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Bayesian Nonparametric Weighted Sampling Inference*

Yajuan Si[†], Natesh S. Pillai[‡] and Andrew Gelman[§]

Abstract

Survey weighting adjusts for known or expected differences between sample and population. Weights are constructed on design or benchmarking variables that are predictors of inclusion probability. In this paper, we assume that the only information we have about the weighting procedure is the values of the weights in the sample. We propose a hierarchical Bayesian approach in which we model the weights of the nonsampled units in the population and simultaneously include them as predictors in a nonparametric Gaussian process regression to yield valid inference for the underlying finite population and capture the uncertainty induced by sampling and the unobserved outcomes. We use simulation studies to evaluate the performance of our procedure and compare it to the classical design-based estimator. We apply our method to the Fragile Family Child Wellbeing Study. Our studies find the Bayesian nonparametric finite population estimator to be more robust than the classical design-based estimator without loss in efficiency.

Key words: survey weighting, poststratification, model-based survey inference, Gaussian process prior, Stan.

1. Introduction

1.1. The problem

Survey weighting adjusts for known or expected differences between sample and population. These differences arise from sampling design, undercoverage, nonresponse, and limited sample size in subpopulations of interest. Weights are constructed on design or benchmarking variables that are predictors of inclusion probability π_i , defined as the probability that unit i will be included in the sample, where inclusion refers to both selection into the sample and response given selection. However, weights have problems. As pointed out by Gelman (2007) and the associated discussions, current approaches for construction and use of weights are not systematic, with much judgment required on which variables to include in weighting, which interactions to consider, and whether and how weights should be trimmed. Our goal here is to develop a unified approach for weighting under the framework of multilevel regression and poststratification. The key challenge is that, in a classical survey weighting setting, the population distribution of the weights is not known, hence the poststratification step must itself be modeled.

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In applied survey research it is common to analyze survey data collected by others in which weights are included, along with instructions such as “This file contains a weight variable that must be used in any analysis” (CBS News/New York Times, 1988) but without complete information on the sampling and weighting process. In classical analysis, externally-supplied weights are typically taken to be inversely proportional to each unit’s probability of inclusion into the sample. Our goal here is to incorporate externally-supplied sampling weights within the Bayesian framework, continuing to make the assumption that these weights represent inverse inclusion probabilities but in a fully model-based framework.

This work has both theoretical and practical motivations. From a theoretical direction, we would like to develop a fully nonparametric version of model-based survey inference. In practice, we would like to get the many benefits of multilevel regression and poststratification (see, e.g., Lax and Phillips 2009a,b) in realistic settings with survey weights. Current Bayesian methods typically ignore survey weights, assume that all weighting information is included in regression adjustment, or make ad hoc adjustments to account for the design effect induced by unequal weights (Ghitza and Gelman, 2013). A fully Bayesian method accounting for survey weights would address a serious existing concern with these methods.

1.2. Background

For one survey response variable of interest, we label the values of unit i in the population as Y_i , for $i = 1, \dots, N$, and in the sample as y_i , for $i = 1, \dots, n$, where N is the population size and n is the sample size. Design-based inference treats Y_i in the population as fixed and the inclusion indicator I_i as random. Model-based survey inference builds models on y_i and uses the model to predict the nonsampled values of Y . Rubin (1983) and Little (1983) point out that the proper model specification of survey outcome should be conditional on the inclusion probabilities, and model formulation within strata defined by the inclusion probabilities is a useful way to avoid misspecification. Assuming the weights are proportional to the inverse of the inclusion probabilities, we use a one to one mapping of the unique values of collected sample weights to formalize the strata. We call the strata as poststratification cells since they are post-constructed by the sample weights. This definition is different from the classical poststratification (also called benchmarking) adjustment, which is an intermediate step during weight construction.

We follow Little (1991, 1993) and develop a unified notation framework for weighting and poststratification of sample surveys. Suppose the units in the population and the sample can be divided into J poststratification cells with population cell size N_j and sample cell size n_j for each cell j , $j = 1, \dots, J$, with $N = \sum_{j=1}^J N_j$ and $n = \sum_{j=1}^J n_j$. For example, in a national political survey, the cells might be a cross-tabulation of 4 age categories, 2 sexes, 4 ethnicity categories, 5 education categories and 50 states, where the resulting number of cells J is $4 \times 2 \times 4 \times 5 \times 50$. The sample sizes n_j ’s can be small or even zero. In the present paper, however, we shall define poststratification cells based on the survey weights in the observed data, where the collected $n_j \geq 1$.

In classical sampling theory, weights are typically defined either as proportional to the inverse probability of inclusion $1/\pi_i$ (Horvitz and Thompson, 1952), or as the benchmarking

ratio $N_{j[i]}/n_{j[i]}$ (Holt and Smith, 1979), where $N_{j[i]}$ and $n_{j[i]}$ are the population size and sample size of benchmarking cell j to which unit i belongs. Inverse-probability weights are determined after the design but before the sampling. Benchmarking weights, however, can be determined only after the data has been collected, when n_j 's are known. When unit nonresponse exists, the probability of inclusion is estimated by combining the probability of selection and the response propensity score (i.e., the probability of response $\Pr(I_i = 1)$). Therefore, the final constructed weights are related to the design variables that affect inclusion and the demographic and other variables that affect response.

As in classical sampling theory, we shall focus on estimating the population mean of a single survey response: $\theta = \bar{Y} = \sum_i Y_i/N$. Let $\theta_j = \bar{Y}_j$ be the population mean within cell j and \bar{y}_j be the sample mean. The overall mean in the population is defined as

$$\theta = \bar{Y} = \sum_j \frac{N_j}{N} \theta_j.$$

Our proposed estimate for θ can be expressed in weighted form

$$\hat{\theta} = \sum_j W_j \hat{\theta}_j,$$

where the cell weights W_j sum to 1. This provides a unified expression for the existing estimation procedures. Classical design-based approaches use the unsmoothed estimates $\hat{\theta}_j = \bar{y}_j$ without any modeling of the survey response, and cell weights W_j 's that depend only on the n_j 's and N_j 's. The population mean estimate is expressed as

$$\hat{\theta}^{\text{design-based}} = \sum_j W_j \bar{y}_j = \sum_i w_i y_i,$$

where $w_i = W_{j[i]}/n_{j[i]}$ is the weight of individual i in cell j . This design-based estimate is unbiased if the cell weights W_j are set as N_j/N , which corresponds to unit weights $w_i \propto N_{j[i]}/n_{j[i]}$. With either the inverse-probability unit weights $w_i \propto 1/\pi_i$ or the benchmarking unit weights $w_i \propto N_{j[i]}/n_{j[i]}$, the classical weighted ratio estimator (Horvitz and Thompson, 1952; Hájek, 1971) is

$$\hat{\theta}^{\text{design}} = \sum_i w_i y_i \Big/ \sum_i w_i. \quad (1)$$

When one corrects for many factors, the unit weights w_i become highly variable, and then the resulting $\hat{\theta}$ becomes unstable. In practice the solution is often to trim the weights or restrict the number of adjustment variables, but then there is a concern that the weighted sample no longer matches the population.

A different approach, which we follow, is to set the cell weights W_j equal to N_j/N and use modeling to obtain the estimates $\hat{\theta}_j$ from the sample means \bar{y}_j and sample sizes n_j , so that

$$\hat{\theta}^{\text{model-based}} = \sum_j \frac{N_j}{N} \hat{\theta}_j.$$

Inside each cell the units weights are equal. Design-based and model-based methods both implicitly assume simple random sampling or equal probability sampling within cells. Thus \bar{y}_j can be a reasonable estimate for θ_j , and when \bar{y}_j is used as an estimate for θ_j in the model-based estimator, it can be shown that this is equivalent to the design-based estimator using benchmarking unit weights $w_i \propto N_{j[i]}/n_{j[i]}$. When cell sizes are small, though, multilevel regression can be used to obtain better estimates of the θ_j 's.

Model-based estimates are subject to bias under misspecified model assumptions. Survey sampling practitioners tend to avoid model specifications and advocate design-based methods. Model-based methods should be able to yield similar results as classical methods when classical methods are reasonable. This means that any model for survey responses should at least include all the information used in weighting-based methods.

In summary, model-based sampling inference is a general approach but can be difficult to implement if the relevant variables are not fully observed in the population. Design-based inference can be appealingly simple but there are concerns about capturing inferential uncertainty, obtaining good estimates in subpopulations and adjusting for large numbers of design factors.

In this paper we develop an approach for fully Bayesian inference using externally-supplied survey weights. In using only the weights, we seek to generalize classical design-based inference, more fully capturing inferential uncertainty and in a more open-ended framework that should allow more structured modeling as desired. For simplicity, we consider a univariate survey response, with the externally-supplied weight being the only other information available about the sample units. Our approach can be generalized to multivariate outcomes and includes additional informative predictors, which will be elaborated in Section 5 for extension work.

If full information is available on design and nonresponse models, this information can be included as predictors in a regression framework, using hierarchical modeling as appropriate to handle discrete predictors (for example, cluster indicators or small geographic areas) to borrow strength in the context of sparse data. However, it is common in real-world survey analysis for the details of sampling and nonresponse to be not supplied to the user, who is given only unit-level weights and perhaps some information on primary sampling units. The methods we develop here are relevant for that situation, in which we would like to enable researchers to perform model-based and design-consistent Bayesian inference using externally-supplied survey weights.

We extend the procedure in Zheng and Little (2003) and Chen et al. (2010), who focus on probability-proportional-to-size selection, in two ways: first, we assume that with unequal probabilities of inclusion the weights are available only for the sample units, which is what happens in practice, and we estimate the distribution of the weights in the population; second, we build a nonparametric Bayesian regression model that is more flexible and computationally efficient than their penalized spline model, which also serves as a special case of our model. Elliott (2007) and Elliott and Little (2000) consider similar splines models in nonparametric regression as well as discretization of weights for weight trimming and smoothing. They all assume the weights are known for the population. Zangeneh and Little (2012) im-

plement Bayesian bootstrapping and subjective screening for estimation of unknown measure sizes when only sample records are available in the probability-proportional-to-size selection scenario, and this is separate from estimation for survey outcome models. We combine the two steps of modeling the distribution of w and regression modeling for $y|w$ using a Gaussian process prior distribution, and we propagate the uncertainties to make inference on the underlying population quantities of interest by a fully Bayesian procedure. We call our procedure Bayesian nonparametric finite population (BNPF) estimation.

We fit the model using the Bayesian inference package Stan (Stan Development Team, 2013a,b), which obtains samples from the posterior distribution using the no-U-turn sampler, a variant of the Hamiltonian Monte Carlo algorithm (Hoffman and Gelman, 2013).

This article is organized as follows. Section 2 describes the model. In Section 3 we investigate the performance of our procedure in simulation studies. Section 4 applies the procedure to an ongoing survey with which we are directly involved. Section 5 concludes with discussion and further extensions.

2. Bayesian model for survey data with externally-supplied weights

Consider a simple survey design using independent sampling with unequal inclusion probabilities for different units. If the covariates that determine the sampling probability are fully observed, the design will be ignorable given this information. As noted in the introduction, we assume we do not have this information but have only the weights, which implicitly contain the information used to account for the nonignorable design effects. This framework is limited (for example, it does not allow one to adjust for cluster sampling) but it is standard in applied survey work, where users are supplied with a publicly released dataset and sampling weights but little or no other design information.

In the collected dataset (which, for mathematical simplicity, we assume is performed with replacement), we observe (w_i, y_i) , for $i = 1, \dots, n$. In our Bayesian hierarchical model below, we simultaneously predict the w_i 's for the $N - n$ nonsampled units and make inference based on the regression model $y_i|w_i$ in the population. We assume the population size N is large enough to ignore the finite population correction factors.

2.1. Model for the weights

Let J denote the number of observed distinct values of the unit weights w_i . We make the assumption that these J unique values are the only possible values of w_i in the population. This assumption is not generally correct (for example, if weights are constructed by multiplying factors for different demographic variables, there may be some empty cells in the sample corresponding to unique products of factors that would appear in the population but not in the sample) but it allows us to proceed without additional knowledge of the process by which the weights were constructed.

In our model, the unique values of the unit weights determine the J poststratification cells for the individuals in the population via a one to one mapping. We do not know the corresponding population cell size N_j 's and so we include them as parameters in the model.

We assume independent sampling for the sample inclusion indicator with probability

$$\Pr(I_i = 1) = \pi_i = c/w_i, \text{ for } i = 1, \dots, N,$$

where c is a positive constant. By definition, $I_i = 1$ for observed samples, i.e., $i = 1, 2, \dots, n$. This implies the following model for sample cell counts n_j :

$$n_j \sim \text{Poisson}(cN_j/w_{(j)}), \text{ for } j = 1, \dots, J,$$

where $w_{(j)}$ is the value of the weight corresponding to cell j , and with $w_{(j)} = w_{j[i]}$ for units i belonging to cell j . We can think of the quantity $n_0 = c \sum_j N_j/w_{(j)}$ as the expected sample size; thus,

$$n_j \sim \text{Poisson} \left(n_0 \frac{N_j/w_{(j)}}{\sum_j N_j/w_{(j)}} \right).$$

This is equivalent to assuming $n \sim \text{Poisson}(c \sum_j N_j/w_{(j)})$, and conditional on n ,

$$\vec{n} = (n_1, \dots, n_J) \sim \text{Multinomial} \left(n; \frac{N_1/w_{(1)}}{\sum_j N_j/w_{(j)}}, \dots, \frac{N_J/w_{(J)}}{\sum_j N_j/w_{(j)}} \right).$$

Our modeling assumption states that in cell j there are N_j units, each with weight $w_{(j)}$, in the population, and we have observed n_j of them. For each cell j , we need to predict the survey outcome for the nonsampled $N_j - n_j$ units with weight $w_{(j)}$. Here c and N_j 's are unknown parameters. Since we assume there are only J unique values of weights in the population, by inferring N_j , we are implicitly predicting the weights for all the nonsampled units.

By definition, $\sum_j n_j = n$. Thus if N_j 's are large,

$$n = \sum_j E(n_j) \approx c \sum_j N_j/w_{(j)}.$$

To simplify our modeling, we define c implicitly using the above equation: for each posterior simulation of $(N_j, w_{(j)})$, for $j = 1, \dots, J$, we set c equal to $\frac{n}{\sum_j N_j/w_{(j)}}$.

2.2. Nonparametric regression model for $y|w$

Let $x_{j[i]} = \log w_{j[i]}$. For a continuous survey response y , we work with the default model,

$$y_i \sim N(\mu(x_{j[i]}), \sigma^2),$$

where $\mu(x_{j[i]})$ is a mean function of $x_{j[i]}$ that we model nonparametrically. We work with the logarithm of survey weight because such weights are typically constructed multiplicatively (as the product of inverse selection probabilities, benchmarking ratio factors, and inverse propensity scores), so that changes in the weights correspond to differences on the log scale.

We can re-express the model using the means and standard deviations of the response within cells as

$$\bar{y}_j \sim N(\mu(x_{j[i]}), \sigma^2/n_j) \text{ and } \sum_{j=1}^J s_j^2/\sigma^2 \sim \chi_{n-1}^2,$$

where the poststratification cell mean $\bar{y}_j = \sum_{i \in \text{cell}_j} y_i/n_j$, cell total variance $s_j^2 = \sum_{i \in \text{cell}_j} (y_i - \bar{y}_j)^2$, and χ_{n-1}^2 is the Chi-square distribution with $n - 1$ degrees of freedom, for $j = 1, \dots, J$. Alternatively, we can allow the error variance to vary by cell:

$$\bar{y}_j \sim N(\mu(x_{j[i]}), \sigma_j^2/n_j) \text{ and } s_j^2/\sigma_j^2 \sim \chi_{n_j-1}^2.$$

If the data y are binary-valued, we denote the sample total in each cell j as $y_{(j)} = \sum_{i \in \text{cell}_j} y_i$ and assume

$$y_{(j)} \sim \text{Binomial}(n_j, \theta_j).$$

Here, $\theta_j = E(y_i) = \Pr(y_i = 1)$ for units i within cell j , thus assuming independent sampling within cell j with the same probability θ_j . We assume

$$\text{logit}(\theta_j) = \mu(x_{j[i]})$$

as the mean function of the logarithm of survey weight and construct hierarchical models as will be described.

Penalized splines have been used to construct nonparametric random slope models in survey inference (Chen et al., 2010; Elliott, 2007; Zheng and Little, 2003; Elliott and Little, 2000). However, in our experience, highly variable weights bring in difficulties for the selection and fitting of spline models.

We avoid parametric assumptions or specific functional forms for the mean function and instead use a Gaussian process (GP) prior on $\mu(x_{j[i]})$. GPs models constitute a flexible class of nonparametric models that avoid the need to explicitly specify basis functions (Rasmussen and Williams, 2006). The class of GPs has a large support on the space of smooth functions and thus has attractive theoretical properties such as optimal posterior convergence rates for function estimation problems (van der Vaart and van Zanten, 2008). They are also computationally attractive because of their conjugacy properties. GPs are further closely related to basis expansion methods. In particular, if one chooses Gaussian priors for the coefficients on the basis functions, then one actually obtains an induced GP prior for μ with a mean and covariance function that depends on the hyperparameters in the Gaussian prior as well as the choice of basis. Rasmussen and Williams (2006) show that GPs include as special cases various well-known models, including Bayesian linear models, spline models, large neural networks (under suitable conditions), and are closely related to others, such as support vector machines. In this regard, our model supersedes those spline models that were earlier used in research on survey analysis.

We assume

$$\mu(x_j) \sim \text{GP}(x_j\beta, C(\kappa, \tau, \delta)),$$

where we have set the mean function equal to a linear regression, $x_j\beta$, with β denoting an unknown coefficient and x_j the logarithm of the unit weights in cell j . Here $C(\kappa, \tau, \delta)$ denotes the covariance function, for which we use an exponential kernel: for any $x_j, x_{j'}$,

$$\text{Cov}(\mu(x_j), \mu(x_{j'})) = \tau^2(1 - \delta)e^{-\kappa|x_j - x_{j'}|} + \tau^2 \delta \mathbf{I}_{j=j'}, \quad (2)$$

where τ , δ , and κ are unknown hyperparameters with positive values. The decay parameter κ (defined as the inverse of the range parameter) controls the local smoothness of the sample paths of $\mu(x)$. Smoother sample paths imply more borrowing of information from neighboring w values. The nugget term $\tau^2\delta$ accounts for unexplained variability between cells. As special cases, with $\delta = 0$ this reduces to the common GP covariance kernel with τ^2 as partial sill and κ as decay parameter but without the nugget term; with $\delta = 1$ this is a penalized Bayesian hierarchical model with independent prior distributions $N(x_j\beta, \tau^2)$ for each $\mu(x_j)$ with regularization. The vector $\vec{\mu} = (\mu(x_1), \dots, \mu(x_J))$ has a J -variate Gaussian distribution

$$\vec{\mu} \sim N(\vec{x}\beta, \Sigma),$$

where $\vec{x} = (x_1, \dots, x_J)$ and $\Sigma_{jj'} = \text{Cov}(\mu(x_j), \mu(x_{j'}))$ as given by (2).

2.3. Posterior inference for finite population

Let \vec{y} be the data vector. The parameters of interest are $\phi = (\sigma, \beta, \kappa, \tau, \delta, c, \vec{N})$, where \vec{N} is the vector of cell sizes (N_1, \dots, N_J) . The likelihood function for the collected data is

$$p(\vec{y}|\phi, w) \propto p(\vec{y}|\mu, \vec{n}, \sigma^2)p(\mu|w, \beta, \kappa, \tau, \delta)p(\vec{n}|w, c, \vec{N}).$$

The joint posterior distribution is

$$p(\phi|\vec{y}, w, N) \propto p(\vec{y}|\mu, \vec{n}, \sigma^2)p(\mu|w, \beta, \kappa, \tau, \delta)p(\vec{n}|w, c, \vec{N})p(\phi).$$

We assume the following prior distribution:

$$\begin{aligned} \beta &\sim N(0, 2.5) \\ \sigma^2 &\sim \text{Inverse Gamma}(1, 0.5) \\ \tau &\sim \text{Half-Cauchy}^+(0, 5) \\ \kappa &\sim \text{Gamma}(0.5, 0.5) \\ \delta &\sim U[0, 1] \\ \pi(N_j) &\propto 1, \text{ for } j = 1, \dots, J. \end{aligned} \quad (3)$$

Here $\text{Half-Cauchy}^+(a, b)$ denotes a Cauchy distribution with mean a and scale b restricted to positive realizations. The half-Cauchy prior distribution for the variance scale parameter τ allows for values close to 0 and heavy tails (Gelman, 2006; Polson and Scott, 2012). We are using uniform prior distributions on the allocation probability δ (between 0 and 1) and on the population poststratification cell sizes N_j 's (with nonnegative values). The population

estimator will be normalized by the summation of the N_j 's, and all are averaged over their posterior distribution (as computed using simulations).

Our objective is to make inference for the underlying population. For a continuous outcome variable, the population mean is defined as

$$\bar{Y} = \frac{\sum_{j=1}^J \bar{Y}_j N_j}{\sum_{j=1}^J N_j} = \frac{1}{\sum_{j=1}^J N_j} \sum_{j=1}^J (\bar{y}_j n_j + \bar{y}_{\text{exc},j} (N_j - n_j)),$$

where $\bar{y}_{\text{exc},j}$ is the mean for nonsampled units in cell j , for $j = 1, \dots, J$. The posterior predictive distribution for $\bar{y}_{\text{exc},j}$ is

$$\bar{y}_{\text{exc},j} | \mu, w_{(j)}, \sigma^2 \sim N(\mu(x_j), \sigma^2 / (N_j - n_j)).$$

Here we assume the population size N and the cell sizes N_j 's are large enough so that $\bar{y}_{\text{exc},j}$ is well approximated by $\mu(x_j)$.

For a binary outcome, we are interested in the proportion of Yes responses in the population:

$$\bar{Y} = \frac{\sum_j Y_{(j)}}{\sum_{j=1}^J N_j} = \frac{1}{\sum_{j=1}^J N_j} \sum_j \left(y_{(j)} + \sum_{i=1}^{N_j - n_j} y_i \right) = \frac{1}{\sum_{j=1}^J N_j} \sum_j (y_{(j)} + y_{\text{exc},(j)}),$$

where $y_{\text{exc},(j)}$ is the total of the binary outcome variable for nonsampled units in cell j , with posterior predictive distribution

$$y_{\text{exc},(j)} | N_j, \theta_j, n_j \sim \text{Binomial}(N_j - n_j, \theta_j).$$

As before, for finite-population inference we approximate $y_{\text{exc},(j)}$ by $(N_j - n_j)\theta_j$.

We compare our BNFP estimator with the classical estimator $\hat{\theta}^{\text{design}}$ in (1), which in theory is design-unbiased (but which in practice can be compromised by the necessary choices involved in constructing classical weights that correct for enough factors without being too variable). We use the design-based variance estimator under sampling with replacement approximation in the R package `survey` (Lumley, 2010), and the standard deviation is specified as

$$\text{sd}^{\text{design}} = \frac{1}{n} \sqrt{\sum_{i=1}^n w_i^2 (y_i - \hat{\theta}^{\text{design}})^2},$$

where the weights w_i have been renormalized to have an average value of 1.

3. Simulation studies

We investigate the statistical properties of our method. First we apply a method proposed by Cook et al. (2006) for checking the statistical procedure and the software used for model fitting. Next we implement a repeated sampling study given the population data to check coverage rates and calibration of our Bayesian procedure.

3.1. Computational coherence check

If we draw parameters from their prior distributions and simulate data from the sampling distribution given the drawn parameters, and then perform the Bayesian inference correctly, the resulting posterior inferences will be correct on average. For example, 95%, 80%, and 50% posterior intervals should contain the true parameter values with probability 0.95, 0.80, and 0.50. We will investigate the three nominal coverage rates of population quantities and hyperparameters and check whether they follow a uniform distribution by simulation.

Following Cook et al. (2006), we repeatedly draw hyperparameters from the prior distributions, simulate population data conditional on the hyperparameters, sample data from the population, and then conduct the posterior inference. We choose $N = 1,000,000$ and $n = 1,000$. For illustrative purposes, suppose there are J^0 poststratification cells and the unit weights $w_{(j)}^0$ are assigned values from 1 to J^0 with equal probabilities. We set $N_j = N/J^0$ for $j = 1, \dots, J^0$. In our computational check we set $J^0 = 10$, a small number of population poststratification cells, to ensure the sampled units will occupy all the population cells, thus avoiding biases caused by unselected cells. Our goal in this simulation is to assess the correctness of our computation. In later simulation studies, we will investigate the performance in the scenario where several population poststratification cells are not occupied by the samples and ignored in the inference.

As mentioned earlier, since the sample size n is fixed, for each iteration the parameter c can be obtained by

$$c = \frac{n}{\sum_{j=1}^J \frac{N_j}{w_{(j)}}} \frac{\sum_{j=1}^J N_j}{N}.$$

The multiplicative factor $\frac{\sum_{j=1}^J N_j}{N}$ appears above because the N_j 's are unnormalized in our parametrization.

After sampling the parameters $(\beta^0, \sigma^0, \tau^0, \kappa^0, \delta^0)$ from their prior distributions described in Section 2, we generate realizations of the mean function $\mu(x_j)$ from a Gaussian distribution with mean vector $x_j \beta^0$ and covariance kernel with parameters $(\tau^0, \delta^0, \kappa^0)$. Then we generate the population data. When the survey responses are continuous, we generate N_j independent synthetic $Y_{j[i]}^0$'s from the normal distribution with mean $\mu(x_j)$ and standard deviation σ^0 . For binary outcomes, we treat the generated $\mu(x_j)$ as logit θ_j and then obtain the probability θ_j in the binomial distribution, for $j = 1, \dots, J^0$. For each cell j , we generate N_j independent binary outcome variables $Y_{j[i]}^0$'s, for $i = 1, \dots, N_j$, with $\Pr(Y_{j[i]}^0 = 1) = \theta_j$. These N_j instances of $w_{(j)}^0$ and the corresponding $Y_{j[i]}^0$'s comprise the population data, denoted as (w_i^0, Y_i^0) , for $i = 1, \dots, N$.

After generating the population data, we draw n samples from the population with probability proportional to $1/w_i^0$ with replacement, for $i = 1, \dots, N$. For the selected units, $i = 1, \dots, n$, we count the unique values of w_i 's defining the poststratification cells and the corresponding number of units in each cell, denoted as $w_{(j)}$ and n_j , for $j = 1, \dots, J$, where J is the number of unique values for w_i 's, i.e., the number of cells. We collect the survey respondents, y_i , for $i = 1, \dots, n_j$, for each cell j .

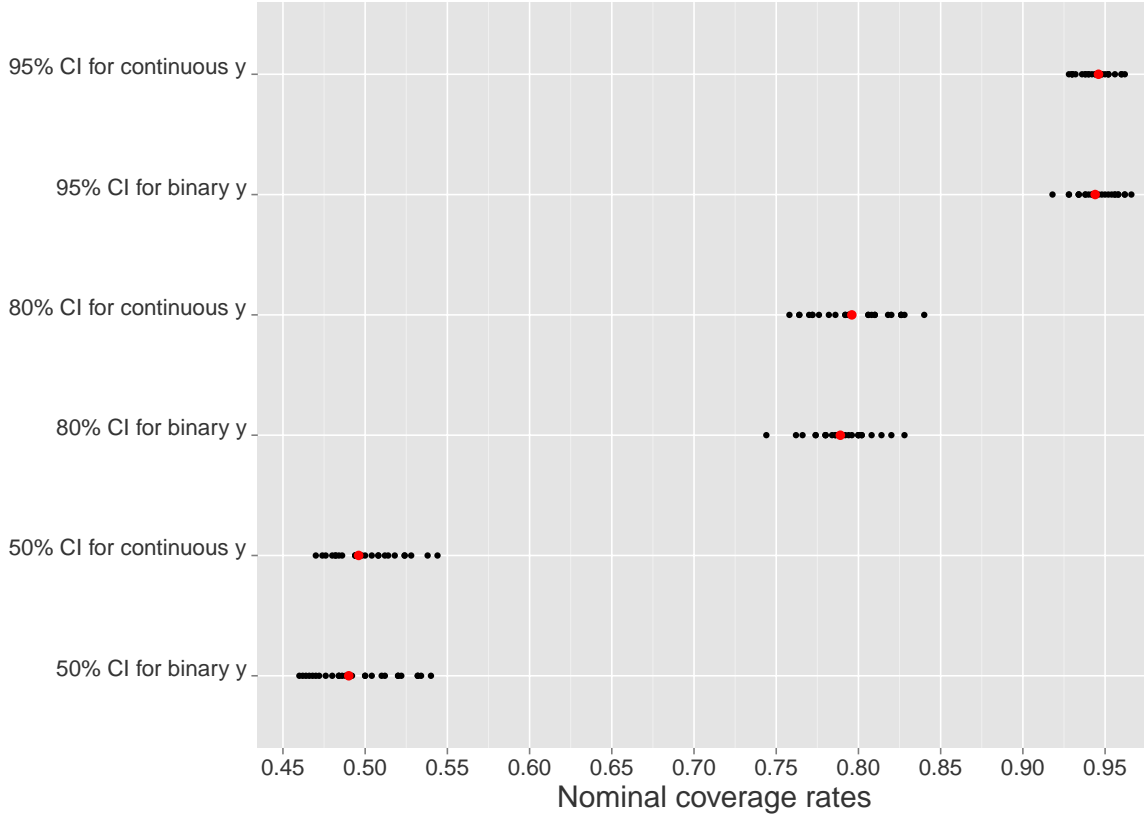


Figure 1: *From the computational coherence check for the simulated-data example, nominal coverage rates of central 95%, 80%, and 50% posterior intervals for the population quantities and hyperparameters in the models for continuous and binary survey responses, correspondingly. The red dots represent the median values.*

We use Stan for the posterior computation. For continuous outcome, we keep the permuted 3,000 draws from 3 separate MCMC chains after 3,000 warm-up draws for each chain. In Stan, each chain takes less than a second on a standard laptop after compiling. For binary outcomes, we keep 6,000 draws from 3 separate MCMC chains after 6,000 warm-up draws for each chain. Each chain takes around 2 seconds after compiling. Even though the sample size is large, we need only to invert a $J \times J$ matrix for the likelihood computations for the GP. This matrix inversion is the computational bottleneck in our method.

First, we monitor the convergence of our MCMC algorithm based on one data sample. The convergence measure we use is \hat{R} based on split chains (Gelman et al., 2013, Section 11.4), which when close to 1 demonstrates that chains are well mixed. The collected posterior draws for our simulations have large enough effective sample sizes n_{eff} for the parameters, which is estimated conservatively by Stan using both cross-chain and within-chain estimates.

The corresponding trace plots also show good mixing behaviors. The posterior mean values are close to the true values. The posterior summaries for the parameters do not change significantly for different initial values of the underlying MCMC algorithm.

After checking convergence, we implement the process repeatedly 500 times to examine the coverage rates. We compute central 95%, 80%, and 50% intervals using the appropriate quantiles of the posterior simulations. The nominal coverage rates of the 95%, 80%, and 50% posterior intervals, shown in Figure 1, are close to their expected values for both the continuous and binary survey responses.

We also find the posterior inference for parameters to be robust under different prior distributions for the hyperparameters, such as the half-normal or gamma distribution for the scale τ or a heavy-tailed prior distribution for β .

3.2. Simulated data from a regression model

In the previous section, we generated a separate population and sample corresponding to each repetition. In this section we fix a finite population generated from a model described below. Then we check the frequentist coverage rates of our Bayesian procedure for the population mean, using repeated samples from this underlying finite population.

For constructing the finite population, we use external data sources to generate the population cell sizes and weights; this allows for cell counts and weights with values close to what is seen in practice. To this end, we borrow a cross tabulation distribution from the 2013 New York City Longitudinal Survey of Well-being (LSW) conducted by the Columbia Population Research Center. The population in this case is that of New York City, defined by the public crosstab tables from the 2011 American Community Survey (ACS). We use the following benchmarking variables: age (3 categories), ethnicity (3 categories), and education (4 categories). The cross tabulation constructs $J^0 = 3 \times 3 \times 4 = 36$ cell weights w^0 . The unit weights are obtained by the benchmarking ratio factors $N_j^{\text{ACS}}/n_j^{\text{LSW}}$'s, where N_j^{ACS} 's are the collected ACS (treated as population) cell counts and n_j^{LSW} 's are the LSW sample cell sizes. The ratio of the largest to the smallest weight is 17.5.

Next we construct our finite population. We set $N = 1,000,000$ and generate N_j 's from a multinomial distribution with probability proportional to N_j^{ACS} , for $j = 1, \dots, J^0$. For binary outcomes, we simulate from the following model:

$$\text{logit Pr}(Y_i^0 = 1) \sim N(-4 + 4x_i^0, 10).$$

For continuous outcomes, we use the model

$$Y_i^0 \sim N(-4 + 4x_i^0, 10),$$

where $x_i^0 = \log w_i^0$. This constitutes our finite population which is fixed for the rest of the simulations. We perform 100 independent simulations, for each repetition drawing 100 samples from the finite population constructed above with units sampled with probabilities proportional to $1/w_i^0$. The prior distributions for the parameters in our model are as listed in (3). Across the 100 repetitions, the mode of selected poststratification cells is 28; the

Data	Estimator	Avg. S.E.	Bias	RMSE	Coverage ₉₅
Continuous	BNFP	0.910	-0.185	0.987	93%
	classical	1.109	0.007	1.054	96%
Binary	BNFP	0.049	0.002	0.048	92%
	classical	0.052	0.006	0.049	92%

Table 1: *For simulated data from a regression model, comparison between the Bayesian nonparametric finite population (BNFP) and classical design-based estimators on the average value of standard error, empirical bias, RMSE and nominal coverage rates of 95% intervals. We present some of these results to more significant figures than we would usually do in practice so as to clarify the comparisons between the different approaches.*

maximum is 34 and the minimum is 21. As noted above, this is a result of the incompleteness of our model, which treats the observed weights as the only possible cells in the population.

For each repetition, we also calculate the values of the classical design-based estimator with its standard error. Table 1 shows the comparison: BNFP has a smaller actual root mean squared error (RMSE) and a smaller estimated standard error than the classical estimate. Even though its posterior intervals are narrower than the confidence intervals of the classical design-based estimator, the Bayesian nonparametric estimator has competitive nominal coverage rates. BNFP has smaller empirical bias for binary outcome and slightly larger bias for continuous outcome than the classical estimate. When we look at the absolute bias, BNFP always generates smaller values than the classical estimate (0.80 vs. 0.89 for the continuous outcome and 0.036 vs. 0.037 for the binary outcome), which indicates that BNFP is more robust. We obtain the same comparison conclusions when we increase the sample size to 2000. When the sample size is large, the variance of the classical estimate will be reduced to be close to but still larger than that of BNFP. When no empty cells occur, BNFP yields good estimates and coverage rates (close to truth) for the population cell sizes N_j 's and cell means μ_j 's.

4. Application to Fragile Families Child Wellbeing Study

The Fragile Families Child Wellbeing Study (Reichmann et al., 2001) follows a cohort of nearly 5,000 children born in the U.S. between 1998 and 2000 and includes an oversample of nonmarital births. The study addresses the conditions and capabilities of unmarried parents, especially fathers, and the welfare of their children. The Core Study consists of interviews with both mothers and fathers at the child's birth and again when children are ages one, three, five, and nine. The sampling design is multistage (sequentially sampling cities, hospitals, and births) and complex, involving stratified sampling, cluster sampling, probability-proportional-to-size sampling, and random selection with pre-determined quota. There are two main kinds of unit weights: national weights and city weights. Applying the national weights (Carlson, 2008) makes the data from the 16 randomly selected cities representative of births occurring in large cities in the U. S. between 1998 and 2000. The city

weights make the records selected inside each city representative of births occurring in this city between 1998 and 2000 and adjust for selection bias, nonresponse rates, benchmarking on mother’s marital status, age, ethnicity, and education information.

For our example here, we work with the city weights and a binary survey response of whether mother received income from public assistance or welfare or food stamp services. We perform two analyses, one for the baseline survey and one for the Year 9 follow-up survey. At baseline, the sample has $n = 297$ births and $J = 161$ poststratification cells corresponding to the unique values of the weights. Most of the nonempty cells in the sample are occupied by only one or two cases. In Year 9, the sample contained $n = 193$ births, corresponding to $J = 178$ unique values for the weights, with each cell containing 1 or 2 units. We implement the BNFP procedure using its default settings (as described in Section 2) by Stan, running four parallel MCMC chains with 10,000 iterations, which we found sufficient for mixing of the chains.

We assess the fit of the model to data using posterior predictive checks (Gelman et al., 1996). We generate replicated data y^{rep} from their posterior predictive distributions given the model and the data and calculate the one sided posterior predictive p -values, $\Pr(T(y^{rep}) \geq T(y)|y, \phi)$, where $T(y)$ is the test statistic and ϕ represents model parameters. A p -value close to 0 indicates a lack of fit in the direction of $T(y)$. Here we use the sample total $y_{(j)}$ in cells j as the test statistics $T(y)$, following a general recommendation to check the fit of aspects of a model that are of applied interest, and we obtain $y_{(j)}^{rep,l}$ based on posterior samples of parameter ϕ^l , for $l = 1, \dots, L$. The posterior predictive p -value is computed as $\frac{1}{L} \sum_{l=1}^L I(y_{(j)}^{rep,l} \geq y_{(j)})$, for each cell $j = 1, \dots, J$. At baseline, among the obtained 161 posterior predictive p -values, the minimum is 0.70. In Year 9, the 178 posterior predictive p -values are all above 0.51. Most p -values are around 0.75, which does not provide significant evidence against the model, indicating the fitting performs well.

At baseline, the BNFP procedure yields a posterior mean for \hat{p} of 0.19 with standard error 0.0240 and 95% posterior interval (0.15, 0.24). The BNFP estimator is larger than the design-based estimator of 0.16, which has a similar standard error of 0.0243. In Year 9, the BNFP posterior mean for \hat{p} is 0.43 with standard error 0.032 and 95% posterior interval (0.37, 0.49). The BNFP estimator is larger than the design-based estimator of 0.32, which has a larger standard error of 0.044. Comparing to the baseline survey when the child was born, the estimates of the proportion of mothers receiving public support services increase when the child was Year 9. This is expected since child care in fragile families needs more social support.

The posterior summaries for the hyperparameters are shown in Table 2. The posterior mean of the scale τ is larger in the follow-up sample than in the baseline, which illustrates larger variability for the cell mean probabilities. As seen from Figure 2, the poststratification cell mean probabilities depend on the unit weights in cells in an irregular structure. Since most sample cell sizes are 1, we see a general increasing pattern between the poststratification cell size proportions $N_{pj}(= N_j / \sum N_j)$ and the unit weights in cell j , for $j = 1, \dots, J$. The uncertainty is large due to the small sample cell sizes. These conclusions hold for both the baseline and the follow-up survey. In the follow-up survey, the correlation between the cell

Data	Parameter	Mean	Median	SD	2.5%	97.5%
Baseline	\hat{p}	0.19	0.19	0.02	0.15	0.24
	β	-0.37	-0.35	0.20	-0.80	0.00
	τ	1.67	1.50	0.76	0.76	3.64
	κ	1.00	0.66	1.10	0.03	4.00
	δ	0.38	0.36	0.22	0.03	0.84
Year 9	\hat{p}	0.43	0.43	0.03	0.37	0.49
	β	-0.30	-0.27	0.44	-1.32	0.60
	τ	3.66	2.85	2.78	1.31	11.83
	κ	0.87	0.58	0.85	0.04	3.10
	δ	0.33	0.32	0.20	0.03	0.75

Table 2: *For the Fragile Families Study, Bayesian nonparametric finite-population (BNFP) inferences for model parameters for responses to the public support question.*

mean probabilities is stronger and more variable compared to those in the baseline survey.

5. Discussion

We have demonstrated a nonparametric Bayesian estimation for population inference for the problem in which inverse-probability sampling weights on the observed units represent all the information that is known about the design. Our approach proceeds by estimating the weights for the nonsampled units in the population and simultaneously modeling the survey outcome given the weights as predictors using a robust Gaussian process regression model. This novel procedure captures uncertainty in the sampling as well as in the unobserved outcomes. We implement the model in Stan, a flexible Bayesian inference environment that can allow the model to be easily expanded to include additional predictors and levels of modeling, as well as alternative link functions and error distributions. In simulation studies, our fully Bayesian approach performs well compared to classical design-based inference. Partial pooling across small cells allows the Bayesian estimator to be more efficient in terms of smaller variance, smaller RMSE, and better nominal coverage rates.

Our problem framework is clean in the sense of using only externally-supplied survey weights, thus representing an open-ended framework for model-based inference that starts from the same point as the fundamental classical model of inverse-probability weighting. There are many interesting avenues for development. When the variables used to construct the weights are themselves available, they can be included in the model (Gelman, 2007). A natural next step is to model interactions among these variables. Multilevel regression and poststratification have achieved success for subpopulation estimations at much finer levels. More design information or covariates can be incorporated. Another direction to explore is to extend our framework when we have only partial census information, for example, certain margins and interactions but not the full cross-tabulations. Our approach can be used to make inference on the unknown census information, such as the population poststratifica-

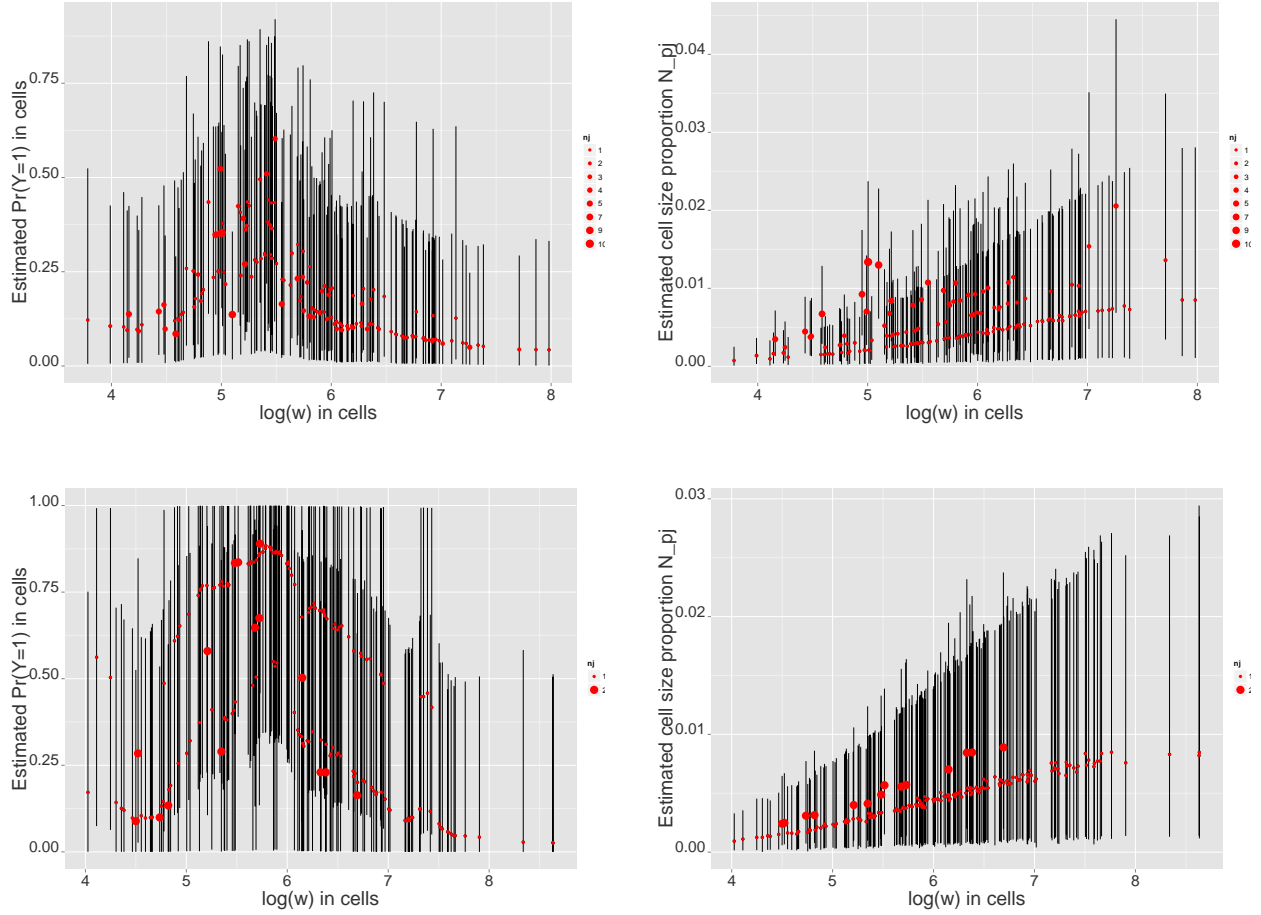


Figure 2: *Estimated Fragile Families survey population poststratification cell mean probabilities θ_j and cell size proportions N_{pj} for unit weights in different cells. Dot sizes are proportional to sample cell sizes n_j 's; the top two plots are for the baseline survey and the bottom two are for the follow-up survey.*

tion or benchmarking cell sizes N_j 's. This also facilitates small area estimation under a hierarchical modeling framework.

Two concerns remain about our method. First, the inferential procedure assumes that all unique values of the weights have been observed. If it is deemed likely that there are some large weights in the population that have not occurred in the sample, this will need to be accounted for in the model, either as a distribution for unobserved weight values, or by directly modeling the factors that go into the construction of the weights. Under an appropriate hierarchical modeling framework, we can partially pool the data and make inference on the empty cells, borrowing information from observed nonempty cells. Second, in difficult problems (those with a few observations with very large weights), our inference will necessarily be sensitive to the smoothing done at the high end, in particular the parametric forms

of the model for the N_j 's and the regression of $y|w$. This is the Bayesian counterpart to the instability of classical inferences when weights are highly variable. In practical settings in which there are a few observations with very large weights, these typically arise by multiplying several moderately-large factors. It should be possible to regain stability of estimation by directly modeling the factors that go into the weights with main effects and partially pooling the interactions; such a procedure should outperform simple inverse-probability weighting by virtue of using additional information not present in the survey weights alone. But that is a subject for future research. In the present paper we have presented a full Bayesian nonparametric inference using only the externally-supplied survey weights, with the understanding that inference can be improved by including additional information.

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