A Spatial Variance-Smoothing Area Level Model for Small Area Estimation of Demographic Rates

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Summary

Accurate estimates of subnational health and demographic indicators are critical for informing policy. Many countries collect relevant data using complex household surveys, but when data are limited, direct weighted estimates of small area proportions may be unreliable. Area level models treating these direct estimates as response data can improve precision but often require known sampling variances of the direct estimators for all areas. In practice, the sampling variances are estimated, so standard approaches do not account for a key source of uncertainty. To account for variability in the estimated sampling variances, we propose a hierarchical Bayesian spatial area level model for small area proportions that smooths both the estimated proportions and sampling variances to produce point and interval estimates of rates of interest. We demonstrate the performance of our approach via simulation and application to vaccination coverage and HIV prevalence data from the Demographic and Health Surveys.

Key words: area level model; Bayesian statistics; small area estimation; spatial statistics.

1 Introduction

Subnational estimates of health and demographic indicators such as vaccination rates or neonatal mortality rates are critical for highlighting disparities and guiding policy interventions. Data on key health outcomes are often collected using national household surveys designed to produce reliable direct weighted estimators for demographic rates of interest. However, often estimates are desired for subregions for which direct weighted estimation may be insufficiently precise. In the survey statistics literature, this problem is known as small area estimation (SAE). Rao & Molina (2015) and Sugasawa & Kubokawa (2023) provide general overviews of SAE, while Pfefferman (2013) and Ghosh (2020) review recent developments. When data are limited, model-based estimators can improve precision compared with direct estimators by explicitly modelling between-area variation and incorporating covariate information. Area level models treat direct weighted estimates as noisy response data, using covariate information and random effects to produce smoothed estimates. The popular Fay–Herriot area level model (Fay &
Herriot, 1979) assumes that for each area, the direct estimator \( \hat{p}_i \) is available and can be modelled using a Gaussian distribution centred around the finite population mean \( p_i \):

\[
\hat{p}_i | p_i, V_i \sim N(p_i, V_i)
\]

where \( V_i \) denotes sampling variances, which are typically assumed to be known. This sampling model is combined with a linking model for the finite population means:

\[
p_i | \beta, \sigma_u^2 \sim N(\mathbf{x}_i^T \beta, \sigma_u^2)
\]

where \( \mathbf{x}_i \) denotes a vector of area level covariate values for area \( i \) and \( \beta \) denotes the corresponding coefficients. The linking model variance \( \sigma_u^2 \) controls the between-area variability. As the direct estimators \( \hat{p}_i \) account for the survey design using sampling weights, area level methods are typically robust to the effects of informative sampling and other design features. Under certain regularity conditions, the resulting estimators are design consistent (Rao & Molina, 2015).

In practice, the variances \( V_i \) are usually estimated using sample-based estimators \( \hat{V}_i \), but the Fay–Herriot model does not account for uncertainty in \( \hat{V}_i \). This is a well known problem in the SAE literature and has motivated a number of extensions of Fay–Herriot that account for unknown sampling variances (Arora & Lahiri, 1997; Bell, 2008; Rivest & Vandal, 2002). However, these approaches are not well-suited for subnational estimation of rates of key health outcomes in a low- and middle-income countries (LMIC) context. In particular, existing methods often rely on the availability of area level covariates for modelling sampling variances and such auxiliary information may not be available if census data are limited or unreliable. Additionally, approaches that model the sampling variances often do not account for uncertainty in the modelled variance estimates, simply treating them as known in the standard Fay–Herriot model. Finally, although the Gaussian approximation for the direct estimator’s sampling distribution may be effective when estimating means of continuous-valued responses, it may be less appropriate when the target estimand is a proportion of binary responses. For estimating a proportion, the direct weighted estimator is typically a weighted sum of binary valued random variables, so its mean and sampling variance can be strongly related. Correctly modelling this mean–variance relationship is critical as it may explain a substantial part of the heterogeneity in sampling variances for a set of estimators.

To address these issues, we propose a fully Bayesian area level model for small area proportions that jointly models the direct estimators and sampling variance estimators. We use spatially structured area level random effects to induce spatial smoothing of both means and variances. In simulations, we find that our proposed method produces interval estimates with improved empirical coverage rates compared with standard Fay–Herriot intervals. Below, we outline our model and review variance-smoothing area level models for SAE. In Section 2, we describe two example estimation problems involving subnational demographic rates to motivate our new approach. Section 3 reviews existing area level models and discusses recent efforts to incorporate variance smoothing for model-based SAE. In Section 4, we detail our spatial variance-smoothing area level model for estimation of small area proportions. We evaluate our approach via simulation studies in Section 5 and by application to data from the Demographic and Health Surveys in Section 6. Finally, we compare our method with existing approaches and discuss potential directions for future research in Section 7.

## 2 Motivation

We consider two motivating examples using data from the Demographic and Health Surveys (DHS) Program. In the first, we use 2018 Nigeria DHS data to estimate regional vaccination...
coverage rates for the first dose of measles-containing-vaccine (MCV1) among children aged 12–23 months (National Population Commission - NPC/Nigeria & ICF, 2019). In the second, we use 2015–2016 Malawi DHS data to estimate HIV prevalence among women aged 15–49 (National Statistical Office NSO/Malawi & ICF, 2017). Figure 1 provides maps of direct survey-weighted estimators for both indicators. In the measles vaccination example, the direct estimates have a large spread and are generally located away from zero or one; in the HIV prevalence example, the direct estimates exhibit less variability and are on average closer to zero.

Figure 1. Direct weighted estimates of vaccination coverage rate for first dose of measles-containing-vaccine (MCV1) among children aged 12–23 months in Nigeria, 2018 (left) and HIV prevalence rate for women aged 15–49 in Malawi, 2015–2016 (right)
In Nigeria and Malawi, the DHS Program uses a stratified two-stage cluster sampling design. Countries are divided into administrative regions which are further partitioned into urban and rural areas. The sampling strata are defined by crossing these regions with urban/rural status. In Nigeria, the divisions used for defining strata are called Admin-1 regions; in Malawi, they are called Admin-2 regions. Each stratum is divided into collections of households called enumeration areas (EAs) or clusters. The first stage of sampling selects a pre-specified number of EAs in each stratum with probability proportional to the number of households in the EA. The second stage of sampling selects a fixed number of households in each sampled EA.

The 2018 Nigeria DHS collected data on measles vaccination status for children in sampled households based on vaccination cards or caregiver recall. In Nigeria, the Admin-1 regions consist of 36 states and the Federal Capital Territory of Abuja. For our analysis, we adhere to the Database of Global Administrative Areas (GADM) boundaries (https://gadm.org/download-country_v3.html). The sampling frame used for the Nigeria DHS was based on a 2006 national census which identified 664,999 EAs. Data were successfully collected in 1389 EAs, but due to security issues during the survey, a number of EAs were dropped. In particular, estimates for the Admin-1 area of Borno may have been affected (see Appendix A.3 of the DHS report National Population Commission - NPC/Nigeria & ICF, 2019).

The 2015–2016 Malawi DHS used voluntary finger prick blood sampling to collect data on HIV prevalence. We desire estimates of HIV prevalence for each of Malawi’s 28 districts, also referred to as Admin-2 areas. For this survey, the sampling frame was obtained from a 2008 census which identified 12,558 EAs distributed between 56 strata. Ultimately, data were collected from 827 EAs, from which a total of 8,497 women aged 15–49 were eligible for HIV testing. Ultimately, 93% of eligible women were tested, but the HIV test results were anonymised, with volunteers not informed of their results and instead receiving access to educational materials and free counselling and testing (National Statistical Office NSO/Malawi & ICF, 2017).

For both Nigeria and Malawi, the DHS provides GPS coordinates for nearly all EAs, but the locations have been adjusted to maintain privacy by adding small distances at random. Figure 2 provides maps of the small area boundaries and jittered sampled EA locations in Nigeria and Malawi.

![Small area boundaries and jittered enumeration area locations for Nigeria (left) and Malawi (right)](image-url)
Malawi. In Malawi, because the island region of Likoma is disconnected from the mainland and has a very small population, we omit its data from our analysis.

3 Existing Work

As the standard Fay–Herriot model treats $V_i$ as known, a number of extensions and alternative approaches have been proposed to relax the assumption of known sampling variances. In this section, we review area level Fay–Herriot type models that account for unknown sampling variances with both continuous and binary response data. Although proportions are constrained so $p_i \in [0, 1]$, it is common to specify models that treat $p_i$ as continuous, and we discuss such models first. We also discuss other extensions to the Fay–Herriot model that influence our proposed model.

3.1 Variance Smoothing for Continuous Responses

The basic Fay–Herriot model has been extended to account for unknown $V_i$ in a number of ways for continuous response data. Some research has focused on adjusting estimates of mean squared error for Fay–Herriot estimators to account for uncertainty in sampling variances (Kleffe & Rao, 1992; Rivest & Vandal, 2002; Wang & Fuller, 2003). The estimated sampling variances $\hat{V}_i$ are typically assumed to be independent of the direct estimators $\hat{p}_i$.

Building upon this research, other papers have proposed to incorporate modelling of sampling variances into the Fay–Herriot model. The most common strategy is to combine the Fay–Herriot model with a model for the sample-based variance estimators $\hat{V}_i$. As an example, You & Chapman (2006) assume the following sampling model for the variance estimators $\hat{V}_i$:

$$\hat{V}_i \sim \frac{V_i}{d_i} \chi^2_{d_i}$$

(3)

where $d_i$ denotes the degrees of freedom for area $i$. In addition, $\hat{V}_i$ are assumed to be independent of the mean estimators $p_i$. If the response values for area $i$ were independently and identically distributed Gaussian random variables, the above model (3) would hold for the variance estimator $\hat{V}_i = s_i^2 / n_i$ with $d_i = n_i - 1$, where $n_i$ denotes the sample size for area $i$. When responses are sampled at random with replacement within areas, such an assumption may be appropriate, but for complicated sampling schemes, different values of $d_i$ or even alternative models may be necessary. You & Chapman (2006) adopted a hierarchical Bayesian approach and placed inverse Gamma priors on the variance parameters $\sigma^2_u \sim IG(r_0, s_0)$ and $V_i \sim IG(r_i, s_i)$, with $r_i$, $s_i$ chosen to be small for all areas $i = 1, \ldots, m$. Notably, they allow the prior for $V_i$ to vary across areas, which makes the sampling variances $V_i$ independent across areas.

The You and Chapman model builds upon a similar model proposed by Arora & Lahiri (1997) and is representative of similar approaches using scaled chi-squared distributions to model the sampling variance estimators $\hat{V}_i$. These approaches typically differ in the priors placed on the true sampling variances $V_i$ or choices of degrees of freedom $d_i$. Bell (2008) reviews and compares a number of sampling variance modeling approaches.

Maiti et al. (2014) assume the same variance sampling model (3) as You and Chapman, but adopt an empirical Bayes approach, setting the prior $\sigma^2_u \sim IG(r, s)$ and estimating $\{r, s, \sigma^2_u\}$ via maximum likelihood. In addition to modelling $\hat{V}_i$, Hwang et al. (2009) and Dass et al. (2012) noted that assuming a common prior for $V_i$ for all areas $i$ could induce shrinkage in the resulting model-based sampling variance estimates and produce improved interval estimates for the small area parameters of interest. In this vein, Sugasawa et al. (2017) explore different priors for the
sampling variances $V_i$, adopting a fully Bayesian approach to estimation. Alternatively, Polettini (2017) induces shrinkage for the sampling variance estimates using a semiparametric Dirichlet process model with random variances.

3.2 Variance Smoothing for Binary Responses

When response values are binary and the target of estimation is a small area proportion, it may be helpful to account for the mean-variance relationship for the direct estimators $\hat{p}_i$. Generalised variance functions (GVF), which model the functional relationship between the expectation and variance of a survey estimator such as $\hat{p}_i$, can be used as an alternative to linearization-based approximations or resampling methods for estimating $V_i$. If the model used is appropriate, the resulting modelled variance estimates could improve upon the direct variance estimates in terms of precision. An introduction to GVF is provided in Chapter 7 of Wolter (2007).

For estimation of proportions, several GVF-like approaches to variance estimation have been previously proposed based on treating the responses like binomial data. Liu et al. (2004) assume the following model for $V_i$:

$$V_i = p_i (1 - p_i) \text{DEFF}_i$$

where $\text{DEFF}_i$ denotes the design effect, defined as the ratio of the variance of $p_i$ under the implemented survey design to the variance of $p_i$ under simple random sampling. As described in their paper, Liu et al. estimate design effects using available information on sample sizes and survey weights and treat them as known. Model-based estimates of $V_i$ can be produced by replacing the unknown $p_i$ values above with their direct estimators. Hawala & Lahiri (2018) propose a similar GVF for count data. Maples (2016) similarly proposes a GVF for producing variance estimates based on estimating the design effect using additional information about any unequal weighting or clustering in the sampling procedure. Franco & Bell (2013) adopt a different strategy using a GVF to compute an effective sample size for each area of interest, which they use to fit a binomial model.

Mohadjer et al. (2012) similarly use a GVF to produce variance estimates for use in an area level model, assuming the following model:

$$\log\left(\frac{V_i}{p_i^2}\right) = \gamma_0 + \gamma_1 \log(\hat{p}_i) + \gamma_2 \log(1 - \hat{p}_i) + \gamma_3 \log(n_i) + \epsilon_i$$

where $\epsilon_i \sim N(0, \sigma^2)$ and $\hat{p}_i$ denotes a predictor of $p_i$ based on a model dependent solely on auxiliary covariate information and not explicitly on any direct estimates.

The GVF approaches described thus far treat the resulting variance estimates as known, so the resulting Fay–Herriot estimates do not account for uncertainty in the variance model. Maples et al. (2009) address this by combining a GVF with a sampling model for the direct variance estimates. In particular, they assume Model (3) holds for the direct variance estimates $\hat{V}_i$ and then propose the following linking model for $V_i$:

$$V_i | \alpha, \gamma \sim IG(\alpha + 1, \alpha \exp(z_i^T \gamma))$$

where $\alpha$ controls the precision of the variance linking model, $z_i$ are area level covariates and $\gamma$ are corresponding coefficients estimated using an empirical Bayes approach. Maples et al. outline a procedure for using bootstrap sampling to estimate effective sample size for each area, which informs their choice for the degrees of freedom $d_i$ in the variance sampling model. They show
that this model produces smoothed variance estimates that could help to correct underestimation by the direct variance estimators.

As an alternative to modelling heterogeneity in the sampling variances, Hirose et al. (2023) propose a variance-stabilising transformation of the direct estimates $\hat{p}_i$. This approach is similarly based on assuming a mean-variance relationship and designing a particular transformation to remove the effect of the mean-variance relationship. However, Hirose et al. apply the same variance-stabilising transformation for all areas, which prevents any variability in the mean-variance relationship and which could be misspecified. In Section 4, we propose an approach more similar to that of Mohadjer et al., which allows for some variability in the mean-variance relationship through the estimated $\gamma$ parameters and random $\varepsilon$ terms.

3.3 Alternative Sampling and Linking Models

The linking and sampling mean models in the Fay–Herriot approach assume responses are continuous, but because $p_i$ are bounded between 0 and 1, it may be inappropriate to treat $\hat{p}_i$ as Gaussian, especially when $p_i$ is close to 0 or 1 and when $V_i$ is large. In the health and demography setting, Mercer et al. (2015) apply a logit transformation to direct estimates of mortality rates before fitting a Fay–Herriot-type model. More generally, You & Rao (2002) and Sugasawa et al. (2018) propose unmatched sampling and linking models, combining the sampling model given by Equation (1) with an alternative linking model that transforms the finite population parameters of interest $p_i$ to make a Gaussian approximation more appropriate. As an example, Liu et al. (2004) considered the following logit-normal linking model:

$$
\logit(p_i) | \beta, \sigma_u^2 \sim N(x_i^T \beta, \sigma_u^2)
$$

Mohadjer et al. (2012) apply this model to estimation of adult literacy rates. Liu et al. also consider alternative models including a beta-logistic model combining a beta sampling model with the above logistic linking model, which accounts for the limited range of $\hat{p}_i$ but will not reflect its true sampling distribution. Franco & Bell (2013) and Chen et al. (2014) consider binomial sampling models, treating observed area level counts as being drawn from a binomial distribution with size parameter given by some measure of effective sample size. As an alternative to unmatched sampling and linking models, Mercer et al. (2015) describe an approach that uses Gaussian sampling and linking models to model $\logit(\hat{p}_i)$ and $\logit(p_i)$.

3.4 Spatial Area Level Models

The Fay–Herriot model has been extended to incorporate spatial and spatiotemporal random effects (Ghosh et al., 1998; Pratesi & Salvati, 2008). These models leverage similarities between areas that are close in space or time, producing smoothed estimates and accounting for potential spatial or spatiotemporal structure in the response data. Chung & Datta (2020) noted that when informative area level covariate information is unavailable but responses are spatially correlated, using spatial random effects models may be especially effective. In LMICs, covariate information is often limited and spatial random effects are often used in area level and unit level modelling. As an example, Mercer et al. (2015) use an area level model with spatiotemporal random effects to estimate child mortality rates in Tanzania (Mercer et al., 2015).

4 Methods

We assume that for all $i = 1, \ldots, m$, we have direct estimates of area level proportions $\hat{p}_i$ and corresponding variance estimates $\hat{V}_i$. We propose a Bayesian joint model for the full data ($\hat{p}$, $\hat{V}$)
that induces spatial smoothing for both the proportion and variance estimates. Our approach uses two sets of unmatched models, one for the estimated proportions $\hat{p}_i$ and one for the variance estimates $\hat{V}_i$, with these models being linked through the use of a generalised variance function. We use a spatial linking model for the proportions that induces spatial smoothing for both the proportions and the estimated variances.

### 4.1 Mean Model

For modelling the direct estimates $\hat{p}_i$, we use unmatched sampling and linking models, combining a Gaussian sampling model with a spatial logit-Gaussian linking model:

$$\hat{p}_i | p_i, V_i \sim \text{N}(p_i, V_i).$$

$$\text{logit}(p) | \beta, \sigma^2_u, \phi \sim \text{N}(X\beta, \Sigma_{BYM2}(\sigma^2_u, \phi)).$$

In the above, $p_i$ denotes the finite population area-specific proportion and $V_i$ denotes the sampling variance of the direct estimator $\hat{p}_i$. We use the shorthand $\text{logit}(p)$ to denote the vector $(\text{logit}(p_1), \ldots, \text{logit}(p_m))^T$, which we assume is drawn from a multivariate Gaussian distribution with mean $X\beta$, where $X$ is an $m \times (r + 1)$ design matrix containing covariate information and $\beta$ is a $(r + 1)$-vector containing the intercept and corresponding coefficients. Finally, $\Sigma_{BYM2}(\sigma^2_u, \phi)$ denotes a spatial covariance matrix dependent on marginal variance parameter $\sigma^2_u$ and spatial correlation parameter $\phi$. We use the BYM2 model, a reparametrisation of the Besag-York-Mollie (Besag et al., 1991) model proposed by Riebler et al. (2016) which determines the structure of $\Sigma_{BYM2}(\sigma^2_u, \phi)$. Below, we review the BYM2 model, rewriting the mean linking model as follows for clarity:

$$\text{logit}(p) = X\beta + u$$

$$u | \sigma^2_u, \phi \sim \text{N}(0, \Sigma_{BYM2}(\sigma^2_u, \phi)).$$

Under the BYM2 model, we assume $u$ can be partitioned into an unstructured component $\hat{u}_1$ and a structured spatial component $\hat{u}_2$:

$$u = \sigma_u \left( \sqrt{1 - \phi} \hat{u}_1 + \sqrt{\phi} \hat{u}_2 \right)$$

We assume $\hat{u}_1 \sim \text{N}(\mathbf{0}, \mathbf{I})$ is a vector of iid Gaussian random area effects and assume an intrinsic conditional autoregressive (ICAR) Gaussian prior for $\hat{u}_2$. The ICAR prior, as proposed by Besag et al. (1991), assumes that spatial components $\hat{u}_{2i}$ and $\hat{u}_{2j}$, representing the values of $\hat{u}_2$ for areas $i$ and $j$, are correlated if areas $i$ and $j$ are defined to be neighbours. Under an ICAR prior, we assume that for a particular area $i$, the mean of $\hat{u}_{2i}$ is equal to the mean of all neighbouring effects and the precision of $\hat{u}_{2i}$ is proportional to the number of neighbours. Using this parameterization, $\sigma^2_u$ denotes the marginal variance of $u$ and $\phi$ represents the proportion of variation assigned to the spatial component.

Under a BYM2 model, $u$ has the covariance matrix

$$\Sigma_{BYM2}(\sigma^2_u, \phi) = \sigma^2_u((1 - \phi)\mathbf{I} + \phi Q_s)$$

Here, $Q_s$ denotes the precision matrix of $\hat{u}_2$ and $Q_s^*$ is its generalised inverse. Note that the precision matrix implied by the ICAR prior, $Q_s$, is singular, yielding an improper prior. To ensure identifiability, we must place a sum-to-zero constraint on $u$. In order to make the marginal
4.2 Variance Model

We similarly use unmatched models for the corresponding variance estimates \( \hat{V}_i \), using a chi-squared sampling model with a log-normal linking model. We use the chi-squared sampling model described in Equation (3), assuming that for all \( i \), the variance estimate \( \hat{V}_i \) is an unbiased estimator of \( V_i \). The linking model assumes the true log \( \log(V_i) \) values are Gaussian distributed with expected values given by a generalised variance function \( f(p_i; n_i; \gamma) \) whose inputs are the area proportion \( p_i \), sample size \( n_i \), and parameters \( \gamma \). We can write down the unmatched models as follows:

\[
\frac{d_i \hat{V}_i}{V_i} | d_i, V_i \sim \chi^2_{d_i}
\]

\[
\log(V_i) | p_i, n_i, \gamma, \sigma^2_{\tau} \sim N(f(p_i; n_i; \gamma), \sigma^2_{\tau})
\]

Here, \( d_i \) denotes the degrees of freedom parameter for area \( i \), which we determine based on the survey design and sample size as discussed below. We use \( \sigma^2_{\tau} \) to denote the variance of the linking model errors which allow for area-specific deviations from the linking model.

We define the generalised variance function as follows:

\[
f(p_i; n_i; \gamma) = \gamma_0 + \gamma_1 \log(p_i(1 - p_i)) + \gamma_2 \log(n_i).
\]

Note that if we set \( \gamma_0 = 0, \gamma_1 = 1, \gamma_2 = -1 \), the right hand side resembles the logarithm of the binomial variance. As such, this GVF can be viewed as a generalised version of the binomial variance. The GVF used here could also be altered to introduce additional covariates or different functional relationships between \( p_i \) and \( V_i \). We can view the variance linking model (15) as a prior that shrinks the estimate \( \hat{V}_i \) towards a model-based prediction dependent on the binomial mean-variance relationship.

As described above, the mean linking model induces spatial smoothing for estimates \( \hat{P}_i \). By combining the mean and variance models and incorporating the means \( P_i \) into the GVF, we induce spatial correlation into the resulting samples of \( V_i \), potentially aiding estimation in areas with fewer samples. When \( \phi \) is zero, no spatial correlation is induced among the sampling variances reflecting an assumption that the mean-variance relationship for binary responses contributes more to the sampling variance than any residual spatial dependence between the variance parameters after accounting for the underlying prevalence. A potential relaxation of this assumption could assume spatial structure in the sampling variances \( V_i \) beyond that induced by \( P_i \), but there is no clear reason for this residual spatial dependence to exist.

We treat the degrees of freedom parameter \( d_i \) as known for all areas \( i \). The appropriate choice for \( d_i \) depends on the sampling design. As mentioned above, if the data for a given area were iid Gaussian (for example, reflecting simple random sampling with replacement), the typical variance estimator would follow a \( \chi^2 \) distribution with \( d_i = n_i - 1 \) degrees of freedom. However, for sampling without replacement and cluster sampling designs, other choices of \( d_i \) may be more appropriate depending on how \( \hat{V}_i \) is computed for each area. Maples et al. (2009) outline a resampling procedure for estimating degrees of freedom for their variance sampling model. When computing variance estimates from DHS data, we use a simplified variance estimator based on
the with-replacement variance estimator for multistage designs presented in eq. (4.6.2) of Särndal et al. (2003), which is computed as a sum over clusters:

\[
\hat{V}_i = \frac{1}{n_{c(i)}(n_{c(i)} - 1)} \sum_{c \in S_{1i}} \left( \frac{\hat{t}_c}{\pi_c} - \hat{t}_i \right)^2
\]  

where \(S_{1i}\) denotes the set of indices of sampled clusters for area \(i\), \(n_{c(i)}\) denotes the number of sampled clusters, and \(\pi_c\) denotes the probability of sampling cluster \(c\). Finally \(\hat{t}_c\) denotes the direct estimator for the total for cluster \(c\) in area \(i\) and \(\hat{t}_i\) denotes the direct estimator for the total of area \(i\). Because this is a sum of squared error terms over \(n_{c(i)}\) clusters, we set \(d_i\) to be equal to \(n_{c(i)} - 1\).

### 4.3 Estimation

We adopt a fully Bayesian approach to estimation by placing priors on the following hyperparameters:

\[ \{\beta, \sigma_u^2, \phi, \gamma, \sigma_t^2\} \sim \Pi(\theta) \]  

where \(\theta\) denotes any parameters used to specify the priors. Details on the priors used in each example are provided in the Supplement. We compute approximate posterior distributions for \(p_i\) for all areas \(i\) using Markov chain Monte Carlo sampling as implemented in the Stan programming language (Carpenter et al., 2017). Functions for fitting the models described above have been collected in an R package and the code for the below simulations and analysis is available at the associated repository on GitHub. In this context, the Bayesian approach offers a number of potential benefits. In particular, we are able to sample from the joint posterior distributions for the proportions of interest for all areas, giving a natural way to quantify uncertainty and also enabling comparisons between areas. Moreover, the sampling approach implemented in Stan is fast and flexible, enabling users to fit and compare potential models quickly.

### 5 Simulations

#### 5.1 Population Generating Model

We use simulations to evaluate our spatial variance smoothing estimator, comparing its performance with that of the direct weighted Hájek estimator and an estimator derived from a model without variance smoothing. For our simulations, we generate an artificial population that mimics data from the 2018 Nigeria DHS. First, we generate synthetic cluster locations across Nigeria using a pixel grid of estimated population counts for Nigeria in 2006 (mimicking the sampling frame used for the DHS survey) (WorldPop and Center for International Earth Science Information Network (CIESIN), 2006). For each of the 73 strata used for the DHS, we sample 300 pixels without replacement with probability proportional to population. These sampled pixels represent enumeration areas or clusters. For each cluster location, we randomly generate cluster sizes \(N_c \sim \text{Poisson}(10)\), yielding a population of \(N = \sum_c N_c\) individuals.

For each individual \(j\) in our population, we generate data using a population generating model motivated by the models used by Corral et al. (2020) (see section 7.2) and Gao & Wakefield (2022). For each cluster \(c\), we simulate cluster level covariate information as follows:
1. The covariate $x_{1,c}$ is the realised value of a binary random variable $X_{1,c}$ with $P(X_{1,c} = 1) = 0.5$;
2. The covariate $x_{2,c}$ is the realised value of a binary random variable $X_{2,c}$ with $P(X_{2,c} = 1) = 0.3 + 0.5 \frac{i(c)}{37}$, where $i(c)$ is the index of the area containing cluster $c$;
3. The covariate $x_{3,c} = x_{3,i(c)}$ is obtained from a $37 \times 1$ ICAR random vector with marginal variance 1 for the Admin-1 areas.
4. The covariate $x_{4,c} = x_{4,i(c)}$ is obtained from a $774 \times 1$ ICAR random vector with marginal variance 1 for the Admin-2 areas.
5. The covariate $x_{5,c}$ is obtained from a random vector generated using a stochastic partial differential equation (SPDE) -based approximation (Lindgren et al., 2011) to a Gaussian process with Matérn covariance with smoothness parameter 1 and marginal variance of 1.

Maps of these covariates are provided in the Supplement. Based on these covariates, we simulate a cluster level risk parameter $q_c$ for each cluster from the following model:

$$\logit(q_c) = \logit(\mu) + 0.25x_{1,c} - 0.25x_{2,c} + 0.5x_{3,c} + 0.25x_{4,c} + 0.25x_{5,c} + u_{i(c)} + v_c$$

where $u_{i(c)} \sim iid N(0, 0.25^2)$ are independent and identically distributed area level random effects for the area $i$ containing cluster $c$, and $v_c \sim iid N(0, 0.5^2)$ represent independent and identically distributed cluster level effects. In the above, $\mu$ denotes the global superpopulation prevalence. The covariates are held constant for all simulations, but the response variables and random area and cluster effects are resampled for each new simulation. We repeatedly generate $Y_{j|q_{i(j)}} \sim Bernoulli(q_{c(j)})$, where $c(j)$ is the cluster of individual $j$. For each simulation, we can thus compute true population Admin-1 area level proportions $p_i$. We induce spatial dependence in the responses via the covariates $x_{3,c}, x_{4,c}$, and $x_{5,c}$, which are each simulated from multivariate Gaussian models with different spatial correlation structures.

To obtain our simulated samples, we use a cluster sampling design. In each simulation, we sample eight clusters from each stratum, keeping all individuals in sampled clusters. We compute sampling weights $w_j$ for each individual from the corresponding inverse inclusion probabilities.

We compare our unmatched joint smoothing model-based estimator with the direct H’ajek estimator and a number of alternative model-based estimates. First, we consider spatial joint sampling (Spatial Unmatched JS) and non-spatial joint sampling (Unmatched JS) models, where the non-spatial version is obtained by replacing the BYM2 prior for the area effects $u$ with an iid multivariate Gaussian prior. We also consider an estimator produced using a model that omits the variance smoothing model entirely, which we refer to as the mean smoothing (MS) model-based estimator. This model is specified using the unmatched models (8) and (9) but treating $V_i$ as known for all $i$. We consider both spatial (Spatial Unmatched MS) and non-spatial versions (Unmatched MS). For all model-based estimators, we adopt a fully Bayesian approach to inference as described in Section 4. We obtain point estimates $\hat{p}_i$ and 90% credible interval estimates $(l_i, u_i)$ by sampling from these approximate posterior distributions. Further details on the estimation procedure are provided in the Appendix.

For each simulation, we calculate several performance metrics, including root mean squared error (RMSE) and mean absolute error (MAE). We also compute the average coverage of the 90% interval estimates and the mean interval lengths (MIL) across all areas. For a single simulation, these metrics are defined as follows:
\[
\text{RMSE}(\hat{p}_i) = \sqrt{\frac{1}{m} \sum (p_i - \hat{p}_i)^2}
\]  
(20)

\[
\text{MAE}(\hat{p}_i) = \frac{1}{m} \sum |p_i - \hat{p}_i|
\]  
(21)

\[
\text{Cov}_{90}(\hat{p}_i) = \frac{1}{m} \sum 1\{p_i \in (l_i, u_i)\}
\]  
(22)

\[
\text{MIL}_{90}(\hat{p}_i) = \frac{1}{m} \sum (u_i - l_i)
\]  
(23)

We consider two sets of simulations with differing global prevalence rates. We let \(\mu = 0.1\) for the first set, which is similar to the overall HIV positivity rate in the Malawi data. For the second set, we let \(\mu = 0.5\), which is similar to the national MCV-1 vaccination rate in the Nigeria data. Table 1 summarises results for our two sets of simulations. In each setting, the results represent the average values of the metrics (20)–(23) across 1,000 simulated populations. We observe that in the low prevalence examples, the spatial unmatched joint model-based estimates perform best in terms of RMSE and MAE. Moreover, prediction intervals constructed based on the direct estimator and the mean-only smoothing model-based estimators tend to exhibit undercoverage, whereas the joint model-based intervals achieve closer to nominal coverage. In the moderate prevalence examples, the joint model-based estimates perform slightly worse than the mean-only model-based estimates in terms of the RMSE and MAE; however, the Hájek and mean-only model intervals show slight undercoverage. The joint modelling approach thus yields slightly more conservative prediction intervals, which may be desirable for decision making.

Additional simulation results for a scenario in which the responses are spatially independent are provided in the Appendix, indicating that in such a case, the spatial modelling does not improve upon the non-spatial versions of the models.

### 6 Applications

We apply our joint smoothing model-based estimator to two examples involving DHS data, demonstrating its use for a low prevalence indicator (Malawi HIV prevalence rates) and for a moderate prevalence indicator (Nigeria measles vaccination rates). We show that our method

| Method                  | RMSE | MAE  | 90% Cov. | MIL  | RMSE | MAE  | 90% Cov. | MIL  |
|-------------------------|------|------|----------|------|------|------|----------|------|
| Direct (Hájek)          | 3.52 | 2.66 | 83       | 10.27| 6.23 | 4.96 | 85       | 19.46|
| Unmatched MS            | 3.31 | 2.44 | 82       | 8.47 | 6.01 | 4.80 | 83       | 17.12|
| Spatial Unmatched MS    | 3.16 | 2.35 | 82       | 8.32 | 5.82 | 4.66 | 83       | 16.85|
| Unmatched JS            | 3.29 | 2.48 | 86       | 9.03 | 6.58 | 5.30 | 86       | 19.53|
| Spatial Unmatched JS    | 3.12 | 2.37 | 87       | 8.94 | 6.30 | 5.07 | 87       | 19.04|
induces spatial smoothing of estimated variances and produces more conservative interval estimates than an approach using an area level model that only smooths means.

For both examples, we compare direct weighted estimation with the model-based smoothing methods described above. We first fit both the spatial mean smoothing unmatched model (Spatial Unmatched MS), which omits the variance model, as well as the full spatial joint smoothing unmatched model (Spatial Unmatched JS). For all models, we use no covariates and we compute approximate posterior distributions for all area level proportions $p_i$ and obtain corresponding point and interval estimates by sampling from these posteriors.

Figure 3 compares point estimates of MCV-1 coverage rates (top) and the length of interval estimates (bottom) for Admin-1 areas among children aged 12–23 months in Nigeria in 2018. Figure 4 similarly provides point estimates of HIV prevalence rates (top) and the length of interval estimates (bottom) for Admin-1 areas for women aged 15–49 in Malawi, 2015–2016. For both examples, the bottom set of maps illustrates the estimated uncertainty of the direct and model-base estimates using the length of 90% credible intervals. In general, we observe that the point estimates agree well for all three methods. However, we observe some spatial smoothing of the interval lengths, suggesting that the joint smoothing model induces spatial smoothing of the direct estimator variances $V_i$.

Figure 5 provides a scatter plot comparing the model-based 90% credible interval lengths produced by the mean smoothing and joint smoothing models with the design-based 90% confidence interval length associated with the Hájek estimator. Here, we see that for the Malawi example (left), the credible interval lengths are similar for the mean smoothing and joint smoothing models. However, for the Nigeria example (right), the joint smoothing intervals are more conservative when the Hájek intervals are short and narrower when the Hájek intervals are long. In addition to the spatial smoothing of interval lengths seen in Figures 3 and 4, this suggests the joint model can help smooth variance estimates globally.

![Figure 3](image-url)

**Figure 3.** Direct and model-based point estimates (top) and length of corresponding 90% interval estimates (bottom) of vaccination coverage rate for first dose of measles-containing-vaccine (MCV1) among children aged 12–23 months in Nigeria, 2018

International Statistical Review (2023), 91, 3, 493–510
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7 Discussion

Our proposed model-based estimator for small area proportions combines several proposed extensions of the basic Fay–Herriot area level model, including using unmatched linking and sampling models to address the non-Gaussian response data (You & Rao, 2002), incorporating spatial smoothing via correlated random effects in the mean linking model (Pratesi & Salvati, 2008), and introducing a variance smoothing model so that the resulting estimators

Figure 4. Direct and model-based point estimates (top) and length of corresponding 90% interval estimates (bottom) of HIV prevalence rate for women aged 15–49 in Malawi, 2015–2016
exhibit both smoothed means and variances (You & Chapman, 2006; Maiti et al., 2014; Sugasawa et al., 2017). We propose a spatial joint smoothing model and adopt a fully Bayesian approach to estimation, which facilitates quick computation of point and interval estimates. Through simulation and application, we have shown that inferences based on our model can improve upon those based on a model that only incorporates smoothing of means. Interval estimates obtained from our model can correct for the undercoverage seen in models that only smooth means, suggesting our model may more accurately account for uncertainty in estimated variances of direct weighted estimators.

For our clustered binary response data, the variance smoothing model we have adopted may help address undercoverage of interval estimates caused by treating variances of direct weighted estimators as known. However, for other designs and contexts, such a model may be inappropriate. In general, the choice of variance sampling and linking models should depend on a number of factors including any clustering and stratification in the design as well as the distribution and presumed mean-variance relationship of the response variables.

Moreover, we acknowledge that our variance smoothing model is a simplification of the true distribution of design-based variances $V_i$, in particular, the use of a chi-squared distribution for the variance sampling model relies upon the assumption that the direct estimator of variance $\hat{V}_i$ for a particular area $i$ is computed as the sum of several squared Gaussian terms. As our data are non-Gaussian, this assumption may be violated and other sampling models for $\hat{V}_i$, such as a Gaussian model, could be explored in future work. Moreover, within each area, we have assumed that the variance for each stratum is equal, but this assumption may be inappropriate for our data because each area of interest is divided into urban and rural subregions, which may be qualitatively different from one another. Finally, the appropriate number of degrees of freedom $d_i$ depends on the specific design used; using resampling methods like those explored by Maples et al. (2009) to choose $d_i$ may help improve the fit of the variance sampling model.

Although we have presented one approach applied to two different types of problems, in practice, for decision making purposes, different estimation problems may have varying priorities. For example, when implementing targeted vaccination programs, it is important to identify communities with especially low vaccination rates, whereas designing policy for providing resources associated with HIV involves identifying communities with high rates of positivity. Given that the variance of a direct prevalence rate estimator may depend on its expected value, various modelling decisions such as choosing to apply a transformation for $\hat{p}_i$ may lead to
different results depending on the expected value of $\hat{p}_i$. As such, it is crucial to carefully consider the distribution of direct estimators before selecting a model. We have used unmatched sampling and linking models for the area level proportions, but we also considered first computing the logit-transformed direct estimators and then applying matched sampling and linking models treating both $\hat{p}_i$ and $p_i$ as Gaussian random variables. In our simulations and application, this approach did not outperform the unmatched models we adopted, but future research could help illustrate when such an approach could be useful.

When mapping subnational health and demographic indicators in LMICs, unit level models, and in particular geostatistical models using spatial Gaussian processes, are often used as they allow estimates to be generated at arbitrary resolutions and can incorporate unit level covariate information. However, such approaches may often struggle to account for design effects such as those caused by clustering and informative sampling. While unit level models may be able to generate prevalence estimates at the individual cluster level, aggregating those cluster level estimates upwards to produce area level estimates may introduce additional errors and lead to improperly calibrated interval estimates (Fuglstad et al., 2022; Paige et al., 2022a, 2022b). Area level models are specified to generate estimates for a preselected set of regions. Moreover, area level models are often simpler and faster to implement than unit level models. For these reasons, we have explored the feasibility of using area level models to generate maps of health indicators such as vaccination rates and disease prevalence rates in LMICs. Our method, like many area level methods, directly accounts for survey design by incorporating available sampling weight information. By incorporating a spatial variance smoothing model and using unmatched sampling and linking models, we are able to address some of the difficulties related to applying area level models for use in this specific context.

Data availability statement

The data that support the findings of this study are available from the DHS and WorldPop. Restrictions apply to the availability of these data, which were used under license for this study. Data are available at https://dhsprogram.com/data with the permission of the DHS and at https://www.worldpop.org with the permission of WorldPop.

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[Received September 2022; accepted October 2023]