Bayesian Analysis of Cluster Sampling

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December 9, 2016

Introduction

One basic goal of survey analysis is making inferences about the finite population from which the sample was drawn, such as means and totals for particular outcomes of interest. We consider the analysis of a survey with a two-stage cluster sampling design, where the first stage involves probability proportional to size (PPS) sampling.

Unlike other areas of statistics, inference in survey sampling is often design-based, meaning it is based on the randomization distribution of whether a unit is included in the sample instead of directly modeling the survey outcomes themselves (Little, 2004). However, a Bayesian approach to survey inference has many advantages over the design-based approach, including the ability to handle complex design features like clustering, better inference for small-sample problems like small area estimation, incorporation of prior information, and large-sample efficiency (Little, 2004).

Bayesian inference of sample surveys considers both the survey inclusion indicators I and the outcomes Y to be random.

However, in many (arguably most) practical situations, the set of design variables X for the entire population are known only to the survey designer, while the analyst has design variables only for the sampled clusters or units. The analyst must therefore model the nonsampled values of X before she can make use of the posterior predictive distributions above for inference about $Q(Y)$. In the case of two-stage PPS cluster sampling, this translates to modeling the measures of sizes M_j for the nonsampled clusters.

Existing Bayesian approaches to this problem (Zangeneh et al., 2011; Zangeneh and Little, 2015) only consider the case of single-stage PPS samples. They also separate estimation of the missing cluster sizes and inference for the finite population quantities into two steps. In contrast, we consider a two-stage PPS sample and integrate the estimation and inference steps into a single model.

Model

Consider a survey outcome y, a known covariate x, and an inclusion indicator I. Let M denote design variables that are known only for sampled units and unknown for nonsampled units. Let θ, ψ, and ϕ denote the parameters for the distributions of y, M, and I, respectively. The complete-data likelihood is then

$$p(y, M, I|x, \theta, \phi) = p(y|x, M, I, \theta)p(M|I, \psi)p(I|\phi).$$

Here we follow the formulation of Zangeneh and Little (2015) in modeling the distribution of the design variables M given the inclusion indicator I instead of the more conventional factorization

$$p(M, I|\xi, \eta) = p(I|M, \xi)p(M|\eta).$$

The difficulty with this formulation is that, in the absence of information on M for nonsampled cases, [something bad happens].

In this paper, we consider the case where the design information M corresponds to cluster sizes in a two-stage PPS design. Specifically, we have a population of J clusters, each of size N_j and a total population of size $N = \sum_j N_j$.

The observed data likelihood then becomes

$$p(y^{obs}, M^{obs}, I|x, \theta, \phi) = \int p(y^{obs}, y^{mis}|x, M, I, \theta)p(M^{obs}, M^{mis}|I, \psi)p(I, \phi)dM^{mis}dy^{mis}$$

We consider two models for the cluster sizes. First, we treat the cluster sizes as discrete random variables coming from a negative binomial distribution: $N_j \sim NegBin(k, p)$. We

also consider a continuous model for the cluster sizes: $N_j \sim LogNormal(\mu, \sigma^2)$.

We consider a population consisting of $J = 1000$ clusters with measure of size M_j ranging from 100 to 1000 under a data generating model given by

$$
\begin{aligned}
Y_i &\sim N(\beta_{0j[i]} + \beta_{1j[i]} w_i, \sigma_y^2) \\
\beta_{0j} &\sim N(\gamma_0 + \gamma_1 \log(M_j), \sigma_{\beta_0}^2) \\
\beta_{1j} &\sim N(\alpha_0 + \alpha_1 \log(M_j), \sigma_{\beta_1}^2),
\end{aligned}
$$

where Y_i is the outcome of interest for unit i, $j[i]$ denotes the cluster j to which unit i belongs, and w_i is a unit-level covariate.[1] A sample of $K < J$ clusters is taken with probability proportional to M_j, and n units are sampled via simple random sampling in each selected cluster. We assume that we know M_j for the K sampled clusters, w_i for every sampled unit and $\overline{w}_j$ for every cluster, and the total measure of size $M = \sum_{j=1}^{J} M_j$. We assume we do not know M_j for nonsampled clusters.

Computational coherence check

To ensure our simulation code is working as expected, we follow the approach of Cook et al. (2006) and conduct a computational coherence check. We repeatedly draw the hyperparameters $\gamma_0, \gamma_1, \alpha_0, \alpha_1, \sigma_y, \sigma_{\beta_0}$, and σ_{β_1} from their priors, simulate population data with the model above, and then fit the model to the full population data (without sampling) using Stan (Stan Development Team, 2015). If our computational procedure is correct, we should be able to recover the true values of the parameters and see approximately 50% of the 50% posterior intervals and 95% of the 95% posterior intervals contain the true parameter values.

In figure 1, we see that the coverage of the 50% and 95% posterior intervals is close to the nominal levels for all the parameters. The point estimates also recover the true values, as seen in figure 2. Here we plot histograms of the posterior means of the hyperparameters

[1] We can write the population mean $\overline{Y}$ in terms of the cluster-level means $\overline{Y}_j$. When Y_i is normally distributed, we can make inferences for $\overline{Y}_j$ based on $\overline{w}_j$, so in this case it's not necessary to know w_i for each unit in the population. In practice, if w is a demographic covariate, it's often the case that we know demographic characteristics of clusters even if we don't know the overall size.

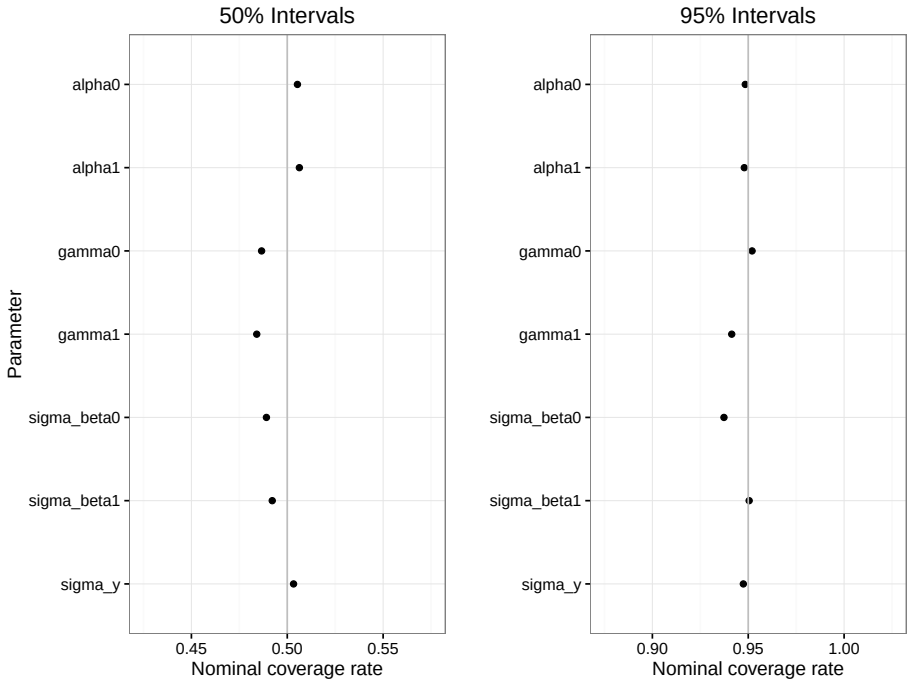

Figure 1: Coverage rates from computational coherence check. Each dot represents the coverage rate of a parameter based on 500 populations generated from repeated draws of the hyperparameters from their prior distributions. The left panel shows coverage rates for 50% posterior intervals and the right panel for 95% posterior intervals.

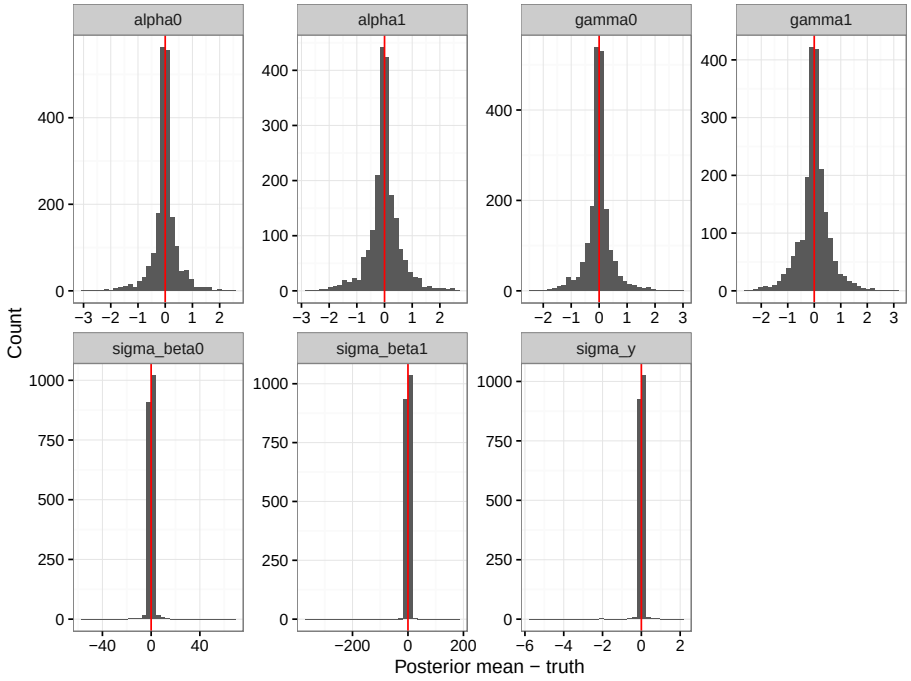

Figure 2: Histograms of posterior means for the hyperparameters across 500 simulations. Because the true hyperparameter values vary across simulations, we plot the difference between the posterior mean and the true value.

across 500 simulations. Because the true values vary across simulations, we plot the differences between the posterior means and the truth; values closer to zero thus indicate more accurate estimates. The parameters in the top row are all drawn from $N(0, 1)$ prior distributions, so the shape of the histograms makes sense. The variance parameters in the bottom row are drawn from Half-Cauchy$(0, 2.5)$ prior distributions, so the occasional extreme outliers we observe are to be expected. Recovering the true parameter values with expected confidence coverage rates indicates that our computational procedure is working as expected.

Bayesian bootstrap

One method for predicting unobserved cluster sizes is the modified Bayesian bootstrap of Zangeneh and Little (2015), based on earlier work by Little and Zheng (2007). Let $w_1, \ldots, w_B$ represent the B unique values of the measures of size M_j observed in a sample of K clusters out of a population of J clusters. Let $n_1, \ldots, n_B$ represent the corresponding counts of these unique sizes, so that $\sum_b n_b = K$. We can then model the counts $n = (n_1, \ldots, n_B)$ as multinomially distributed with parameters $\psi = (\psi_1, \ldots, \psi_B)$. The ψ's are given a noninformative Haldane prior, so $p(\psi_1, \ldots, \psi_B) = Dir(0, \ldots, 0)$. The posterior distribution is then

$$p(\psi_1, \ldots, \psi_B | n_1, \ldots, n_B) = Dir(n_1, \ldots, n_B),$$

and the counts of the unique sizes for the $J - K$ nonsampled clusters, $n^* = (n_1^*, \ldots, n_B^*)$, can be drawn from the posterior predictive distribution

$$\begin{aligned} p(n^*|n) &= \int p(n^*|\psi) p(\psi|n) d\psi \\ &= \int \text{Multin}(n^*|J - K, \psi) \text{Dir}(\psi|n) d\psi. \end{aligned}$$

Directly drawing from this distribution, however, would not account for the PPS sampling design. To adjust for this, Little and Zheng (2007) draw values of ψ from their posterior

$\text{Dir}(\psi|n)$ and then replace ψ_b with

$$\psi_b^* = \frac{c\psi_b(1-\pi_b)}{\pi_b},$$

where

$$\pi_b = \frac{KM_b}{M}$$

is the selection probability for units with measure of size M_b and c is a constant ensuring that $\sum_{b=1}^{B} \psi_b = 1$. This approach essentially adjusts the probability of resampling an observed size M_b by the odds of a cluster of that size not being sampled, so smaller sizes are upweighted relative to larger ones. However, this approach restricts the draws for the nonsampled cluster sizes to come from the set of observed cluster sizes.

Figure 3 shows density plots of the estimated finite population mean $\overline{Y}$ across 2,000 simulations. Because true value of $\overline{Y}$ varies across simulations, we again plot the difference between the estimated value and the truth, and the panels are for scenarios where we sample 20, 50, and 100 units per sampled cluster. As we would hope, the densities are sharply peaked around zero. The coverage rates for the 50% and 95% posterior intervals shown in Table are close to nominal rates, with 50% intervals slightly more conservative than the 95% ones.

Units per cluster	50% interval	95% interval
20	0.61	0.93
50	0.65	0.97
100	0.66	0.98

Table 1: Coverage rates of 50% and 95% posterior intervals for the finite population mean, calculated across 2,000 simulations.

Negative binomial

An alternative to the Bayesian bootstrap is to take a superpopulation approach to estimating the nonsampled cluster sizes. Because the clusters are sampled PPS, we know that the sizes we observe in the sample are biased toward the larger sizes in the population. G. P. Patil (1978) consider a random variable X with pdf $f(x)$ and a probability $w(x)$ of

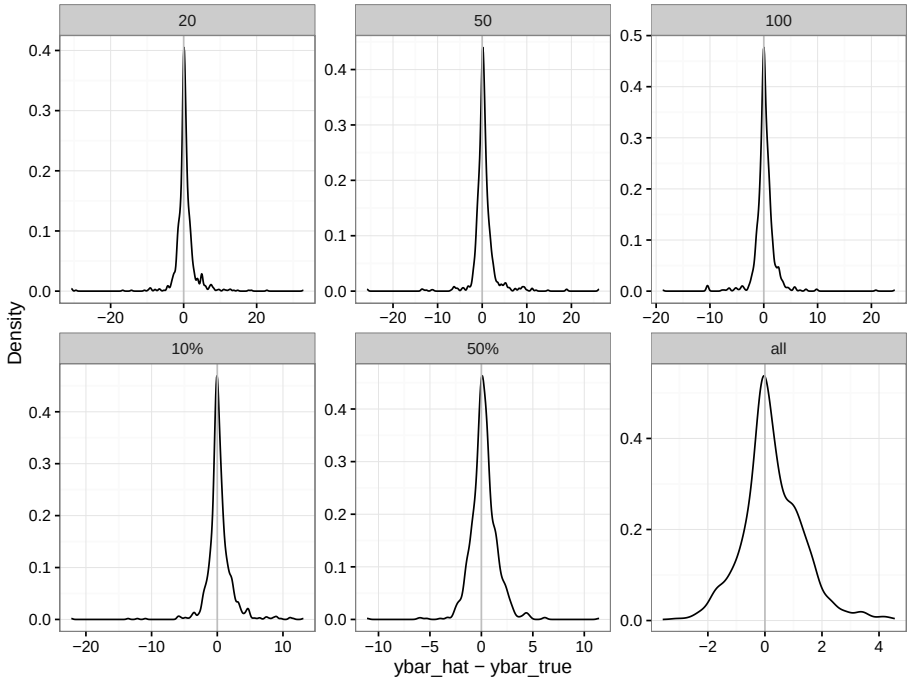

Figure 3: Density plots of the estimated finite population mean across 2,000 simulations. Because true value of $\overline{Y}$ varies across simulations, we again plot the difference between the estimated value and the truth. The panels are for scenarios where we sample 20, 50, and 100 units per sampled cluster.

recording the observation $X = x$ and give the density of X^w, the recorded observation, as

$$f^w(x) = \frac{w(x)f(x)}{\omega},$$

where ω is the normalizing constant. They define the case where $w(x) = x$ as the size-biased distribution. We can see how this distribution is derived in the case of PPS sampling, where the probability of sampling a cluster of size M_j is cM_j, where c is a normalizing constant. The probability of a cluster of size M_j occurring in the superpopulation is $f(M_j)$, so the overall probability of observing a cluster of size M_j in the PPS sample is proportional to $M_j f(M_j)$ and equal to

$$\frac{M_j f(M_j)}{\sum_{M'} M' f(M')},$$

where in this case the denominator is just the expected value of M'.

One reasonable superpopulation distribution for cluster sizes is the negative bino-

mial distribution, a count model that allows for overdispersion. If the superpopulation distribution is $NB(k, p)$ so that

$$Pr(X = x|k, p) = \binom{k + x - 1}{x}(1 - p)^x p^k,$$

then the size-biased distribution of X^w works out to $p(X^w) \sim 1+NB(k+1, p)$ (G. P. Patil, 1978).

The advantage of this approach is that it allows for cluster sizes not observed in the sample to be estimated for the nonsampled units.

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