help of LOO criterion using Stan, rstan, and loo. Now we present important findings from the selected ‘best’ working model, Model 3.

Table 7: Posterior summary statistics for the model parameters of Model 3 – the best Model chosen by LOO criterion

|                | mean | se_mean | sd  | 10%  | 15%  | 85%  | 90%  | n_eff | Rhat |
|----------------|------|---------|-----|------|------|------|------|-------|------|
| α₁             | -2.443 | 0.067  | 0.804 | -3.392 | -3.235 | -1.588 | -1.409 | 143.335 | 1.025 |
| α₂             | -1.213 | 0.066  | 0.792 | -2.159 | -1.983 | -0.396 | -0.170 | 143.777 | 1.025 |
| α₃             | -1.035 | 0.066  | 0.795 | -1.989 | -1.825 | -0.192 | 0.003  | 146.529 | 1.025 |
| α₄             | -1.390 | 0.065  | 0.793 | -2.355 | -2.177 | -0.575 | -0.365 | 148.812 | 1.024 |
| α₅             | -1.454 | 0.066  | 0.796 | -2.412 | -2.243 | -0.626 | -0.408 | 143.693 | 1.025 |
| α₆             | -1.975 | 0.065  | 0.807 | -2.991 | -2.788 | -1.118 | -0.925 | 152.647 | 1.024 |
| α₇             | -1.137 | 0.069  | 0.908 | -2.257 | -2.066 | -0.183 | 0.030  | 170.529 | 1.022 |
| α₈             | -1.614 | 0.072  | 1.090 | -2.992 | -2.680 | -0.523 | -0.255 | 230.229 | 1.015 |
| co-morb        | -0.598 | 0.048  | 0.628 | -1.385 | -1.225 | 0.058  | 0.189  | 169.583 | 1.021 |
| surv-wts       | -0.097 | 0.001  | 0.037 | -0.147 | -0.136 | -0.057 | -0.049 | 1,795.149 | 1.000 |
| rep %          | -0.957 | 0.036  | 0.537 | -1.640 | -1.507 | -0.406 | -0.279 | 219.864 | 1.016 |
| ξ₁             | 0.210  | 0.001  | 0.019 | 0.185  | 0.190  | 0.230  | 0.234  | 1,120.665 | 1.002 |
| ξ₂             | 0.119  | 0.001  | 0.020 | 0.093  | 0.098  | 0.140  | 0.144  | 1,022.191 | 1.002 |
| σᵣ             | 0.185  | 0.005  | 0.055 | 0.120  | 0.131  | 0.240  | 0.256  | 103.554 | 1.018 |

Table 7 gives the posterior summary statistics for the selected best model, Model 3. The ‘mean’ column gives the posterior means, ‘se_mean’ column gives the Monte-Carlo
standard errors, the ‘sd’ column gives the posterior standard deviations (standard errors), the next 4 columns give the 4 percentiles, the column $n_{\text{eff}}$ gives the Effective Sample Sizes ($n_{\text{eff}}$) – the number of independent samples that was used to replace the total $n$ dependent MCMC draws having the same estimation power as the $n$ autocorrelated samples (Stan Development Team (2022)) and finally the column ‘Rhat’ gives a measure of chain-equilibrium ($R$) – a value near 1 (but < 1.05) means that the chains have mixed well, and the posterior samples can be used with confidence for the posterior analyses (Stan Development Team (2022)).

We use the posterior estimates to calculate our state-wise parameter of interest $\bar{Y}_i$ for all the 50 states and DC – this essentially gives us the state-wise vaccine hesitancy estimates. These numbers along with their corresponding standard errors are displayed in Table 8. For easy comparison, the direct survey based estimates from Table 1 are also given in the same table.

Next, we compare our HB model-based state-wise estimates with the UAS-survey-weighted state-wise estimates. We plot the point estimates in the same graph. From the Figure 1 we observe that even though state-level UAS estimates for which enough sample are available are reliable, some of them, for which little to no samples were available in the UAS data, are unreasonably low/high due to the low sample sizes. Compared to that, our HB method produced stable estimates even for states with small or no sample. The corresponding 95% credible intervals of the HB estimates are also given in the same plot.

From the Figure 1 we can see how much improvement our HB estimates bring in over the direct UAS-survey based estimates in terms of standard errors of the hesitancy
Figure 2: In x-axis, we have states in increasing order of UAS sample sizes. In y-axis, we have ratios of standard errors of direct UAS-survey based estimates to our HB model estimates. The horizontal dark line intersects the y-axis at 1.

estimates. The largest improvements came for the states that had fewer samples in the UAS survey data. We can still observe smaller standard error estimates even for the states with larger sample sizes.

Clearly, in Table 8 we can see improvements over Table 1 mentioned in subsection 3.2. Delaware does not have an unrealistic estimate of 1 (with an absurd s.e. of 0) anymore and Alaska, DC, etc. – they all have much more believable estimates and smaller values of standard errors.

Table 9 gives a subset of the above table 8 detailing a few important states for which the differences between our HB and direct UAS-survey based estimates are most prominent. We also provide summary statistics of Direct UAS estimates and our HB estimates in Table 10. The summary statistics for standard errors of the Direct UAS estimates and our HB estimates are given in Table 11. From these latter two tables, we observe that our HB method improves over the direct method both in terms of point estimates and and associated standard errors.

5 Concluding remarks

In this paper, we present a new hierarchical Bayesian estimation of finite population proportions for small areas. We make use of an appropriate data linkage technique that combines a primary (probability) survey with multiple relevant data sources, including a big non-probability survey data from social media. In our model for the respondents, we include weights from the primary survey and factors potentially influencing the binary outcome variable of interest in order to reduce informativeness of the sample. The proposed model is used to produce a hierarchical synthetic estimate that is robust to model misspecification errors and thus reducing reliance on the assumed model. Inspirations were drawn from many seminal works in the field. Finally, we demonstrate our method-
Table 8: HB hesitancy estimates and direct UAS design-based estimates along with their standard errors for all the 50 states and Washington D.C.

| State                  | HB_hesitancy | sd   | direct | dir_se |
|------------------------|--------------|------|--------|--------|
| Alabama                | 0.671        | 0.025| 0.718  | 0.060  |
| Alaska                 | 0.608        | 0.016| 0.207  | 0.187  |
| Arizona                | 0.616        | 0.028| 0.614  | 0.072  |
| Arkansas               | 0.686        | 0.029| 0.820  | 0.046  |
| California             | 0.588        | 0.012| 0.629  | 0.016  |
| Colorado               | 0.600        | 0.029| 0.638  | 0.074  |
| Connecticut            | 0.589        | 0.029| 0.553  | 0.088  |
| Delaware               | 0.650        | 0.017| 1      | 0      |
| District of Columbia   | 0.690        | 0.015| 0.497  | 0.219  |
| Florida                | 0.623        | 0.024| 0.701  | 0.035  |
| Georgia                | 0.681        | 0.024| 0.774  | 0.038  |
| Hawaii                 | 0.583        | 0.019| 0.416  | 0.263  |
| Idaho                  | 0.593        | 0.035| 0.393  | 0.118  |
| Illinois               | 0.648        | 0.027| 0.726  | 0.045  |
| Indiana                | 0.668        | 0.027| 0.731  | 0.048  |
| Iowa                   | 0.596        | 0.030| 0.565  | 0.071  |
| Kansas                 | 0.637        | 0.025| 0.777  | 0.050  |
| Kentucky               | 0.658        | 0.029| 0.774  | 0.049  |
| Louisiana              | 0.682        | 0.023| 0.827  | 0.071  |
| Maine                  | 0.589        | 0.038| 0.745  | 0.076  |
| Maryland               | 0.647        | 0.024| 0.671  | 0.096  |
| Massachusetts          | 0.563        | 0.031| 0.504  | 0.077  |
| Michigan               | 0.650        | 0.023| 0.685  | 0.043  |
| Minnesota              | 0.610        | 0.029| 0.667  | 0.065  |
| Mississippi            | 0.711        | 0.026| 0.908  | 0.031  |
| Missouri               | 0.648        | 0.029| 0.617  | 0.057  |
| Montana                | 0.631        | 0.031| 0.762  | 0.063  |
| Nebraska               | 0.626        | 0.028| 0.785  | 0.078  |
| Nevada                 | 0.610        | 0.022| 0.737  | 0.085  |
| New Hampshire          | 0.600        | 0.020| 0.765  | 0.131  |
| New Jersey             | 0.566        | 0.030| 0.549  | 0.067  |
| New Mexico             | 0.633        | 0.023| 0.760  | 0.096  |
| New York               | 0.597        | 0.025| 0.610  | 0.042  |
| North Carolina         | 0.680        | 0.026| 0.784  | 0.037  |
| North Dakota           | 0.621        | 0.032| 0.831  | 0.086  |
| Ohio                   | 0.650        | 0.022| 0.658  | 0.036  |
| Oklahoma               | 0.638        | 0.029| 0.551  | 0.089  |
| Oregon                 | 0.590        | 0.031| 0.621  | 0.079  |
| Pennsylvania           | 0.666        | 0.024| 0.756  | 0.030  |
| Rhode Island           | 0.605        | 0.013| 0.474  | 0.321  |
| South Carolina         | 0.662        | 0.030| 0.721  | 0.058  |
| South Dakota           | 0.591        | 0.034| 0.440  | 0.122  |
| Tennessee              | 0.621        | 0.031| 0.605  | 0.055  |
| Texas                  | 0.636        | 0.024| 0.656  | 0.037  |
| Utah                   | 0.583        | 0.029| 0.638  | 0.090  |
| Vermont                | 0.574        | 0.022| 0.385  | 0.204  |
| Virginia               | 0.608        | 0.027| 0.607  | 0.048  |
| Washington             | 0.592        | 0.029| 0.654  | 0.053  |
| West Virginia          | 0.652        | 0.033| 0.686  | 0.064  |
| Wisconsin              | 0.827        | 0.026| 0.741  | 0.041  |
| Wyoming                | 0.618        | 0.019| 0.795  | 0.184  |
Table 9: HB hesitancy estimates and direct UAS design-based estimates along with their standard errors for a subset of the states (small areas).

| State                  | HB hesitancy | sd   | direct | dir se |
|------------------------|--------------|------|--------|--------|
| Alabama                | 0.671        | 0.025| 0.718  | 0.060  |
| California             | 0.588        | 0.012| 0.629  | 0.016  |
| Delaware               | 0.650        | 0.017| 1      | 0      |
| District of Columbia   | 0.690        | 0.015| 0.497  | 0.219  |
| Florida                | 0.623        | 0.024| 0.701  | 0.035  |
| Georgia                | 0.681        | 0.024| 0.774  | 0.038  |
| Texas                  | 0.636        | 0.024| 0.656  | 0.037  |

Table 10: Summary statistics of direct UAS-survey based estimates of hesitancy and our HB based estimates of hesitancy.

|            | Min. | 1st.Qu. | Median | Mean | 3rd.Qu. | Max. |
|------------|------|---------|--------|------|---------|------|
| direct     | 0.207| 0.606   | 0.671  | 0.661| 0.761   | 1    |
| HB         | 0.563| 0.597   | 0.623  | 0.627| 0.650   | 0.711|

Table 11: Summary statistics of standard errors of direct UAS-survey based estimates of hesitancy and standard errors of our HB based estimates of hesitancy.

|            | Min. | 1st.Qu. | Median | Mean | 3rd.Qu. | Max. |
|------------|------|---------|--------|------|---------|------|
| direct     | 0    | 0.046   | 0.065  | 0.081| 0.089   | 0.321|
| HB         | 0.012| 0.023   | 0.027  | 0.026| 0.029   | 0.038|
ology to produce proportion estimates from a COVID-19 survey, along with utilizing information from various other disparate sources. The methodology developed here is general and can be applied to a variety of similar finite population proportion estimation problems. We are currently investigating an extension of the proposed methodology to deal with categorical variables with more than two categories.

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