Smoothed model-assisted small area estimation of proportions

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Abstract: In countries where population census data are limited, generating accurate subnational estimates of health and demographic indicators is challenging. Existing model-based geostatistical methods leverage covariate information and spatial smoothing to reduce the variability of estimates but often ignore the survey design, while traditional small area estimation approaches may not incorporate both unit-level covariate information and spatial smoothing in a design consistent way. We propose a smoothed model-assisted estimator that accounts for survey design and leverages both unit-level covariates and spatial smoothing. Under certain regularity assumptions, this estimator is both design consistent and model consistent. We compare it with existing design-based and model-based estimators using real and simulated data.

1. INTRODUCTION

Subnational estimates of health and demographic indicators such as immunization coverage are critical for policy decisions and assessing inequality between regions. When census data are unavailable, household surveys can provide information at the national level, but may not be designed to produce reliable subnational estimates, especially when estimating the prevalence of rare events. Estimates are often desired for “small areas,” regions, or subpopulations for which sample sizes are limited. This problem, called small area estimation (SAE), is well studied in the survey statistics literature; Pfeffermann (2013) and Rao & Molina (2015) review recent advances and Wakefield, Okonek & Pedersen (2020) consider SAE for mapping disease prevalence. SAE
methods have been used to map a wide variety of outcomes including poverty indicators (Bell, Basel & Maples, 2016; Marhuenda et al., 2017; Corral et al., 2021), health outcomes (Congdon & Lloyd, 2010), and crop production estimates (Erciulescu, Franco & Lahiri, 2021).

When response data are limited, “direct” weighted estimators, which rely solely upon a particular area’s response data to estimate a mean or total for that area, can be unreliable. “Indirect” modelling methods can produce more precise estimators by incorporating covariate information or smoothing across areas using random effects. Small area models can be divided into two general categories: area-level models and unit-level models. Area-level methods model area-specific quantities such as survey-weighted area means, while unit-level methods can model individual responses when microdata are available.

Area-level models smooth the direct weighted estimators and the resulting model-based estimators inherit favourable design properties. Since only aggregate quantities are modelled, fewer distributional assumptions about response data are needed. Unit-level models incorporate higher resolution covariate information and can directly model binary responses or count data. For many low- and middle-income countries (LMIC), geostatistical unit-level models with satellite-observed covariates (such as nighttime light emissions) and spatial random effects are popular for mapping outcomes such as disease prevalence (Diggle & Giorgi, 2016), vaccination rates (Utazi et al., 2020), and neonatal and child mortality (Golding et al., 2017).

When using unit-level models, neglecting to acknowledge the survey design can lead to biased or poorly calibrated estimators. There are two potentially intertwined issues: informative sampling and clustering. Under informative sampling, when the sample response is correlated with the inclusion probability even after conditioning on model covariates, unit-level model-based estimators may be biased unless the estimation procedure is adjusted to account for this dependence (Pfeffermann & Sverchkov, 2007; Parker, Janicki & Holan, 2020). Similarly, when cluster sampling is used, failing to account for within-cluster correlation may result in improperly calibrated interval estimates.

To address these difficulties, we propose a two-stage smoothed model-assisted estimator that draws from both area-level and unit-level methods. Our approach incorporates unit-level covariate information and spatial smoothing by first using a working unit-level model to generate model-assisted estimates, which we smooth using a spatial area-level model. Our method can be viewed as a bridge between SAE approaches and the geostatistical models commonly used in global health research. We adopt a fully Bayesian approach to estimation and inference, showing how Bayesian methods and software commonly used in geostatistics and global health research can be adapted to SAE.

The remainder of this article details our proposed method and draws connections between our approach and existing methods. In Section 2, we introduce our motivating example of estimating the spatial distribution of measles vaccination rates in Nigeria based on Demographic and Health Surveys (DHS) Program data. In Section 3, we describe and review existing SAE methods. In Section 4, we outline our smoothed model-assisted estimator. We compare our estimator with existing methods by simulation in Section 5 and by application to the estimation of measles vaccination rates in Section 6. We discuss our method and suggest future areas of research in Section 7.

2. MOTIVATION

We introduce our motivating example, which is estimation of measles vaccination coverage for subnational areas in Nigeria using data from the DHS program, as previously described by Fuglstad, Li & Wakefield (2021). The challenges encountered in this setting are characteristic of other estimation problems involving health and demographic indicators in LMIC, based on household surveys.

In many LMIC, the DHS program conducts regular surveys to collect data on demographic and health variables, including vaccination coverage. The DHS program generally uses a
stratified two-stage cluster sampling design. Countries are divided into principal administrative divisions, usually called Admin-1 regions. These Admin-1 regions are further divided into urban and rural divisions, and sampling is stratified by groups defined by crossing Admin-1 region with urban/rural status. Each stratum is further divided into collections of households called enumeration areas (EAs) or clusters. In each stratum, a specified number of EAs is sampled with probability proportional to the number of households in the EA. Finally, the households in each selected EA are re-enumerated, and a specified number of households is sampled from each. Final inclusion probabilities and sampling weights are calculated for each household. Cluster and strata membership labels are published for each sampled household, but the sizes of the EAs are not available.

Our goal is to generate estimates of subnational vaccine coverage rates for the first dose of measles-containing vaccine (MCV1) among children aged 12–23 months in Nigeria using data from the 2018 Nigeria DHS (You and Zhou, 2019). The 2018 DHS collected data on vaccination status for children in sampled households based on vaccination cards or caregiver recall. We desire estimates at the Admin-1 level, which in Nigeria comprises 36 states and the Federal Capital Territory of Abuja, as defined using the Database of Global Administrative Areas (GADM) boundaries (https://gadm.org/download_country_v3.html). The sampling frame used for the 2018 DHS was based on a national census conducted in 2006, which divided Nigeria into 664,999 EAs and 74 strata. Data were successfully collected in 1389 EAs; a number of clusters were dropped because of security issues during the household listing operation. As a result, as noted in Appendix A.3 of the Nigeria DHS Final Report, estimates for the Admin-1 area of Borno may not be representative of the omitted EAs. Geographic coordinates are available for almost all EAs, but locations have been displaced by small distances to maintain privacy. Figure 1 provides a map of the Admin-1 boundaries and displaced EA locations in Nigeria for which data are available.

Although DHS data are often adequate for computing reliable direct estimators of national rates, sufficient data may not be available at subregional levels to give estimates with sufficient precision. Model-based approaches can generate estimates with reduced variability. However, the multistage stratified cluster design used by the DHS program complicates estimation. Urban EAs are oversampled relative to rural EAs, and in Nigeria, urban areas show higher rates of vaccination than rural areas (Dong & Wakefield, 2021). As such, model-based approaches may need to account for this systematic difference as well as the potential effects of informative sampling and clustering.

3. EXISTING APPROACHES

3.1. Notation

We focus on estimation of area-specific proportions. Let $U = \{1, \ldots, N\}$ denote a set of indices for a finite population of size $N$. We assume $U$ is partitioned into $m$ disjoint administrative areas, $U = U_1 \cup \cdots \cup U_m$, with $U_i$ being the set of $N_i$ indices corresponding to units in area $i$. We use $y_{ij}$ to denote the value of a variable of interest for unit $j$ in area $i$. In our vaccination coverage example, $y_{ij} \in \{0, 1\}$ are binary variables, with a value of 1 indicating vaccination. Our targets of estimation are the area-specific vaccination coverage rates $p_i$:

$$p_i = \frac{1}{N_i} \sum_{j \in U_i} y_{ij}. \quad (1)$$

We use $S = \{j_1, \ldots, j_n\} \subset U$ to denote a random set of $n$ sampled indices, letting $S = S_1 \cup \cdots \cup S_m$ be the corresponding partition by administrative area. We assume a probability sampling scheme, where $S$ is random, and for all $i$ and $j \in U_i$, we let $\pi_{ij}$ be the inclusion
Figure 1: Map of Nigeria with Admin-1 level boundaries. Points indicate enumeration area locations for which data on measles vaccination are available.

probability of unit \( j \) in area \( i \). Finally, we let \( w_{ij} = 1/\pi_{ij} \) denote the sampling weight or inverse inclusion probability for unit \( j \) in area \( i \).

3.2. Area-Level Model-Based Estimation

The direct Hájek estimator (Hájek, 1971) extends the Horvitz–Thompson estimator (Horvitz & Thompson, 1952), using sampling weights to approximate the totals in Equation (1):

\[
\hat{p}_i^H = \frac{\sum_{j \in S_i} w_{ij} y_{ij}}{\sum_{j \in S_i} w_{ij}}. \tag{2}
\]

For many sequences of designs and populations, \( \hat{p}_i^H \) is a design-consistent estimator of \( p_i \) (for a discussion of design consistency, see the Appendix). The standard Fay–Herriot model combines a sampling model for the direct estimators with a linking model for the true finite population means \( p_i \) (Fay & Herriot, 1979). We can specify the combined model as follows:

\[
\hat{p}_i^H = p_i + \epsilon_i \quad \text{and} \quad \sum_{i} \epsilon_i = 0 \quad \text{and} \quad \sum_{i} \frac{\epsilon_i}{p_i} = 0.
\]

\[\epsilon_i \sim N(0, \sigma^2).
\]
where for \( i = 1, \ldots, m \), \( u_i \overset{\text{i.i.d.}}{\sim} \mathcal{N}(0, \sigma^2_u) \) are independently and identically distributed (i.i.d.) area-specific random effects that are also independent of sampling errors \( \epsilon_i \sim \mathcal{N}(0, V_i) \). We let \( V \) denote the design variance of \( \hat{p}^H_i \), which is assumed known. In practice, \( V \) is estimated. Finally, \( x_i \) represents a vector of area-specific covariates, and \( \beta \) denotes the corresponding vector of coefficients. This model assumes \( p_i \) is normally distributed, but in our case, \( p_i \in [0, 1] \), so it may be necessary to transform \( \hat{p}^H_i \), for example, via the logit (Dong and Wakefield, 2021). Given large sample sizes, the Fay–Herriot model has been used to smooth \( \hat{p}^H_i \) directly if it is not close to 0 or 1, and \( V \) is small (Bell, Basel & Maples, 2016).

This basic area-level model can be used to generate model-based estimates either by taking a frequentist approach and computing the empirical best linear unbiased predictor (EBLUP), or by using a Bayesian approach to produce the posterior distribution of \( p_i \). Assuming design consistency of the direct estimator and a sequence of designs and populations such that \( V \rightarrow 0 \), the EBLUP is also a design-consistent estimator of \( p_i \) (Section 6.1, Rao & Molina, 2015). The basic area-level model has been extended to spatial and spatiotemporal correlation structures (Ghosh et al., 1998; Petrucci & Salvati, 2006; Pratesi & Salvati, 2008). Chung & Datta (2020) found that a spatial model can improve estimation when there is spatial structure in the direct estimators not explained by observed covariates. Porter et al. (2014) extended the Fay–Herriot model to include functional covariates based on readily available sources such as satellite imagery.

### 3.3. Unit-Level Model-Based Estimation

When microdata are available, unit-level models can improve upon area-level models (Hidiroglou & You, 2016). For continuous responses, the nested error regression model, also called the basic unit-level model, was proposed by Battese, Harter & Fuller (1988):

\[
y_{ij} = x_{ij}^T \beta + u_i + \epsilon_{ij}.
\]  
(5)

In the above, \( x_{ij} \) denotes covariate values for individual units \( j \), and \( \beta \) denotes the corresponding coefficients. The area-level random effects are denoted \( u_i \overset{\text{i.i.d.}}{\sim} \mathcal{N}(0, \sigma^2_u) \) representing an area-level random effect. Finally, \( \epsilon_{ij} \overset{\text{i.i.d.}}{\sim} \mathcal{N}(0, \sigma^2_\epsilon) \) represent random and independent errors. For multistage designs, unit-level models could also include random effects for each stage of sampling, as suggested by Marhuenda et al. (2017). Area-level predictions can be generated by aggregating unit-level predictions. For a binary response, a binomial unit-level model can be specified:

\[
y_{ij} | x_{ij}, \beta, u_i \sim \text{Binomial}(1, q_{ij}),
\]
(6)

\[
\text{logit}(q_{ij}) = x_{ij}^T \beta + u_i,
\]
(7)

where \( q_{ij} \) denotes an individual-level risk parameter. Aggregation is more difficult in the binary case, as covariate information is needed for all units in the population.

Estimators based on basic area-level models are often design-consistent, but unit-level models do not generally produce design-consistent estimators. Parker, Janicki & Holan (2020) provide a comprehensive overview of existing strategies used to account for informative sampling when using unit-level models. Pseudolikelihood methods, as described by Binder (1983) and Skinner (1989), incorporate survey weights into estimation of linear and generalized linear models, as reviewed by Lumley & Scott (2017). This approach has been extended to estimation for both linear mixed models (Pfeffermann et al., 1998) and generalized linear mixed models.
(Asparouhov, 2006; Rabe-Hesketh & Skrondal, 2006) with multiple levels of random effects for multistage sampling designs. Separate weights may be needed to account for cluster-level effects and unit-level effects. As noted by Slud (2020), under informative multistage sampling, mixed model parameters may be nonidentifiable if only final single inclusion weights are available, as is the case for the DHS data. In addition, using unscaled weights can lead to bias in variance parameter estimation (Korn & Graubard, 2003; Asparouhov, 2006). Alternatives include estimation via pairwise likelihood using pairwise inclusion probabilities (Rao, Verret & Hidiroglou, 2013; Yi, Rao & Li, 2016) or direct modelling of survey weights (Pfeffermann & Sverchkov, 2007). These methods acknowledge the design, but are sensitive to scaling of weights or require availability of higher order or pairwise weights.

Unit-level models such as those in Equation (5) have been extended to account for spatial variation. Chandra, Salvati & Chambers (2007) use a nested error regression model with spatial area effects, and Chandra et al. (2012) use a geographically weighted regression approach, but the resulting estimators do not use survey weights, and the effect of informative sampling is unclear. Huang (2019) outlines an approach using pairwise likelihood to estimate spatial correlation parameters for a cluster-level model.

Global health researchers have recently turned to unit-level modelling using satellite-derived covariate information and latent spatial Gaussian processes for mapping health indicators. Typically, the sampling design is assumed to be ignorable with respect to the models used. Outcomes are often assumed to vary smoothly in space, enabling researchers to produce maps at resolutions as fine as 1 km by 1 km (Diggle & Giorgi, 2019; Utazi et al., 2020). Although the continuous spatial modelling approach enables prediction at any location, interpretation is complicated: the surface is assumed to exist even at locations where no individual is present.

Unit-level models can adjust for clustering using cluster random effects or alternative likelihoods that account for overdispersion; however, it is not obvious how to aggregate cluster effects to generate predictions. Furthermore, such models may not explicitly account for urban/rural stratification when using DHS data. Paige et al. (2022) and Dong & Wakefield (2021) show that urbanicity can be associated with health outcomes, leading to bias if the stratification is not incorporated into the model. An additional complication results from changing levels of urbanization over time. In many LMIC, increasing urbanization means that covariates commonly used as surrogates for urbanicity, such as the intensity of nighttime light, may not align with the original partition used to define strata.

4. SMOOTHED MODEL-ASSISTED ESTIMATION

Below, we describe a small area estimator that accounts for survey design while incorporating unit-level covariate information and smoothing via random effects. In essence, our two-stage smoothed model-assisted method uses an area-level model to smooth estimates obtained via a unit-level model-assisted approach. We first use a working model with unit-level covariates to calculate a generalized regression estimator and then use a linking model to induce smoothing on the model-assisted estimators. As long as the model-assisted estimators are design-consistent and their design variances converge to zero, our smoothed model-assisted estimators will also be design-consistent. We thus provide an alternative to existing SAE methods, which only require the final inclusion weights. Our proposed model incorporates unit-level covariates and spatial random effects while also explicitly accounting for the sampling design.

4.1. Stage 1: Model-Assisted Estimation

While the unit-level models described in Section 3 may produce biased estimators under model misspecification, model-assisted estimators are motivated by working superpopulation models but are specified to ensure design consistency and unbiasedness even when the working model
is incorrect. For a review of model-assisted methods, see Särndal, Swensson & Wretman (2003) or Breidt & Opsomer (2017). A common model-assisted approach is the difference estimator

$$\hat{\beta}_i^{\text{DIFF}} = \frac{1}{N_i} \left\{ \sum_{j \in U_i} \hat{y}_{ij} + \sum_{j \in S_i} w_{ij}(y_{ij} - \hat{y}_{ij}) \right\},$$

(8)

where $\hat{y}_{ij}$ represents the working model prediction for unit $j$ in area $i$. The difference estimator for area $i$ combines model-based predictions from the working model with a direct estimator of the mean of the residuals in the area. Breidt & Opsomer (2017) showed that under certain regularity conditions, the difference estimator is design-consistent. In particular, they assumed design consistency of the direct estimator of the residual mean in addition to assuming the asymptotic equivalence between predictions from the working model estimated from sample data and those of predictions similarly estimated from the full population. The popular generalized regression (GREG) estimator can be framed as an example of a difference estimator using a working linear regression model to generate predictions (Särndal, Swensson & Wretman, 2003). In the case of binary response data, Lehtonen & Veijanen (1998) proposed the use of a working logistic regression model to compute a logistic generalized regression (LGREG) estimator. Kennel & Valliant (2010) extended the LGREG for use with cluster samples, and Myrskylä (2007) compared the LGREG and GREG with binary responses, finding that when the model fit is strong, the LGREG is preferable.

For the first stage of our smoothed model-assisted approach for estimating small area proportions, we compute a model-assisted estimator using a working logistic regression model of the form

$$P(y_{ij} = 1|x_{ij}, \beta) = q_{ij}$$

(9)

$$\text{logit}(q_{ij}) = x_{ij}^T \beta.$$  

(10)

Since we use a single working model for all areas, our approach resembles the “modified GREG” estimator described by Rao & Molina (2015), also referred to as the survey regression estimator. We estimate model parameters by solving survey-weighted estimating equations, as implemented in the \texttt{svyglm} function from the R package \texttt{survey}. This parameter estimation strategy is an example of the pseudolikelihood approach. We then generate working predictions $\hat{y}_{ij} = \text{expit}(x_{ij}^T \hat{\beta})$ for all $i$ and $j \in U_i$, where $\text{expit}(x) = (1 + e^{-x})^{-1}$ is the inverse of the logit function.

Based on these working predictions, we construct the model-assisted estimator

$$\hat{p}_i^{\text{MA}} = \frac{1}{\hat{N}_i} \left( \sum_{j \in U_i} \hat{y}_{ij} + \sum_{j \in S_i} w_{ij}(y_{ij} - \hat{y}_{ij}) \right),$$

(11)

where $\hat{N}_i = \sum_{j \in S_i} w_{ij}$, yielding a Hájek-like estimator. Under certain regularity conditions, this estimator is design-consistent; for further details see the Appendix.

Model-assisted estimators are typically asymptotically design-unbiased and design-consistent, but quantification of uncertainty can be difficult. Linearization-based variance approximations generally do not account for uncertainty resulting from model estimation manifest in the first sum on the right of Equation (8) (Myrskylä, 2007). The working model should be carefully selected because overfitting can also result in underestimation of uncertainty. For our model-assisted
estimator, we estimate variance by modifying the with-replacement variance estimator of a total as described by Kennel & Valliant (2010) for use with a mean:

\[ \hat{V}(\hat{p}_{i}^{\text{MA}}) = \frac{1}{N_i^2 (n_i - 1)} \sum_{j \in S_i} (w_{ij} e_{ij} - \hat{e}_i)^2, \]  

(12)

where

\[ \hat{e}_i = \frac{1}{n_i} \sum_{j \in S_i} w_{ij} e_{ij}, \]  

(13)

\( n_i \) denotes sample size for area \( i \), and \( e_{ij} = \hat{y}_{ij} - y_{ij} \). This estimator is designed for unclustered sampling designs; when applying our approach to DHS data, we adapt Kennel and Valliant’s cluster sampling variance estimator. Note that this variance estimator ignores variability due to the estimation of \( \hat{N}_i \) and the regression parameters. In practice, variance estimation may be improved via resampling methods such as the bootstrap.

4.2. Stage 2: Spatial Logistic Area Level Model

After computing the model-assisted estimators and their associated variance estimators, we use a Fay–Herriot model to smooth across areas. Since our targets of estimation \( p_i \) are bounded between 0 and 1, we incorporate a logit transformation into both the sampling and linking models. In essence, we apply a spatial area-level model to logit-transformed model-assisted estimators. Our linking and sampling models can be specified as follows:

\[ \text{logit}(p_i) = x_i^\top \beta + u_i, \]  

(14)

\[ \text{logit}(\hat{p}_{i}^{\text{MA}}) = \text{logit}(p_i) + \epsilon_i, \]  

(15)

where for \( i = 1, \ldots, m \), \( x_i = (1, x_{i1}, \ldots, x_{ip})^\top \) represents a length \( p + 1 \) vector of area-specific covariates, and \( \beta = (\beta_0, \beta_1, \ldots, \beta_p)^\top \) denotes the vector containing the intercept and corresponding fixed effect coefficients. We use \( u = (u_1, \ldots, u_m)^\top \) to denote random area-level effects, which we assume to be spatially correlated and drawn from a multivariate Gaussian distribution, \( u \sim \mathcal{N}(0, \Sigma(\sigma_u^2, \phi)) \). Here, \( \sigma_u \) and \( \phi \) denote parameters controlling the spatial correlation matrix \( \Sigma \) as specified in Equation (21). Finally, we use \( \epsilon_i \) to denote independent sampling errors \( \epsilon_i \sim \mathcal{N}(0, V_i) \), where \( V_i = \text{Var}(\text{logit}(\hat{p}_{i}^{\text{MA}})) \), which we treat as known. In practice, we estimate \( V_i \) by first estimating \( \hat{V}(\hat{p}_{i}^{\text{MA}}) \) using Equation (12) and then applying the delta method to obtain the approximation

\[ V_i \approx \frac{\hat{V}(\hat{p}_{i}^{\text{MA}})}{(\hat{p}_{i}^{\text{MA}} (1 - \hat{p}_{i}^{\text{MA}}))^2}. \]  

(16)

We adopt a hierarchical Bayesian approach to inference by defining hyperparameter priors, yielding the following alternative representation:

\[ \text{logit}(\hat{p}_{i}^{\text{MA}}) \mid p_i, V_i \sim \mathcal{N}(\text{logit}(p_i), V_i), \quad i = 1, \ldots, m \]  

(17)

\[ \text{logit}(p_i) \mid \beta, \sigma_u^2, \phi \sim \mathcal{N}(X \beta, \Sigma(\sigma_u^2, \phi)), \]  

(18)

\[ \beta, \sigma_u^2, \phi \sim \pi(\xi), \]  

(19)

where we use \( \text{logit}(p_i) \) to denote the vector \( (\text{logit}(p_1), \ldots, \text{logit}(p_m))^\top \), and \( X \) to denote the \( m \times (p + 1) \) matrix of area-level covariates. We assume that the estimators \( \text{logit}(\hat{p}_{i}^{\text{MA}}) \) for each
area $i$ are independent. Finally, $\pi(\xi)$ denotes the hyperparameter priors, and $\xi$ represents the corresponding parameters, which should be specified based on the specific application at hand.

By specifying different structures for $\Sigma$, we can obtain different models for the spatial dependence in $\logit(p_i)$. Typically, we specify an $m \times m$ adjacency matrix representing adjacency relationships between the areas. We model the area-level random effects $u$ using the BYM2 model, a reparameterization of the Besag–York–Mollié (Besag, York & Mollié, 1991) model proposed by Riebler et al. (2016) for the area-level random effects vector $u$:

$$u = \sigma_u \left( \sqrt{1 - \phi\bar{u}_1} + \sqrt{\phi\bar{u}_2} \right). \quad (20)$$

Here, we assume $\bar{u}_1 \sim \mathcal{N}(0, I)$ is a random area effect with no spatial structure. We use $\bar{u}_2$ to denote a structured spatial component, which follows an intrinsic conditional autoregressive (ICAR) model (intuitively, the mean of $\bar{u}_2$ is set to the mean of all neighbouring effects, and the precision is specified to be proportional to the number of neighbours). As such, $\sigma_u$ controls the marginal variance of $u$, and $\phi$ controls the proportion of variation assigned to the structured component. Under this model, $u$ has the covariance matrix

$$\text{Var}(u|\sigma_u, \phi) = \sigma_u((1 - \phi)I + \phi Q^{-*}), \quad (21)$$

where $Q^{-*}$ is the Moore–Penrose pseudoinverse of $Q_\sigma$, the precision matrix of $\bar{u}_2$. As discussed by Riebler et al. (2016), $Q_\sigma$ is singular, making the ICAR prior for the random effects improper, so we place a sum to zero constraint on the elements of $u$ to ensure identifiability in the posterior. Moreover, the marginal variance of each effect $u_i$ depends on its number of neighbours, so to make the overall variance parameter $\sigma_u$ interpretable, $Q_\sigma$ is scaled (following the procedure described in Section 3.2 of Riebler et al. (2016)) to make the geometric mean of the marginal variances equal to 1.

Following Riebler et al. (2016) and Simpson et al. (2017), we place penalized complexity (PC) priors on $\sigma_u$ and $\phi$. These priors penalize the Kullback–Leibler distance of a full model from a simpler base model and shrink $\phi$ and $\sigma_u$ to zero. We place a flat prior on $\beta$ so that $\pi(\beta) \propto 1$.

The approach presented here is specified for spatially structured binary response data, but the overall strategy of using area-level models to smooth model-assisted estimators can be adapted to other types of data. If the response is continuous, rather than binary, the same approach can be applied using a working linear regression model in the first stage and using a similar second-stage model, but without applying the logit transformations, as proposed by Fay (2018). Other models for spatial random effects could be used, including, for example, those previously introduced into Fay–Herriot models by Ghosh et al. (1998) and Pratesi & Salvati (2008). As mentioned above, Chung & Datta (2020) provide a recent comparison of several spatial random effects models used within the Fay–Herriot model. Examples of previous uses of ICAR spatial random effects within area-level models are provided in You & Zhou (2011), Porter et al. (2014), Mercer et al. (2015), and Li et al. (2019).

5. SIMULATIONS
5.1. Population Generating Model

Below, we use simulations to compare our smoothed model-assisted estimator with existing direct, model-assisted, and model-based estimators. The set-up is motivated by simulations used by Corral et al. (2021). Using the WorldPop 100m population counts grid for Nigeria.
corresponding to the 2006 census (WorldPop, 2018), we sampled 300 pixels without replacement with probability proportional to population in each of 73 strata defined by crossing the 37 Admin-1 areas with urban/rural status (one area corresponding to Lagos is entirely urban). Each sampled pixel represents a simulated cluster location. For each simulated cluster, we simulated its cluster size $n$ from a Poisson distribution with mean 15. For each cluster $c$ in area $i$, we simulated a cluster-level risk $q_{ic}$ using the model

$$
\logit(q_{ic}) = x_{1,ic} - x_{2,ic} + 0.5x_{3,ic} + 0.25x_{4,ic} + 0.25x_{5,ic} + 1.5x_{6,ic} + 0.1x_{7,ic} + 0.1x_{8,ic} + u_i + \varepsilon_{ic},
$$

(22)

where $u_i \sim \mathcal{N}(0, 0.1^2)$ are i.i.d. area-level random effects, and $\varepsilon_{ic} \sim \mathcal{N}(0, 0.5^2)$ represent i.i.d. cluster-level effects. The covariates were specified as follows:

1. The covariate $x_{1,ic}$ was the realized value of a binary random variable $X_{1,ic}$ with $P(X_{1,ic} = 1) = 0.5$;
2. The covariate $x_{2,ic}$ was the realized value of a binary random variable $X_{2,ic}$ with $P(X_{2,ic} = 1) = 0.3 + 0.5(i/37)$;
3. The covariate $x_{3,ic} = x_{3,i}$ was obtained from a $37 \times 1$ random vector modelled as an ICAR random effect with marginal variance 1 for the Admin-1 areas;
4. The covariate $x_{4,ic} = x_{4,i}$ was obtained from a $774 \times 1$ random vector modelled as an ICAR random effect with marginal variance 1 for the Admin-2 areas;
5. The covariate $x_{5,ic}$ was obtained from a random vector generated using a stochastic partial differential equation (SPDE)-based approximation to a Gaussian process with Matérn covariance (smoothness 1) and marginal variance of 1;
6. The covariate $x_{6,ic}$ was obtained from a random vector generated from the same procedure as $x_{5,ic}$ and was used to simulate informative sampling;
7. The covariate $x_{7,ic}$ denotes estimated travel times to cities in 2015 (Weiss et al., 2018);
8. The covariate $x_{8,ic}$ denotes proportion of people per grid square living in poverty in 2010 (Tatem et al., 2017).

The covariates $x_1$ and $x_2$ represent informative nonspatial covariates, while $x_3$, $x_4$, $x_5$, and $x_6$ exhibit spatial correlation. The covariates $x_3$ and $x_6$ were based on real covariates commonly used for modelling health outcomes in LMIC. Based on the above cluster-level risks, we generated responses $Y_{icj} \sim \text{Bernoulli}(q_{ic})$, where $Y_{icj}$ denotes the response for unit $j$ in cluster $c$ in area $i$. As described above, our population consisted of 300 clusters of varying sizes. From this population, we repeatedly sampled 10 clusters from each stratum, using all response values from each sampled cluster. We used an informative sampling scheme in which we oversampled clusters with large values for $x_{6,ic}$: clusters with values of $x_{6,ic}$ in the top quartile were three times as likely to be sampled as clusters in the bottom three quartiles. The spatial correlation of the $x_6$ values induces spatial structure in the model residuals unless this oversampling is addressed when estimating model parameters. Based on this design, we computed sampling probabilities and design weights $w_{ij}$ for each individual. In practice, we generated the covariate values and cluster sizes once and then sampled a list of indices identifying the sampled clusters. These indices and cluster characteristics were held constant across simulations, but the response variables, area effects, and cluster effects were repeatedly resampled.

5.2. Estimation Procedure

For each simulation, we computed the true population Admin-1 area-level proportions $p_i$ and compared with several estimators computed from the sampled data. For all estimators that
rely on covariate modelling, we considered two potential models: a reduced model and a full model. The full model includes all covariates except \( x_4 \). We removed the area-specific covariate \( x_4 \) in order to induce spatial correlation in the model residuals. The reduced model includes all covariates except \( x_4 \) and \( x_6 \), so it does not account for the effect of oversampling the stratum defined by \( \{ x_{6,ic} > \text{median}(x_{6,ic}) \} \), meaning the design is not ignorable after conditioning on model covariates. Conversely, the full model partially accounts for this by including \( x_6 \) as a covariate. Furthermore, for all model-based approaches incorporating smoothing via random effects, we considered both nonspatial smoothing using i.i.d. Gaussian area-level random effects and spatial smoothing using the BYM2 model for area-level random effects.

Below, we describe the estimators used for comparison. First, we computed the direct weighted Hájek estimator. We also computed model-assisted estimators (MA) using both the full and reduced models. Next, we computed several area-level model-based estimators. Applying the spatial logistic area-level model described in Section 4.2 to the Hájek estimator yielded a spatial smoothed Hájek (SH) estimator. Similarly, by applying the same model to the model-assisted estimator, we obtained our proposed spatial smoothed model-assisted estimator (SMA). For comparison, we also computed nonspatial versions of smoothed estimators by assuming i.i.d. Gaussian random effects in the logistic area-level linking model given in Equation (14).

Finally, we computed a number of unit-level model-based estimators, using a Binomial model as well as two models designed to account for effects of clustering: one with beta-distributed random effects, and the other with normal random effects on the linear predictor scale.

We here briefly describe these models, which have been used in SAE previously as discussed by Dong & Wakefield (2021). The beta-binomial model, which accounts for response-data overdispersion, potentially related to clustering, can be specified as follows. We assume that each unit in a given cluster \( c \) in area \( i \) has the same risk \( q_{ic} \):

\[
Y_{icj} | q_{icj} \sim \text{Bernoulli}(q_{ic}),
\]

\[
q_{ic} | \mu_{ic}, d \sim \text{Beta}(\mu_{ic}, d),
\]

\[
\text{logit}(\mu_{ic}) = x_{ic}^\top \beta + u_i,
\]

where we parameterized the beta distribution via

\[
E(q_{ic} | \mu_{ic}, d) = \mu_{ic},
\]

\[
\text{Var}(q_{ic} | \mu_{ic}, d) = \frac{\mu_{ic}(1 - \mu_{ic})}{d + 1},
\]

where \( d \) denotes a dispersion parameter. The lognormal-binomial model (called the lono-binomial model by Dong & Wakefield (2021)) assumes instead that

\[
y_{icj} | x_{ic}, \beta, u_i \sim \text{Bernoulli}(r_{ic})
\]

\[
\text{logit}(r_{ic}) = q_{ic} + \epsilon_{ic} = x_{ic}^\top \beta + u_i + \epsilon_{ic},
\]

where for all areas \( i \) and clusters \( c \), \( r_{ic} \) denotes a cluster-level parameter defined as the sum of the cluster-level prevalence \( q_{ic} \) and i.i.d. Gaussian cluster-level error \( \epsilon_{ic} \). For the binomial,
beta-binomial, and lognormal-binomial models, we implement two versions with nonspatial i.i.d. and spatial BYM2 area-level random effects $u$. For all unit-level models, area-level estimates were made by making predictions of $q_{ic}$ for all clusters in the population and then aggregating upwards to the area level.

Additional information on the estimation procedures, including information on the software used and priors for model hyperparameters, can be found in the Supplementary Material.

5.3. Results

For each method, we computed point estimates $\hat{p}_i$ as well as 90% interval estimates ($\hat{p}_i^-, \hat{p}_i^+$). For each vector of estimates $\hat{p}_i$, we computed the root mean squared error (RMSE) and mean absolute error (MAE). We also computed the coverage of the 90% interval estimates and the mean interval lengths (MIL) across all areas.

$$RMSE(\hat{p}_i) = \sqrt{\frac{1}{m} \sum_i (p_i - \hat{p}_i)^2}, \quad (30)$$

$$MAE(\hat{p}_i) = \frac{1}{m} \sum_i |p_i - \hat{p}_i|, \quad (31)$$

$$Coverage_{90}(\hat{p}_i) = \frac{1}{m} \sum_i 1\{p_i \in (\hat{p}_i^-, \hat{p}_i^+)\}, \quad (32)$$

$$MIL_{90}(\hat{p}_i) = \frac{1}{m} \sum_i (\hat{p}_i^+ - \hat{p}_i^-). \quad (33)$$

We summarize these error metrics by averaging their values across all 1000 simulated populations. For all estimators incorporating covariate information, we provide comparisons for both reduced (Table 1) and full models (Table 2) across the 1000 generated response vectors. Note that the Hájek and SH estimators do not make use of any covariates. In general, introducing covariate information reduces the error of point estimates, and the methods using the full set of covariates achieve the lowest error. For the reduced models in Table 1, the nonspatial SMA estimator does not improve on the MA estimator, suggesting that the smoothing via independent random effects is not particularly beneficial. However, the spatial SMA estimator performs best, suggesting that when there are relevant design variables that are left out of the fitted model, the SMA approach may improve upon direct or unit-level approaches. We would also expect the spatial estimator to perform well when there is residual spatial dependence. The non-spatial SMA estimator, which uses independent area effects, may be less efficient because the spatial covariates were omitted from the reduced model.

In Table 2, we observe that the spatial unit-level models perform best, suggesting that when all relevant design variables are included in the model and the design is truly ignorable, unit-level approaches may be preferred. However, the Spatial SMA approach still offers benefits over the Hájek and MA approaches. In terms of calibration, the Hájek, model-assisted, and area-level model-based estimators have coverage rates close to the nominal 90% rate. However, some of the unit-level model-based interval estimates exhibit undercoverage, especially when only the reduced set of covariates was used. For the full set of covariates, the estimators based on the binomial display undercoverage, while the beta-binomial and lognormal-binomial interval estimates achieve close to nominal coverage.

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Table 1: Averaged RMSE (×100), MAE (×100), coverage rates, and MIL (×100) of estimators of area-level means across 1000 simulated populations with spatially correlated binary responses based on sample data obtained via informative sampling for methods using no covariates or only the reduced set of covariates (omitting one of the spatial covariates used in population generation).

| Method          | RMSE  | MAE  | 90% Coverage | MIL   |
|-----------------|-------|------|--------------|-------|
| Direct (Hájek)  | 4.44  | 3.28 | 86           | 13.99 |
| MA              | 3.70  | 2.81 | 87           | 11.82 |
| Nonspatial      |       |      |              |       |
| SH              | 4.84  | 3.44 | 89           | 14.66 |
| SMA             | 3.71  | 2.79 | 87           | 12.27 |
| Binomial        | 4.22  | 3.11 | 75           | 8.24  |
| Betabinomial    | 4.13  | 3.05 | 83           | 10.10 |
| Lono-Binomial   | 4.42  | 3.23 | 81           | 9.95  |
| Spatial         |       |      |              |       |
| SH              | 4.24  | 3.13 | 91           | 13.40 |
| SMA             | 3.47  | 2.65 | 87           | 11.49 |
| Binomial        | 4.14  | 3.02 | 76           | 8.06  |
| Betabinomial    | 3.96  | 2.88 | 85           | 9.84  |
| Lono-Binomial   | 4.38  | 3.18 | 81           | 9.72  |

Note: The lowest RMSE and MAE are in bold italics.

Table 2: Averaged RMSE (×100), MAE (×100), coverage rates, and MIL (×100) of estimators of area-level means across 1000 simulated populations with spatially correlated binary responses based on sample data obtained via informative sampling for methods using the full set of covariates.

| Method          | RMSE  | MAE  | 90% Coverage | MIL   |
|-----------------|-------|------|--------------|-------|
| MA              | 3.17  | 2.41 | 87           | 9.68  |
| Nonspatial      |       |      |              |       |
| SMA             | 3.18  | 2.41 | 87           | 9.92  |
| Binomial        | 2.68  | 2.02 | 88           | 7.99  |
| Betabinomial    | 2.69  | 2.04 | 89           | 8.43  |
| Lono-Binomial   | 4.42  | 3.23 | 81           | 9.95  |
| Spatial         |       |      |              |       |
| SMA             | 3.03  | 2.28 | 88           | 9.47  |
| Binomial        | 2.62  | 1.96 | 88           | 7.76  |
| Betabinomial    | 2.62  | 1.96 | 90           | 8.21  |
| Lono-Binomial   | 2.62  | 1.96 | 89           | 8.10  |

Note: The lowest RMSE and MAE are in bold italics.

6. APPLICATION: VACCINATION COVERAGE IN NIGERIA

We applied our smoothed model-assisted estimator to generate Admin-1 level estimates of measles vaccination rates using the 2018 Nigeria DHS data described in Section 2. In this case, \( y_{ij} \) represents the observed vaccination status of child \( j \) in area \( i \). We used two main unit-level covariates obtained from grid-based estimates of travel times to cities in 2015 (Weiss et al., 2018) and the proportion of people per grid square living in poverty in 2010 (Tatem...
et al., 2017). The associated fixed effect estimates were significantly different from zero in a survey-weighted logistic regression with measles vaccination as outcome; however, these covariates were themselves estimated using geostatistical models, so any associations should be interpreted with caution. We also used a map of estimated population density (WorldPop) to derive a binary covariate that classifies each pixel as either urban or rural.

When using unit-level covariates to predict binary response variables, covariate information on the entire population is required to generate estimates. In our setting, when recent and reliable population data may not be available, satellite imagery can provide covariates on a pixel grid spanning the domain. Instead of predicting the response on each child separately, we generated predictions for each pixel and averaged over the pixel-level predictions for a given area. When averaging, we weighted each pixel’s prediction by the estimated number of children aged 1–5 in the pixel using maps created by WorldPop. We harmonized the covariate rasters and population density rasters to a common pixel grid, the 1 km by 1 km grid provided by WorldPop. We also used the map of estimated population density to derive a binary covariate that classified each pixel as either urban or rural by assigning the highest density pixels in a given area to be urban so that the total proportion of population classified as urban in each area matched the proportion reported in the 2018 Nigeria DHS report.

Using these data, we compared a number of the estimation methods outlined above. We first considered the Hájek estimator \( \hat{p}_i^H \) and the model-assisted estimator \( \hat{p}_i^{MA} \) where the working model is a logistic regression model. We then considered smoothed Hájek estimators and smoothed model-assisted estimators obtained by fitting the model specified in (14) and (15) for \( \hat{p}_i^H \) and \( \hat{p}_i^{MA} \), respectively. For each, we considered both i.i.d. and BYM2 models for the area-level random effects \( \mathbf{u} \), yielding four estimators: smoothed Hájek with i.i.d. area effects (SH) and BYM2 area effects (Spatial SH) as well as smoothed model-assisted with i.i.d. area effects (SMA) and BYM2 area effects (Spatial SMA).

Finally, we considered a geostatistical model; to account for clustering, we use the spatial beta-binomial model described above with a BYM2 prior for the area-level random effects \( \mathbf{u} \). Since pixels do not necessarily coincide with clusters, we cannot use the lono-binomial model, which requires us to identify the sampling frame of clusters in order to aggregate estimates appropriately.

Figure 2 compares point estimates of measles vaccination rates (left) and the length of interval estimates (right) for Admin-1 areas among children aged 12–23 months in Nigeria in 2018. Point and interval estimates for all methods are provided in the Supplementary Material. We omit results for the non-spatial mixed models, as their results are similar to those of the spatial models. On the right side, we quantify uncertainty using the length of 90% credible intervals (for the smoothed and unit-level models) and design-based 90% confidence intervals (for the Hájek and model-assisted estimators) for Admin-1 areas in Nigeria in 2018. The interpretation of uncertainty estimates requires some care because the intervals for the Hájek and model-assisted estimators only estimate design-based uncertainty, while the smoothed and beta-binomial intervals are drawn from posterior distributions which also account for model parameter uncertainty. The point estimates for all the methods are similar but the interval estimate lengths vary considerably. In particular, incorporating unit-level covariates shrinks the interval estimates as seen when comparing the Hájek and model-assisted estimators. The interval lengths are shortest for the unit-level model, while the smoothed Hájek and smoothed model-assisted intervals are more conservative.

Figure 3 compares the interval lengths for the Hájek estimates with the lengths of interval estimates produced by the other methods, illustrating that the unit-level model (beta-binomial) intervals are considerably shorter than those produced by the rest of the methods. In particular, our smoothed model-assisted intervals are more conservative; as our simulations show, when relevant design variables are omitted from unit-level models, resulting prediction intervals can
Figure 2: Estimated measles vaccination rates (left) and 90% prediction interval lengths for estimated measles vaccination rates (right) among children aged 12–23 months for Admin-1 areas in Nigeria in 2018.

Figure 3: Comparison of reference Hájek design-based 90% confidence interval length (x-axis) with model-assisted and model-based interval estimate lengths (y-axis) for four methods for measles vaccination rates.
exhibit undercoverage, whereas the corresponding smoothed model-assisted intervals may be better calibrated. In DHS surveys, clusters are generally sampled with probability proportional to the size, but the cluster sizes are typically not published. As such, cluster size may be a relevant design variable that we are unable to incorporate into unit-level models. The smoothed model-assisted point estimates and interval estimates may thus be preferable to the unit-level model estimates. Among the unit-level models, we recommend the use of the beta-binomial estimates, which account for potential clustering effects.

7. DISCUSSION

We have proposed a smoothed model-assisted estimator for small area means that incorporates unit-level covariate information and smoothing via random effects while retaining favourable design optimality properties. Our method seeks to bridge SAE and model-based geostatistics literatures, drawing from and offering benefits to both perspectives.

The basic question of how best to estimate area-specific quantities given limited data arises in many settings; in a sense, any subpopulation with limited sample data may be considered a small area. For example, multilevel regression and poststratification has been used to generate local estimates of opinion using survey data with high nonresponse or nonprobability sampling (Si, 2020). Our smoothed model-assisted approach is particularly tailored for estimating subnational health and demographic indicators. In this context, properties such as asymptotic design unbiasedness and design consistency are high priorities for national statistics offices that create and distribute estimates. Using spatial and spatiotemporal smoothing and unit-level covariate information in SAE may offer large benefits in areas with limited data. Finally, the household surveys used in this setting typically have high response rates, informative sampling weights, and geographic information.

Although the above simulations and application illustrate the potential benefits of our approach, in some settings the new method may offer limited improvement. When data are not available in every area for which estimates are desired, it is still computationally possible to sample from the smoothing model posterior for unsampled areas. However, as they do not incorporate actual observations from the area in question, such estimates cannot meaningfully be called design-consistent. Typical unit-level models enable predictions to be made for unsampled areas. When sampling is not informative, such predictions may be preferable to those that would result from our approach. Another limitation is that our estimator requires careful specification of the working model. When the model is overly flexible, typical approximations that ignore variability from model estimation will underestimate the variance of model-assisted estimators. The resulting smoothed model-assisted estimators may thus be overconfident. Finally, when reliable population information is unavailable, as may be the case when estimating health and demographic indicators in LMIC, it is common to use satellite-derived covariate rasters and aggregate pixel-level predictions to compute area-level estimates. This aggregation process is affected by measurement error in the covariates, misalignment between population density maps and household locations, and the resolution of the pixel grid. The effects of aggregation on the resulting area-level estimates are not well understood; Paige et al. (2022) consider potential implications.

When unit-level covariates are strongly associated with a variable of interest, using covariate modelling in SAE offers accuracy and efficiency gains. However, unit-level models do not generally produce design-consistent estimators. Various solutions have been proposed, including pseudolikelihood and pseudo-Bayesian methods, pairwise likelihood methods, and direct modelling of the sample distribution. Pseudolikelihood methods are sensitive to scaling, and pairwise likelihood estimation requires knowledge of pairwise sampling probabilities, while uncertainty quantification for pseudo-Bayesian approaches relies on applying ad hoc corrections. Direct modelling of the sample distribution may necessitate undesirable model assumptions. As such,
more work is needed to understand how best to use unit-level covariate modelling in a setting where design optimality properties are prioritized.

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APPENDIX

**Survey Asymptotics**

Let \( \hat{p}_i(s) \) denote an estimator of \( p_i \) depending on the observed sample \( s \). The expectation with respect to sampling \( E_d \) can be defined as

\[
E_d(\hat{p}_i(s)) = \sum_s P_d(s)\hat{p}_i(s),
\]

where \( P_d \) is a probability mass function mapping samples \( s \) to their probabilities. The design variance \( V_d \) can be analogously defined.

In the survey statistics literature, it is also common to define survey asymptotics in terms of a sequence of nested samples and populations that are both increasing in size (Särndal, Swensson & Wretman, 2003; Breidt & Opsomer, 2017). Let \( U^{(\infty)} = 1, 2, \ldots \) be an infinite sequence of elements with associated \( y \) values \( y_1, y_2, \ldots, \) and let \( U^{(1)}, U^{(2)}, \ldots \) be a sequence of populations where \( U^{(k)} \) contains the first \( N^{(k)} \) elements of \( U^{(\infty)} \) and \( U^{(1)} \subset U^{(2)} \subset \cdot \cdot \cdot \). For each \( U^{(k)} \), let \( P_d(\cdot) \) be a sampling design that assigns probabilities to each possible sample \( s^{(k)} \). Assume that the sample size \( n^{(k)} \) is fixed and \( n^{(1)} < n^{(2)} < \cdot \cdot \cdot \). Thus \( k \to \infty \) implies \( n^{(k)} \to \infty \) and \( N^{(k)} \to \infty \).

Let \( \theta^{(k)} \) be a function of the elements of \( U^{(k)} \), and let \( \hat{\theta}^{(k)} \) be an estimator of \( \theta^{(k)} \) based on the sample \( s^{(k)} \). An estimator \( \hat{\theta}^{(k)} \) is asymptotically design-unbiased for \( \theta^{(k)} \) if

\[
\lim_{k \to \infty} [E_d(\hat{\theta}^{(k)}) - \theta^{(k)}] = 0 \quad \text{(A2)}
\]

and \( \hat{\theta}^{(k)} \) is design-consistent if for any fixed \( \epsilon > 0 \):

\[
\lim_{k \to \infty} P_d(|\hat{\theta}^{(k)} - \theta^{(k)}| > \epsilon) = 0. \quad \text{(A3)}
\]

Särndal, Swensson & Wretman (2003) note that these conditions depend on the specification of the sequences of estimators, population values, and designs; conditions on the limiting behaviour of the finite population values and inclusion probabilities are typically needed to ensure consistency.

**Design Consistency of Survey Regression LGREG Estimator**

We now consider the design consistency of the model-assisted estimator specified by Equation (11) and discuss the relevant regularity assumptions. Our proof adapts the one presented by Kennel and Valliant (2020, Appendix) for a multivariate logistic model-assisted
estimator for clustered samples. Rather than showing design consistency for $\hat{p}_i^{MA}$, we, instead, consider the area-specific total estimator $\hat{t}_i^{MA}$:

$$\hat{t}_i^{MA} = \sum_{j \in U_i} \hat{y}_{ij} + \sum_{j \in S_i} w_{ij}(y_{ij} - \hat{y}_{ij}).$$

(A4)

Let $\hat{y}_{ij}$ denote predictions from our working logistic regression model

$$P(y_{ij} = 1|x_{ij}, \beta) = q_{ij},$$

(A5)

$$\text{logit}(q_{ij}) = x_{ij}^T \beta.$$ (A6)

If we had full population data, we could estimate $\beta$ by maximizing the population log-likelihood to obtain finite population parameters $B$:

$$B = \arg \max_{\beta} \sum_i \sum_{j \in S_i} \ell'(y_{ij}; \beta).$$

(A7)

Since we have data only for sampled units, in practice, we maximize the survey-weighted log-likelihood to obtain $\hat{B}$, an estimator of $B$:

$$\hat{B} = \arg \max_{\beta} \sum_i \sum_{j \in S_i} \frac{1}{\pi_{ij}} \ell'(y_{ij}; \beta).$$

(A8)

To reflect the dependence of our predictions on the estimated regression parameters, we introduce the following notation, letting $\hat{y}$ denote predictions if we observed the finite population parameters $B$:

$$\hat{y}_{ij} = \mu(x_{ij}, \hat{B})$$

(A9)

$$\hat{y}_{ij} = \mu(x_{ij}, B).$$

(A10)

We assume an asymptotic regime with a fixed number $m$ of areas, where area $i$ has sample size $n_i$ and population size $N_i$. We let $N$ denote the overall population size and $n$ denote the overall sample size. We assume a sequence of designs and populations such that $N, N_i \to \infty$ and assume the following conditions:

1. The regression parameter estimates satisfy $\hat{B} = B + O_P(n^{-1/2})$. Moreover, $B \to \beta$ as $N \to \infty$.
2. For each area $i$, for each $j$, $|\partial \mu / \partial t| \leq h(x_{ij}, \beta)$ for all $t$ in a neighbourhood centred on $\beta$ such that $(1/N_i) \sum_{j \in U_i} h(x_{ij}, \beta) = O(1)$.
3. For each area $i$, the sum of $w_{ij}\hat{y}_{ij}$ is design consistent for the sum of $\hat{y}_{ij}$ and the sum of $w_{ij}y_{ij}$ is design consistent for the sum of $y_{ij}$.

Note that Assumption 1 requires that the working model parameter estimator converges to some limit. Since we may sample from many different areas, we assume that the same working model is used for all areas or, alternatively, that the survey design calls for proportional sampling of all areas $a$. Assumption 2 requires that the derivative term $|\partial \mu / \partial t| \leq h(x_{ij}, \beta)$ is bounded in each
small area. Assumption 3 requires that Horvitz–Thompson-type estimators are design-consistent under the sequence of designs specified.

By Taylor’s theorem, for all \( j \in U_i \), there is some vector \( B^*_{ij} \) such that

\[
\hat{y}_{ij} = \bar{y}_{ij} + \left[ \frac{\partial \mu}{\partial t} \bigg|_{t=B^*_{ij}} \right] ^T \text{vec}(\hat{B} - B).
\] (A11)

Here, \( \frac{\partial \mu}{\partial t} \) is a \((p + 1) \times 1\) vector of the partial derivatives of \( \mu \) with respect to the components of \( t \). By summing over all units \( j \in U_i \) and dividing by the population size \( N_i \), we obtain the following:

\[
\frac{1}{N_i} \sum_{j \in U_i} \hat{y}_{ij} = \frac{1}{N_i} \sum_{j \in U_i} \bar{y}_{ij} + \frac{1}{N_i} \sum_{j \in U_i} \left[ \frac{\partial \mu}{\partial t} \bigg|_{t=B^*_{ij}} \right] ^T \text{vec}(\hat{B} - B).
\] (A12)

Under Assumptions 1 and 2, we have that

\[
\frac{1}{N_i} \sum_{j \in U_i} \hat{y}_{ij} - \frac{1}{N_i} \sum_{j \in U_i} \bar{y}_{ij} = O_p(n^{-1/2})
\] (A13)

and

\[
\frac{1}{N_i} \sum_{j \in S_i} w_{ij} \hat{y}_{ij} - \frac{1}{N_i} \sum_{j \in S_i} w_{ij} \bar{y}_{ij} = O_p(n^{-1/2})
\] (A14)

implying that

\[
\frac{1}{N_i} \left[ \sum_{j \in U_i} \hat{y}_{ij} - \sum_{j \in S_i} w_{ij} \hat{y}_{ij} \right] = \frac{1}{N_i} \left[ \sum_{j \in U_i} \bar{y}_{ij} - \sum_{j \in S_i} w_{ij} \bar{y}_{ij} \right] + O_p(n^{-1/2}).
\] (A15)

We can thus rewrite \( i_i^{MA} \) as follows:

\[
\frac{1}{N_i} i_i^{MA} = \frac{1}{N_i} \left[ \sum_{j \in U_i} \hat{y}_{ij} + \sum_{j \in S_i} w_{ij}(y_{ij} - \hat{y}_{ij}) \right]
\] (A16)

\[
= \frac{1}{N_i} \left[ \sum_{j \in S_i} w_{ij}y_{ij} + \sum_{j \in U_i} \hat{y}_{ij} - \sum_{j \in S_i} w_{ij} \hat{y}_{ij} \right]
\] (A17)

\[
= \frac{1}{N_i} \left[ \sum_{j \in S_i} w_{ij}y_{ij} + \sum_{j \in U_i} \bar{y}_{ij} - \sum_{j \in S_i} w_{ij} \bar{y}_{ij} \right] + O_p(n^{-1/2}).
\] (A18)

Therefore, as long as Assumption 3 holds, \( i_i^{MA} \) will converge to the desired population total.