Supplementary Materials to 'Model-Based Inference for Small Area Estimation with Sampling Weights'

Y. Vandendijck^{a,*}, C. Faes^a, R. S. Kirby^b, A. Lawson^c, N. Hens^{a,d}

^aInteruniversity Institute for Biostatistics and statistical Bioinformatics, Hasselt University, Diepenbeek, Belgium

^bDepartment of Community and Family Health, College of Public Health, University of South Florida, Tampa, FL

^cDepartment of Public Health, University of South Carolina, Charleston, SC
^dCentre for Health Economic Research and Modeling Infectious Diseases, Vaccine and
Infectious Disease Institute, University of Antwerp, Wilrijk, Belgium

 ${\it Email address:} \ {\tt yannick.vandendijck@uhasselt.be} \ ({\tt Y. Vandendijck})$

^{*}Corresponding author

1. B-spline Basis Functions

To specify the non-parametric function $f(\cdot)$ in (13) and (14) we make use of penalized splines using B-spline basis functions. We implement B-spline basis functions of degree two with a second order difference penalty. The non-parametric function $f(\cdot)$ is of the form

$$f(\tilde{w}_{ik}) = \sum_{b=1}^{K_B} \theta_b B_b(\tilde{w}_{ik}), \tag{1}$$

where $B_1(\cdot), \ldots, B_{K_B}(\cdot)$ are the B-spline basis functions of degree two (m = 1) (see for example, Eilers and Marx, 1996; or Hastie et al., 2001) and $\theta_1, \ldots, \theta_{K_B}$ are unknown regression coefficients. We take $K_B = 20$. Since $K_B = 20$, we need to define $K_B - 3$ internal knots which are taken at equally spaced quantiles. The smoothness of $f(\cdot)$ is achieved by imposing a penalty on the regression coefficients $\theta_1, \ldots, \theta_{K_B}$ of the form $\lambda \boldsymbol{\theta}^T \mathbf{D}_q^T \mathbf{D}_q \boldsymbol{\theta}$, where λ is a smoothing parameter and \mathbf{D}_q is the q-th order differencing matrix (see for example, Eilers and Marx, 1996).

For fitting purposes, we express (1) in mixed model form. The goal is to express (1) as

$$f(\tilde{\boldsymbol{w}}) = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\alpha},\tag{2}$$

where **X** and **Z** are design matrices, $\boldsymbol{\beta}$ are fixed effects parameters and $\boldsymbol{\alpha}$ are random effects parameters with $\alpha_b \sim \mathcal{N}(0, \sigma_\alpha^2)$, for $b = 1, \ldots, K_B - 2$. Set $\boldsymbol{\Omega} = \mathbf{D}_q^T \mathbf{D}_q$, where $\boldsymbol{\Omega}$ is thus a $K_B \times K_B$ matrix. It follows from the penalized spline literature (Ruppert et al., 2003) that $\mathrm{rank}(\boldsymbol{\Omega}) = K_B - 2$. The eigendecomposition of $\boldsymbol{\Omega}$ is of the form $\boldsymbol{\Omega} = \mathbf{V}\mathbf{D}\mathbf{V}^T$, where \mathbf{D} is a diagonal matrix with the eigenvalues on the main diagonal and \mathbf{V} contains the corresponding normalized eigenvectors such that $\mathbf{V}\mathbf{V}^T = \mathbf{I}$. \mathbf{D} contains exactly $K_B - 2$ positive entries and two zero entries on its main diagonal. Let \mathbf{D}_Z be the $(K_B - 2) \times (K_B - 2)$ submatrix of \mathbf{D} corresponding to these positive entries. In addition, define $\mathbf{V} = [\mathbf{V}_X | \mathbf{V}_Z]$ where \mathbf{V}_X corresponds with the columns of \mathbf{V} with the zero eigenvalues and \mathbf{V}_Z corresponds with the columns of \mathbf{V} with the positive eigenvalues. The design matrices in (2) are given by

$$X = BV_X$$
 and $Z = BV_ZD_Z$, (3)

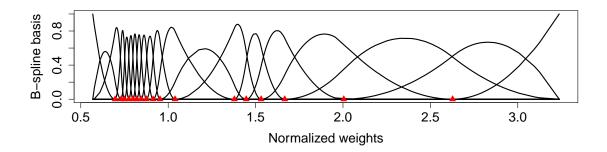
where **B** is a matrix with (i, b)th entry $B_{ib} = B_b(\tilde{w}_{ik})$. The matrix \mathbf{BV}_X is a basis for the space of straight lines and we can thus simplify by setting

 $\mathbf{X}_i = [1 \ \tilde{w}_{ik}]$. Expression (2) can now be written as

$$f(\tilde{w}_{ik}) = \beta_0 + \tilde{w}_{ik}\beta_w + \sum_{b=1}^{K_b - 2} \alpha_b z_b(\tilde{w}_{ik}), \tag{4}$$

where $z_b(\tilde{w}_{ik})$ corresponds with (i, b)th entry of **Z**. Expression (4) corresponds with equation (17) in the manuscript.

In Figure 1 we present the B-spline basis and the \mathbf{Z} matrix basis for a randomly generated dataset in the simulation study.



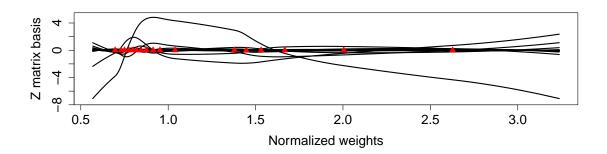


Figure 1: Representation of the B-spline basis and the \mathbf{Z} matrix basis for a randomly generated dataset in the simulation study. The internal knots are shown as solid triangles.

2. Software Implementation

The Bayesian hierarchical model for the outcomes (12) - (17) and the multinomial model (20) described in Sections 3.1 and 3.2 are fit using the integrated nested Laplace approximations (INLA) approach by Rue et al. (2009). INLA yields a computationally convenient alternative to Markov chain Monte Carlo (MCMC) techniques. This method combines Laplace approximations and numerical integration in a very efficient manner to carry out a Bayesian analysis. A multinomial likelihood, needed to fit the multinomial model (20), is not directly available in INLA. Instead, we employ the multinomial-Poisson transformation of Baker (1994) to fit model (20). We used R version 3.1 to fit the models using the INLA package (Martino and Rue, 2009).

We recommend representing the survey data as binomial data where the grouping is done on the small areas and on the unique values of the weights (the strata). The hierarchical models (12)-(14) using the random walk of order one (RW1) are fit by the following code:

```
formula = (y \sim f(wn, model="rw1", scale.model=TRUE, hyper= list( prec = list( prior="loggamma", param=c(1,0.01)))) + f(region.unstruct, model="iid", param=c(0.5,0.008)) + f(region.struct, model="besag", graph=graph.loc, param=c(0.5,0.008))) inla(formula, family="binomial", data=surveydata, Ntrials=n, control.predictor=list(compute=TRUE, link=1), control.compute=list(config=TRUE))
```

The variables region.unstruct and region.struct are identical and include indices for the different (small) areas. In the formulation of the random walk we specify scale.model=TRUE to ensure that the model fit is unaffected by the scaling of the weights (Sørbye, 2013). The graph.loc is a graph-file including the neighbourhood structure of the area under research.

The hierarchical models (12)-(14) using the penalized splines are fit by the following code:

```
formula = (y ~ f(idnum, model="z", Z=ZSpline,
  initial=5, param=c(1,0.01))
  + f(region.unstruct, model="iid", param=c(0.5,0.008))
  + f(region.struct, model="besag", graph=graph.loc,
  param=c(0.5,0.008)) )
inla(formula, family="binomial", data=surveydata, Ntrials=n,
```

```
control.predictor=list(compute=TRUE, link=1), control.compute=list(config=TRUE)) The vector idnum is a sequence from 1 to \sum_{k=1}^K L_k.
```

To fit the sample cell counts n_{lk} and predict the N_{lk} , model (20) is fit using the following code (see www.r-inla.org for more information on fitting multinomial data with INLA):

```
formula = (n \sim -1 + f(idx, model="iid", hyper = list(prec = list(initial = log(0.0001), fixed = TRUE))) + f(jdx, x, model="iid", constr = FALSE, hyper = list(prec = list(initial = log(0.0001), fixed = TRUE)))) mod.N = inla(formula, family = "poisson", data = surveydata, control.predictor=list(compute=TRUE,link=1), control.compute = list(config=TRUE))
```

The vector idx includes indices of the different small areas, the vector jdx is a sequence from 1 to $\sum_{k=1}^{K} L_k$ and the vector x is a vector of ones.

To obtain the \hat{p}_{lk^*} in the off-sample areas we use expression (18) in the manuscript. The values \hat{p}_{lk^*} are then calculated using the posterior distributions of the parameters. Predicting the values \hat{p}_{lk^*} in this manner properly accounts for the spatial structure of the data which is modelled using the random effect v (Gomez-Rubio et al., 2010). Sampling from the posterior distributions is done by using the inla.posterior.sample() function.

R-code to fit models (5)-(10) is based on the code available at http://faculty.washington.edu/jonno/software.html as described in Mercer et al. (2014).

The ICAR model given in equation (6) of the manuscript can be rewritten as an intrinsic Gaussian Markov random field (IGMRF). This means that the joint distribution of $\mathbf{v} = (v_1, \dots, v_K)^T$ can be written as

$$\pi\left(\mathbf{v}|\sigma_v^2\right) \propto \exp\left(-\frac{1}{2\sigma_v^2}\sum_{k\sim k'}(v_k-v_{k'})^2)\right),$$

where the sum goes over all pairs of adjacent areas $k \sim k'$. This can be written in the form

$$\pi\left(\mathbf{v}|\sigma_v^2\right) \propto \exp\left(-\frac{1}{2\sigma_v^2}\mathbf{v}^T\mathbf{R}\mathbf{v}\right),$$

where **R** is a so-called structure matrix. For the ICAR model given in equation (6) the diagonal entries of **R** are equal to m_k and the off-diagonal elements are equal to -1 if $k \sim k'$ and zero otherwise (Gelfand et al., 2010; Schrödle and Held, 2011).

As mentioned in the manuscript, to ensure identifiability of the overall intercept β_0 , a sum-to-zero constraint is set on the random effects v_k . In INLA this is done by writing the density of the IGMRF as the density of a proper GMRF under the linear constraint

$$\pi \left(\mathbf{v} | \mathbf{A} \mathbf{v} = \mathbf{e} \right),$$

where for the ICAR model for \mathbf{v} the components of the linear constraint are $\mathbf{A} = (1, ..., 1)$ and $\mathbf{e} = 0$, i.e. all random effects v_k sum up to zero. Sampling from this GMRF using this linear constraint is done using techniques described in Rue (2001), Rue and Held (2005) and Rue et al. (2009). The basis for the sampling procedure is the Cholesky factorization of the precision matrix of the GMRF above.

3. R-code and Simulated Dataset

We have added a simulated dataset ('survey_data_YV_et_al_SpatialStatistics .txt' and 'arrond_data_YV_et_al_SpatialStatistics.txt'). The R-code ('Rcode_main _YV_et_al_SpatialStatistics.R' and 'Rcode_source_YV_et_al_SpatialStatistics.R') to fit the models described in the manuscript are also available in the online Supplementary Materials of this manuscript. The HIS dataset used for the real data application cannot be provided since these data cannot be made publicly available.

The simulated dataset is generated according to simulation model (P5) combined with the sampling model (S3). The simulated dataset contains 4806 responses obtained from 40 of the 43 districts of Belgium. In Figure 2, we present the boxplot of the predicted prevalences by district using the different estimators. In Figure 3, we present a map with the predicted prevalences using the model based approach (13) with a penalized spline model.

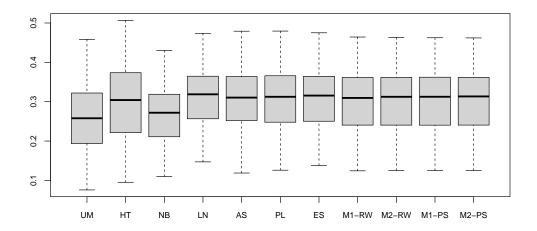


Figure 2: Boxplots of the predicted prevalences by district using different estimators for a simulated dataset generated according to simulation model (P5) combined with the sampling model (S3).

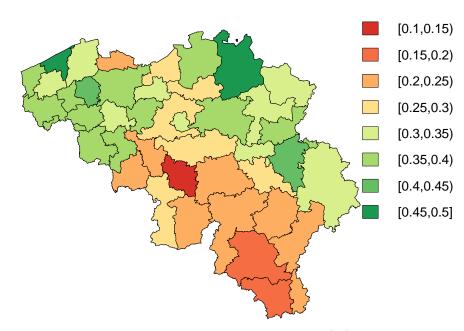


Figure 3: Predicted prevalences using the model based approach (13) with a penalized spline model.

4. Simulation Study: Calculation of Survey Weights

The survey design weight, w_{ik}^d , of a sampled individual i of area k is equal to the inverse of the probability of inclusion π_{ik} of this individual in the sample. Thus $w_{ik}^d = 1/\pi_{ik}$. As presented in Section 4 of the manuscript, the sample design for the simulation study has the following relevant components: (1) selecting districts from which samples are drawn; and (2) selecting individuals from the districts selected in the previous step. The probability of inclusion is thus given by

$$\pi_{ik} = \pi_k^{(1)} \times \pi_{ik}^{(2)},\tag{5}$$

where $\pi_k^{(1)}$ is the probability of selecting the kth district and $\pi_{ik}^{(2)}$ is the conditional probability (given that district k is sampled) of selecting the ith individual to the sample.

We sample n_{area} (39,40,41,42,43) from the 43 districts with probability-proportional-to-size sampling where the size variables are the population sizes of the districts. In this manner, districts with a large population size are sampled with probability one, whereas districts with a small population size have a probability smaller than one. The probabilities $\pi_k^{(1)}$ are presented in Table 1. It can be observed that, of course, the probabilities depend on the value of n_{area} . For completeness, we present in Figure 4 a map presenting the indices of the districts in Belgium.

At the second stage, n_k individuals are sampled in the selected districts using the hypothetical sampling proportions in different age groups and gender as presented in Table 2 of the manuscript. Let us focus, for example, on scenario (S3). An individual i belonging to the male group of [0-20[-year-olds has a conditional probability of

$$\pi_{ik}^{(2)} = \frac{n_k \times 0.16}{N_L^{male,[0-20]y}} \tag{6}$$

of being sampled. An individual i belonging to the female group of [50-65[-year-olds has a conditional probability of

$$\pi_{ik}^{(2)} = \frac{n_k \times 0.06}{N_k^{female,[50-65]y}}.$$
(7)

of being sampled. The conditional probabilities $\pi_{ik}^{(2)}$ are calculated in a similar manner for the other age groups in Table 2 of the manuscript and also for

scenarios (S2) and (S4). For scenario (S1), the simple random sampling approach, the conditional probability for an individual i is just

$$\pi_{ik}^{(2)} = \frac{n_k}{N_k}. (8)$$

The survey design weights, w_{ik}^d , are adjusted with a post-stratification factor f_{ps} to form the final weights used in the analysis, namely $w_{ik} = w_{ik}^d \times f_{ps}$, with the strata of the post-stratification defined by the age-groups [0-10[, [10-20[, [20-30[, [30-40[, [40-50[, [50-60[, [60-70[, [70-80[, 85+ and gender in the total population.

Table 1: Probabilities $\pi_k^{(1)}$ when n_{area} districts from the 43 districts are sampled with probability-proportional-to-size where the size variables are the population sizes of the districts

stricts.		7.5	7.5	7.5	7.5	
District	Population	$\pi_k^{(1)}$ when				
index	size	$n_{area} = 39$	$n_{area} = 40$	$n_{area} = 41$	$n_{area} = 42$	$n_{area} = 43$
11	931567	1.000	1.000	1.000	1.000	1.000
21	811076	1.000	1.000	1.000	1.000	1.000
62	584398	1.000	1.000	1.000	1.000	1.000
23	560138	1.000	1.000	1.000	1.000	1.000
44	496608	1.000	1.000	1.000	1.000	1.000
24	458265	1.000	1.000	1.000	1.000	1.000
52	420214	1.000	1.000	1.000	1.000	1.000
13	407672	1.000	1.000	1.000	1.000	1.000
71	384503	1.000	1.000	1.000	1.000	1.000
25	352018	1.000	1.000	1.000	1.000	1.000
12	306413	1.000	1.000	1.000	1.000	1.000
92	283793	1.000	1.000	1.000	1.000	1.000
34	277786	1.000	1.000	1.000	1.000	1.000
31	271437	1.000	1.000	1.000	1.000	1.000
63	266334	1.000	1.000	1.000	1.000	1.000
41	262337	1.000	1.000	1.000	1.000	1.000
53	249153	1.000	1.000	1.000	1.000	1.000
46	224356	1.000	1.000	1.000	1.000	1.000
72	220231	1.000	1.000	1.000	1.000	1.000
73	190051	1.000	1.000	1.000	1.000	1.000
42	186553	1.000	1.000	1.000	1.000	1.000
55	174142	1.000	1.000	1.000	1.000	1.000
56	146253	1.000	1.000	1.000	1.000	1.000
35	142946	1.000	1.000	1.000	1.000	1.000
36	140684	1.000	1.000	1.000	1.000	1.000
57	140673	1.000	1.000	1.000	1.000	1.000
45	114390	1.000	1.000	1.000	1.000	1.000
33	104320	1.000	1.000	1.000	1.000	1.000
61	100543	1.000	1.000	1.000	1.000	1.000
91	100298	1.000	1.000	1.000	1.000	1.000
37	88034	0.989	1.000	1.000	1.000	1.000
43	79428	0.893	1.000	1.000	1.000	1.000
51	79372	0.892	1.000	1.000	1.000	1.000
54	70016	0.787	0.885	1.000	1.000	1.000
64	68767	0.773	0.869	0.994	1.000	1.000
93	61733	0.694	0.780	0.893	1.000	1.000
38	56751	0.638	0.717	0.821	0.963	1.000
84	55743	0.626	0.704	0.806	0.946	1.000
81	52301	0.588	0.661	0.756	0.888	1.000
83	50911	0.572	0.643	0.736	0.864	1.000
85	48692	0.547	0.615	0.704	0.826	1.000
32	48082	0.540	0.607	0.695	0.816	1.000
82	41103	0.462	0.519	0.594	0.697	1.000

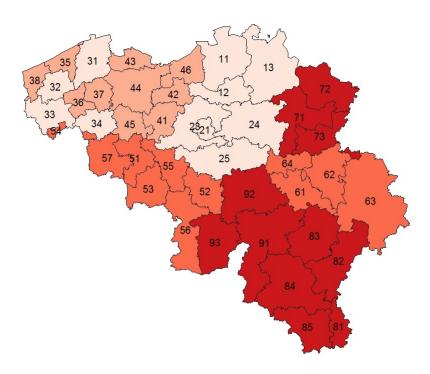
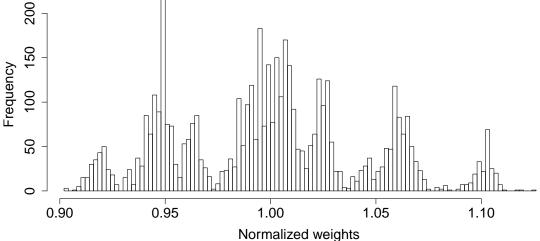


Figure 4: Map presenting the indices of the districts in Belgium.

5. Simulation Study: Histograms of Simulated Weights

In this section we present histograms of the distribution of the generated weights for all sampling scenarios for one randomly generated dataset in the simulation study (Figures 5 - 8). The histograms of the normalized weights \tilde{w}_{ik} are presented. The values of the generated weights for this dataset vary between 0.90 and 1.12 for scenario (S1), between 0.43 and 7.88 for scenario (S2), between 0.57 and 3.24 for scenario (S3) and between 0.55 and 1.93 for scenario (S4). The shapes of the histograms and the ranges of the normalized weights are fairly similar for other generated datasets.



Histogram of normalized weights for scenario (S1)

Figure 5: Histogram of the normalized weights \tilde{w}_{ik} for one randomly generated dataset under sampling scenario (S1).

Histogram of normalized weights for scenario (S2)

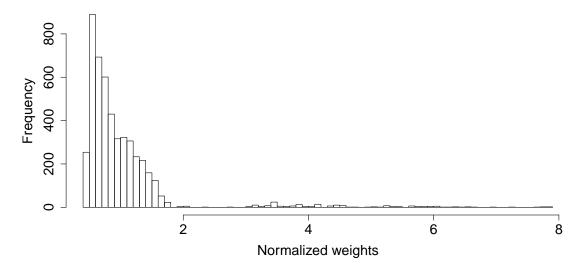


Figure 6: Histogram of the normalized weights \tilde{w}_{ik} for one randomly generated dataset under sampling scenario (S2).

Histogram of normalized weights for scenario (S3)

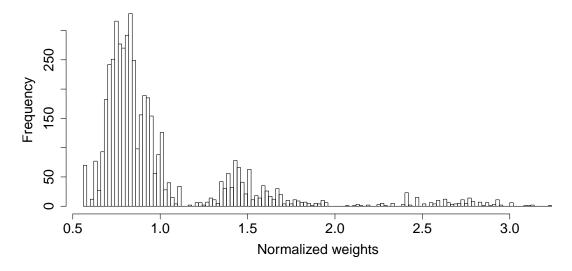


Figure 7: Histogram of the normalized weights \tilde{w}_{ik} for one randomly generated dataset under sampling scenario (S3).

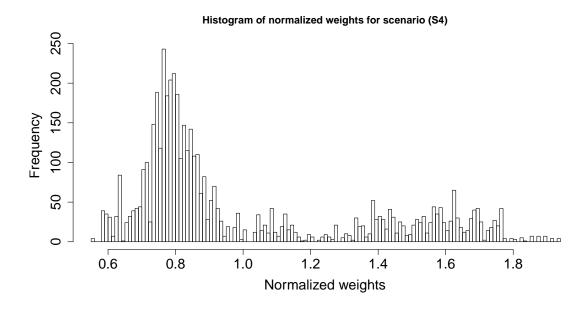


Figure 8: Histogram of the normalized weights \tilde{w}_{ik} for one randomly generated dataset under sampling scenario (S4).

6. Simulation Study: Extra Results for (P1), (P2) and (P3)

In this section we present the results of the nominal coverage and average length of the 95% credible intervals (CIs) which are shown in Table 2. The HT estimator has a nominal coverage around 95% for all scenarios. The unweighted mean and naive binomial have poor coverages for the combinations (P2) and (P3) with (S2) and (S3) due to the bias of the estimators in these settings. The nominal coverage of the LN, AS, PL and ES methods are above 95% for almost all scenarios. The proposed model-based approach using the random walk does not perform well for some scenarios. The model-based approach using the penalized splines, on the other hand, has an overcoverage. Despite this overcoverage, the average lengths of the CIs of the model-based approach performing well in terms of coverage is smaller than the length of the HT estimator CIs.

Table 2: The nominal coverage and length of the 95% credible intervals for 11 estimators based on 100 simulated datasets using the prevalence models (P1), (P2), (P3) and the four sampling scenarios. The results are averaged over all districts.

НТ NB LN M2 $\overline{M1}$ M2 M1RW1 RW1PSPSNominal coverage (P1) (S1) 0.96 1.00 1.00 0.99 1.00 1.00 1.00 1.00 1.00 1.00 (P1) (S2)0.960.95 1.00 0.98 0.96 0.98 0.980.990.991.00 1.00 (P1) (S3) 0.96 0.95 1.00 0.99 0.98 1.00 1.00 0.99 0.99 1.00 1.00 (P1) (S4)0.96 0.96 1.00 1.00 0.99 1.00 1.00 1.00 1.00 1.00 1.00 (P2) (S1) 0.95 0.95 1.00 0.991.00 0.99 0.990.99 1.00 1.00 0.99 (P2)0.70 (S2)0.94 0.14 0.96 0.92 0.96 0.95 0.840.94 1.00 1.00 (P2)(S3)0.840.95 0.570.990.96 0.990.990.980.99 1.00 1.00 (P2) (S4)0.94 0.95 0.98 1.00 0.98 1.00 0.99 0.98 0.98 0.98 0.98 (P3) (S1) 0.96 0.96 1.00 1.00 0.99 1.00 1.00 1.00 0.99 0.990.99(P3) 0.74 0.96 (S2)0.94 0.18 0.96 0.92 0.95 0.85 0.93 1.00 1.00 (P3) (S3) 0.96 0.99 0.99 0.870.64 0.96 0.990.98 0.991.00 1.00 (P3) 0.99 0.99 (S4) 0.96 0.98 0.99 0.99 0.98 0.99 0.99 0.95 1.00 Average length (S1) 0.08 0.08 0.13 0.08 0.08 0.08 0.08 0.08 0.08 (P1) 0.180.18 0.09 (P1) (S2)0.180.210.07 0.09 0.13 0.090.09 0.090.08 0.08 (P1) (S3) 0.18 0.19 0.07 0.08 0.13 0.08 0.08 0.09 0.08 0.08 0.08 (P1) (S4)0.180.190.08 0.08 0.130.08 0.08 0.08 0.08 0.08 0.08 (P2) 0.21 0.09 0.09 0.09 (S1)0.21 0.09 0.14 0.11 0.110.100.10 (P2) (S2) 0.19 0.26 0.12 0.15 0.12 0.12 0.13 0.150.14 0.08 0.13 (P2) 0.20 (S3) 0.23 0.090.10 0.10 0.100.130.120.120.150.13(P2) (S4)0.20 0.22 0.09 0.10 0.15 0.10 0.10 0.110.11 0.11 0.11(P3) 0.20(S1)0.200.090.08 0.140.09 0.09 0.100.100.10 0.10 (P3) (S2) 0.18 0.25 0.08 0.11 0.12 0.12 0.12 0.12 0.14 0.120.13 (P3) (S3)0.19 0.22 0.08 0.10 0.140.10 0.10 0.120.120.11 0.11(P3) 0.10(S4)0.19 0.21 0.08 0.09 0.14 0.09 0.09 0.100.100.10

7. Simulation Study: Sensitivity to Prior Distributions

To investigate the sensitivity of our proposed methods to the choice of prior distribution of the precision parameters, we vary the priors and compare the prevalence estimates. In addition to the Gamma(0.5, 0.008) priors on the precisions σ_u^{-2} and σ_v^{-2} , we also consider the priors Gamma(2.0, 0.4), Gamma(0.3, 0.001) and a flat prior on the log precision scale. The Gamma priors yield a 95% range on the σ_u and σ_v scale of (0.27, 1.29) and (0.02, 17.72), respectively. For σ_w^{-2} and σ_α^{-2} , we also consider the priors Gamma(2.0, 0.4), Gamma(0.3, 0.001) and a flat prior on the log precision scale while keeping the priors for σ_u^{-2} and σ_v^{-2} at the original choice of Gamma(0.5, 0.008). For each prior setting, we calculate the averaged squared deviation of the small area prevalence estimates with the estimates of the original prior choices given in Section 3.1 of the manuscript, namely

$$\frac{1}{K} \sum_{k=1}^{K} \left(\bar{p}_k^o - p_k^* \right)^2, \tag{9}$$

where \bar{p}_k^o and p_k^* are the estimated prevalences in area k using the original and modified prior settings, respectively. In Table 3 we report these deviations for one simulated dataset using scenario (P5) combined with (S3). We observe that the estimated small area prevalences are insensitive to the chosen priors. Assessing the sensitivity to prior distributions for other simulated datasets and under different data simulation scenarios yields similar results.

Table 3: The averaged squared deviations of small area prevalence estimates of modified prior settings with the original prior settings for σ_u , σ_v and σ_w . The results are obtained from one simulated dataset using scenario (P5) combined with (S3). (M1: model-based model 1; M2: model-based model 2)

0.0 0.0	9.4e-7 $9.2-7$	8.1e-7 $9.8e-7$	3.8e - 6		5.8e - 5	5.8e-5 5.5e-5	5.8e-5 5.5e-5 8.6e-7	5.8e-5 5.5e-5 8.6e-7 4.9e-6	5.8e-5 5.5e-5 8.6e-7 4.9e-6 5.5e-7	5.8e - 5 5.5e - 5 8.6e - 7 4.9e - 6 5.5e - 7 3.2e - 6	5.8e - 5 5.5e - 5 8.6e - 7 4.9e - 6 5.5e - 7 3.2e - 6	5.8e - 5 5.5e - 5 8.6e - 7 4.9e - 6 5.5e - 7 3.2e - 6 9.1e - 8	5.8e-5 5.5e-5 5.6e-7 4.9e-6 3.5e-7 3.2e-6 3.1e-8 4.2e-6
0.0													
0.0	9.7e - 7	4.2e - 7	5.7e - 6	5.76-5	5	5.1e-5	5.1e-5 9.1e-7	5.1e-5 9.1e-7 4.0e-6	5.1e-5 9.1e-7 4.0e-6 8.3e-7	5.1e-5 9.1e-7 4.0e-6 8.3e-7 2.2e-7	5.1e-5 9.1e-7 9.1e-7 4.0e-6 8.3e-7 2.2e-7 9.8e-8	5.1e-7 9.1e-7 4.0e-6 8.3e-7 2.2e-7 9.8e-8 1.4e-7	5.11e-5 9.11e-7 4.0e-6 8.3e-7 2.2e-7 9.8e-8 1.4e-7 7.1e-6
$\operatorname{Gamma}(1.0,0.01)$	Gamma(1.0,0.01)	Gamma(1.0,0.01)	Gamma(1.0,0.01)	Gamma(1.0,0.01)	` ` `	$\operatorname{Gamma}(1.0,0.01)$	$\begin{array}{l} \operatorname{Gamma}(1.0,0.01) \\ \operatorname{Gamma}(1.0,0.01) \end{array}$	Gamma $(1.0,0.01)$ Gamma $(1.0,0.01)$ Gamma $(1.0,0.01)$	Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(1.0,0.01)	Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(2.0,0.4)	Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(2.0,0.01) Gamma(2.0,0.4) Gamma(0.3,0.001)	Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(0.3,0.001)	Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(0.3,0.001) Gamma(1.0,0.01) Gamma(1.0,0.01)
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Gamma(0)	Gamma(0)	Gamma(0	Gamma(2	Gamma(2		Gamma(2	Gamma(2 Gamma(0	Gamma(2 Gamma(0 Gamma(0	Gamma(2 Gamma(0 Gamma(0 Gamma(0	Gamma(2. Gamma(0 Gamma(0 Gamma(0 Gamma(0	Gamma(0 Gamma(0 Gamma(0 Gamma(0 Gamma(0 Gamma(0	Gamma(2) Gamma(0) Gamma(0) Gamma(0) Gamma(0) Gamma(0) flat prior	Gamma(2) Gamma(0) Gamma(0) Gamma(0) Gamma(0) flat prior
	0.0	Gamma(0.5,0.008) $Gamma(1.0,0.01)$ $Gamma(2.0,0.4)$ $Gamma(1.0,0.01)$	Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01)	Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01) Gamma(0.5,0.008) Gamma(1.0,0.01)	Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01) Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01)	Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01) Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01)	Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01) Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01) Gamma(0.5,0.008) Gamma(1.0,0.01)	Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01) Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01) Gamma(0.3,0.001) Gamma(1.0,0.01) Gamma(0.5,0.008) Gamma(1.0,0.01) Gamma(2.0,0.4) Gamma(1.0,0.01)	Gamma(0.5,0.008) Gamma(1.0,0.01) 0.0 0.0 0.0 Gamma(2.0,0.4) Gamma(1.0,0.01) 9.7e-7 6.7e-7 9.4e-7 Gamma(0.3,0.001) Gamma(1.0,0.01) 4.2e-7 7.5e-7 8.1e-7 Gamma(0.5,0.008) Gamma(1.0,0.01) 5.7e-6 5.4e-5 6.8e-6 Gamma(0.3,0.001) Gamma(1.0,0.01) 5.1e-5 5.5e-5 5.8e-5 Gamma(0.5,0.008) Gamma(1.0,0.01) 9.1e-7 1.1e-6 8.6e-7 Gamma(2.0,0.4) Gamma(1.0,0.01) 4.0e-6 2.3e-6 4.9e-6 Gamma(0.3,0.001) Gamma(1.0,0.01) 8.3e-7 1.2e-6 6.5e-7	Gamma(0.5,0.008) Gamma(1.0,0.01) 0.0 0.0 0.0 0.0 Gamma(2.0,0.4) Gamma(1.0,0.01) 9.7e_7 6.7e_7 9.4e_7 Gamma(0.5,0.004) Gamma(1.0,0.01) 9.7e_7 7.5e_7 8.1e_7 Gamma(0.5,0.08) Gamma(1.0,0.01) 5.7e_6 5.4e_5 6.8e_6 Gamma(2.0,0.4) Gamma(1.0,0.01) 5.7e_5 5.6e_5 5.8e_5 Gamma(0.5,0.08) Gamma(1.0,0.01) 9.1e_7 1.1e_6 8.6e_7 Gamma(0.5,0.04) Gamma(1.0,0.01) 8.3e_7 1.2e_6 6.5e_7 Gamma(0.3,0.001) Gamma(1.0,0.01) 8.3e_7 1.2e_6 6.5e_7 Gamma(0.5,0.008) Gamma(2.0,0.4) 3.2e_6 6.5e_7 3.2e_6	Gamma(0.5,0.008) Gamma(1.0,0.01) 0.0 0.0 0.0 Gamma(2.0,0.4) Gamma(1.0,0.01) 9.7e-7 6.7e-7 9.4e-7 Gamma(0.3,0.01) Gamma(1.0,0.01) 5.7e-6 5.4e-5 6.8e-6 Gamma(0.5,0.08) Gamma(1.0,0.01) 5.7e-5 5.6e-5 5.8e-5 Gamma(0.3,0.04) Gamma(1.0,0.01) 5.1e-5 5.5e-5 5.5e-5 Gamma(0.5,0.04) Gamma(1.0,0.01) 9.1e-7 1.1e-6 8.6e-7 Gamma(0.5,0.004) Gamma(1.0,0.01) 8.3e-7 1.2e-6 6.5e-7 Gamma(0.5,0.008) Gamma(2.0,0.4) 2.2e-7 1.7e-7 3.2e-6 Gamma(0.5,0.008) Gamma(0.3,0.001) 9.8e-8 2.0e-7 9.1e-8	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

8. Simulation Study: Off-sample Results

In this section we present the simulation results for the off-sample areas separately. As discussed in Section 4 of the manuscript, we generate in each simulated dataset zero to four off-sample areas. In the S=100 simulations we generated in this manner there was a total of 214 off-sample areas. The MSE, bias and coverage results of the estimates of these off-sample areas are presented in Tables 4-7. We present these results separately to be able to evaluate the described approaches with respect to predictions in areas where no data is available. In this manner an evidence evaluation of the proposed method to estimate the prevalence in off-sample areas is given. The conclusion from these results are similar to the conclusion presented in Section 4.2 of the manuscript.

Table 4: The average squared bias and mean squared error for 11 estimators based on 100 simulated datasets using the prevalence models (P1), (P2), (P3) and the four sampling scenarios. These results are based on the estimates of the off-sample areas in the simulation study.

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		UM	НТ	NB	LN	AS	PL	ES	M1	M2	M1	M2
									RW1	RW1	$_{\mathrm{PS}}$	$_{\mathrm{PS}}$
Bias^2	$(\times 10^{3})$											
(P1)	(S1)			0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01
(P1)	(S2)			0.01	0.05	0.01	0.01	0.01	0.00	0.22	0.00	0.01
(P1)	(S3)			0.00	0.02	0.01	0.00	0.00	0.00	0.01	0.00	0.00
(P1)	(S4)			0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00
(P2)	(S1)			0.07	0.07	0.04	0.06	0.06	0.07	0.07	0.07	0.07
(P2)	(S2)			3.89	0.09	0.07	0.07	0.07	0.62	0.14	0.13	0.13
(P2)	(S3)			1.67	0.09	0.06	0.08	0.07	0.13	0.09	0.08	0.08
(P2)	(S4)			0.20	0.06	0.04	0.05	0.05	0.08	0.06	0.06	0.06
(P3)	(S1)			0.09	0.09	0.04	0.07	0.07	0.08	0.08	0.08	0.08
(P3)	(S2)			2.96	0.09	0.04	0.06	0.06	0.55	0.22	0.11	0.10
(P3)	(S3)			1.19	0.09	0.03	0.06	0.06	0.10	0.06	0.06	0.05
(P3)	(S4)			0.13	0.07	0.03	0.05	0.05	0.08	0.06	0.05	0.05
MSE	$(\times 10^{3})$											
(P1)	(S1)			0.05	0.05	0.18	0.05	0.05	0.05	0.05	0.05	0.05
(P1)	(S2)			0.04	0.11	0.17	0.07	0.08	0.06	0.69	0.05	0.05
(P1)	(S3)			0.04	0.07	0.14	0.06	0.06	0.08	0.15	0.06	0.06
(P1)	(S4)			0.03	0.06	0.15	0.04	0.04	0.08	0.07	0.04	0.04
(P2)	(S1)			0.14	0.13	0.25	0.13	0.12	0.14	0.14	0.14	0.14
(P2)	(S2)			3.93	0.19	0.40	0.22	0.21	0.80	0.42	0.19	0.20
(P2)	(S3)			1.72	0.20	0.35	0.20	0.19	0.28	0.22	0.17	0.16
(P2)	(S4)			0.25	0.12	0.23	0.11	0.11	0.20	0.13	0.13	0.14
(P3)	(S1)			0.14	0.14	0.20	0.12	0.12	0.13	0.13	0.13	0.13
(P3)	(S2)			3.00	0.20	0.41	0.20	0.20	0.83	0.45	0.17	0.16
(P3)	(S3)			1.23	0.17	0.21	0.15	0.15	0.47	0.14	0.11	0.11
(P3)	(S4)			0.17	0.13	0.22	0.11	0.11	0.27	0.14	0.13	0.13

Table 5: The average squared bias and mean squared error for 11 estimators based on 100 simulated datasets using the prevalence models (P4), (P5), (P6) and the four sampling scenarios. These results are based on the estimates of the off-sample areas in the simulation study.

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		UM	$_{ m HT}$	NB	LN	AS	PL	ES	M1	M2	M1	M2
									RW1	RW1	$_{\mathrm{PS}}$	$_{\mathrm{PS}}$
Bias ²	$(\times 10^3)$											
(P4)	(S1)			3.80	4.10	3.94	3.78	3.85	3.79	3.79	3.79	3.80
(P4)	(S2)			4.44	4.55	4.27	4.01	4.10	5.87	7.37	4.30	4.32
(P4)	(S3)			4.08	4.17	4.07	3.85	3.88	5.76	5.51	4.07	4.06
(P4)	(S4)			4.01	4.42	4.03	4.01	4.04	4.69	4.76	3.96	3.95
(P5)	(S1)			5.99	6.34	6.50	6.03	6.02	5.94	5.96	6.01	6.04
(P5)	(S2)			7.22	7.23	6.93	6.90	6.92	8.71	7.61	6.59	6.56
(P5)	(S3)			6.03	6.61	6.42	6.34	6.33	9.54	8.32	6.12	6.09
(P5)	(S4)			6.01	6.69	6.59	6.23	6.20	7.30	7.21	6.46	6.41
(P6)	(S1)			5.28	5.68	5.60	5.32	5.36	5.25	5.26	5.29	5.31
(P6)	(S2)			6.00	6.14	5.78	5.87	5.90	7.07	7.08	5.30	5.30
(P6)	(S3)			5.00	5.59	5.38	5.36	5.33	7.11	6.71	4.92	4.87
(P6)	(S4)			5.01	5.51	5.32	5.14	5.18	6.51	6.26	5.21	5.20
MSE	$(\times 10^3)$											
(P4)	(S1)			4.28	4.50	4.26	4.27	4.33	4.27	4.27	4.27	4.28
(P4)	(S2)			4.98	5.17	4.64	4.73	4.79	6.07	9.04	4.82	4.84
(P4)	(S3)			4.52	4.60	4.35	4.32	4.31	6.00	6.26	4.52	4.51
(P4)	(S4)			4.38	4.84	4.33	4.46	4.48	5.17	5.27	4.34	4.31
(P5)	(S1)			6.65	6.92	6.96	6.67	6.64	6.75	6.74	6.79	6.83
(P5)	(S2)			7.77	8.17	7.60	8.03	7.94	8.99	8.70	7.37	7.37
(P5)	(S3)			6.61	7.35	7.00	7.20	7.17	10.07	9.09	6.80	6.76
(P5)	(S4)			6.63	7.33	7.09	6.99	6.94	8.51	8.10	7.14	7.08
(P6)	(S1)			5.81	6.13	5.98	5.85	5.86	5.83	5.84	5.88	5.90
(P6)	(S2)			6.52	7.33	6.49	7.22	7.15	7.39	8.21	6.02	6.05
(P6)	(S3)			5.50	6.17	5.82	6.07	5.98	7.50	7.33	5.53	5.48
(P6)	(S4)			5.54	6.06	5.78	5.75	5.81	7.64	7.14	5.80	5.80

Table 6: The nominal coverage and length of the 95% credible intervals for 11 estimators based on 100 simulated datasets using the prevalence models (P1), (P2), (P3) and the four sampling scenarios. These results are based on the estimates of the off-sample areas in the simulation study.

C BIIII	aracron											
		UM	HT	NB	LN	AS	PL	ES	M1	M2	M1	M2
									RW1	RW1	PS	PS
Nomin	al cove	rage										
(P1)	(S1)			1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
(P1)	(S2)			1.00	1.00	1.00	1.00	1.00	1.00	0.89	1.00	1.00
(P1)	(S3)			1.00	1.00	1.00	1.00	1.00	1.00	0.99	1.00	1.00
(P1)	(S4)			1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
(P2)	(S1)			1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
(P2)	(S2)			0.38	1.00	1.00	1.00	1.00	0.91	0.97	1.00	1.00
(P2)	(S3)			0.89	1.00	1.00	1.00	1.00	1.00	0.99	1.00	1.00
(P2)	(S4)			1.00	1.00	1.00	1.00	1.00	0.99	1.00	1.00	1.00
(P3)	(S1)			1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
(P3)	(S2)			0.51	1.00	1.00	1.00	1.00	0.94	0.96	1.00	1.00
(P3)	(S3)			0.92	1.00	1.00	1.00	1.00	0.96	1.00	1.00	1.00
(P3)	(S4)			1.00	1.00	1.00	1.00	1.00	0.98	1.00	1.00	1.00
Averag	ge lengt	h										
(P1)	(S1)			0.10	0.10	0.20	0.10	0.10	0.10	0.10	0.10	0.10
(P1)	(S2)			0.09	0.12	0.22	0.13	0.13	0.11	0.12	0.09	0.09
(P1)	(S3)			0.09	0.10	0.20	0.10	0.10	0.11	0.11	0.09	0.09
(P1)	(S4)			0.10	0.10	0.20	0.10	0.10	0.11	0.11	0.10	0.10
(P2)	(S1)			0.12	0.12	0.23	0.12	0.12	0.12	0.12	0.12	0.12
(P2)	(S2)			0.10	0.17	0.27	0.18	0.18	0.12	0.15	0.12	0.12
(P2)	(S3)			0.11	0.13	0.24	0.13	0.14	0.12	0.10	0.12	0.12
(P2)	(S4)			0.11	0.12	0.23	0.13	0.13	0.12	0.11	0.14	0.14
(P3)	(S1)			0.11	0.11	0.22	0.11	0.11	0.11	0.11	0.11	0.11
(P3)	(S2)			0.10	0.17	0.26	0.17	0.17	0.12	0.14	0.11	0.12
(P3)	(S3)			0.10	0.13	0.23	0.13	0.13	0.12	0.12	0.12	0.11
(P3)	(S4)			0.11	0.12	0.22	0.12	0.12	0.12	0.12	0.13	0.13

Table 7: The nominal coverage and length of the 95% credible intervals for 11 estimators based on 100 simulated datasets using the prevalence models (P4), (P5), (P6) and the four sampling scenarios. These results are based on the estimates of the off-sample areas in the simulation study.

C BIIII	aradioi											
		UM	HT	$^{ m NB}$	LN	AS	PL	$_{\rm ES}$	M1	M2	M1	M2
									RW1	RW1	PS	PS
Nomin	al cove	rage										
(P4)	(S1)			0.97	0.96	1.00	0.97	0.97	0.97	0.97	0.97	0.97
(P4)	(S2)			0.94	0.92	1.00	0.96	0.94	0.72	0.73	0.95	0.95
(P4)	(S3)			0.97	0.96	1.00	0.98	0.98	0.80	0.87	0.97	0.97
(P4)	(S4)			0.98	0.97	1.00	0.98	0.98	0.87	0.90	0.98	0.98
(P5)	(S1)			0.98	0.95	1.00	0.98	0.98	0.98	0.97	0.97	0.97
(P5)	(S2)			0.96	0.97	1.00	0.97	0.98	0.55	0.76	0.96	0.96
(P5)	(S3)			0.98	0.98	1.00	0.99	0.99	0.59	0.78	0.99	0.99
(P5)	(S4)			0.98	0.97	1.00	0.98	0.98	0.85	0.88	0.99	0.99
(P6)	(S1)			0.97	0.96	1.00	0.97	0.97	0.97	0.98	0.96	0.97
(P6)	(S2)			0.96	0.95	1.00	0.97	0.98	0.52	0.76	0.95	0.95
(P6)	(S3)			0.98	0.97	1.00	0.99	0.99	0.64	0.80	0.99	0.99
(P6)	(S4)			0.97	0.95	1.00	0.97	0.96	0.85	0.85	0.98	0.97
Averag	ge lengt	h										
(P4)	(S1)			0.29	0.29	0.33	0.29	0.29	0.29	0.29	0.29	0.29
(P4)	(S2)			0.30	0.31	0.34	0.32	0.31	0.23	0.25	0.30	0.30
(P4)	(S3)			0.29	0.30	0.33	0.30	0.30	0.29	0.31	0.29	0.29
(P4)	(S4)			0.30	0.30	0.33	0.30	0.30	0.32	0.32	0.29	0.30
(P5)	(S1)			0.35	0.34	0.39	0.35	0.35	0.35	0.35	0.35	0.35
(P5)	(S2)			0.31	0.37	0.41	0.37	0.37	0.17	0.30	0.35	0.35
(P5)	(S3)			0.32	0.35	0.40	0.35	0.36	0.23	0.30	0.34	0.35
(P5)	(S4)			0.33	0.35	0.39	0.35	0.35	0.34	0.34	0.34	0.34
(P6)	(S1)			0.32	0.32	0.36	0.32	0.32	0.32	0.32	0.32	0.32
(P6)	(S2)			0.28	0.35	0.39	0.36	0.35	0.17	0.31	0.32	0.33
(P6)	(S3)			0.29	0.33	0.37	0.33	0.33	0.19	0.33	0.32	0.32
(P6)	(S4)			0.31	0.32	0.36	0.32	0.32	0.30	0.34	0.32	0.32

9. Application: Results per District

In Tables 8-11 we present the point estimates and associated credible interval per district for the application dataset. For completeness, we mention that in Figure 4 a map presenting the indices of the districts in Belgium is provided.

Table 8: Predicted as thma prevalences by district in Belgium using the 2001 Belgian Health Interview Survey. \hat{p}_k : point estimate; ll: lower limit of the 95% credible interval;

ul: upper limit of the 95% credible interval.

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District	Population	Sample		UM			HT			NB	
index	size	size	\hat{p}_k	11	ul	\hat{p}_k	11	ul	\hat{p}_k	11	ul
11	931567	895	3.02	2.08	4.36	2.49	1.68	3.68	3.41	2.44	4.56
12	306413	202	3.47	1.66	7.10	4.41	2.05	9.23	4.12	2.54	6.20
13	407672	200	3.50	1.67	7.17	2.97	1.37	6.32	4.09	2.51	6.19
21	811076	2949	6.17	5.36	7.10	5.95	5.09	6.94	6.07	5.27	6.95
23	560138	337	5.34	3.39	8.32	5.61	3.39	9.14	5.08	3.50	7.15
24	458265	250	4.40	2.45	7.78	2.66	1.39	5.06	4.54	2.95	6.63
25	352018	290	9.31	6.46	13.24	9.85	6.39	14.87	7.32	5.14	10.37
31	271437	199	6.03	3.45	10.33	6.13	2.88	12.56	5.24	3.43	7.85
32	48082	103	0.00			0.00			3.45	1.78	5.63
33	104320	0							4.57	2.38	8.33
34	277786	106	4.72	1.97	10.87	4.93	1.78	12.88	4.66	2.78	7.40
35	142946	150	6.67	3.62	11.97	5.07	2.56	9.79	5.40	3.40	8.41
36	140684	50	2.00	0.28	13.10	1.78	0.24	11.85	4.20	2.26	7.03
37	88034	56	3.57	0.88	13.33	4.26	1.04	15.79	4.43	2.46	7.40
38	56751	0							4.57	2.34	8.48
41	262337	96	4.17	1.56	10.63	2.70	0.83	8.43	4.56	2.67	7.28
42	186553	0							4.59	2.43	8.30
43	79428	56	7.14	2.68	17.67	6.51	2.26	17.36	5.12	2.93	8.80
44	496608	454	3.08	1.83	5.14	3.00	1.69	5.28	3.73	2.47	5.26
45	114390	54	3.70	0.92	13.79	4.88	1.11	19.02	4.54	2.55	7.53
46	224356	209	5.26	2.93	9.26	5.32	2.71	10.17	4.86	3.14	7.28
51	79372	151	8.61	5.06	14.28	6.02	3.39	10.49	6.30	4.10	9.75
52	420214	627	6.86	5.13	9.12	7.78	5.57	10.77	6.28	4.76	8.16
53	249153	293	4.78	2.85	7.91	6.35	3.46	11.38	4.80	3.19	6.93
54	70016	97	5.15	2.15	11.83	3.98	1.56	9.77	4.79	2.82	7.76
55	174142	187	8.56	5.30	13.52	8.92	5.44	14.28	6.45	4.32	9.68
56	146253	181	3.31	1.49	7.19	3.06	1.24	7.35	4.20	2.53	6.41
57	140673	201	4.48	2.34	8.39	4.30	2.20	8.21	4.62	2.92	6.94
61	100543	54	1.85	0.26	12.20	6.22	0.89	32.95	4.22	2.29	6.96
62	584398	618	6.15	4.51	8.34	4.88	3.40	6.96	5.73	4.29	7.51
63	266334	454	5.51	3.75	8.02	5.39	3.29	8.70	5.21	3.73	7.11
64	68767	100	3.00	0.97	8.93	1.96	0.61	6.09	4.22	2.42	6.69
71	384503	399	2.51	1.35	4.60	3.52	1.84	6.65	3.42	2.16	4.95
72	220231	154	2.60	0.98	6.73	1.39	0.48	3.96	3.83	2.20	6.01
73	190051	105	4.76	1.99	10.97	3.99	1.52	10.05	4.63	2.77	7.39
81	52301	210	5.71	3.27	9.79	5.82	3.14	10.57	5.17	3.35	7.74
82	41103	260	3.85	2.08	6.99	3.15	1.62	6.04	4.30	2.74	6.32
83	50911	307	7.17	4.77	10.64	7.23	4.61	11.18	6.07	4.23	8.60
84	55743	309	2.59	1.30	5.09	2.05	0.99	4.20	3.65	2.24	5.39
85	48692	212	6.13	3.59	10.27	5.32	3.03	9.17	5.39	3.50	8.08
91	100298	0							4.63	2.44	8.36
92	283793	294	2.38	1.14	4.91	3.78	1.23	11.05	3.58	2.17	5.31
93	61733	134	2.99	1.12	7.70	3.51	0.84	13.48	4.15	2.40	6.49
			•			•			•		

Table 9: Predicted asthma prevalences by district in Belgium using the 2001 Belgian Health Interview Survey. \hat{p}_k : point estimate; ll: lower limit of the 95% credible interval;

ul: upper limit of the 95% credible interval. Sample District Population LN AS PLindex size size 11 11 ul ul ul \hat{p}_k \hat{p}_k 2.16 2.02 11 931567 895 3.20 4.59 2.65 1.65 3.86 2.93 4.02 12 306413 202 4.55 3.02 6.75 4.35 2.46 6.754.39 2.71 6.75 13 407672 200 4.07 2.43 6.453.29 1.46 5.80 3.70 2.165.80 5.91 21 811076 2949 5.09 6.80 5.87 6.73 5.87 5.09 6.76 5.07 23 560138 337 5.30 3.78 7.425.41 3.52 7.705.21 3.567.412.14 24 458265 250 4.19 2.46 6.653.39 1.48 5.96 3.60 5.49 25 352018 290 7.89 5.83 10.82 8.41 5.88 11.42 7.89 5.51 11.09 31 5.34 3.21 271437199 3.627.945.528.455.263.368.01 32 48082 103 3.49 2.89 4.19 3.38 2.77 4.05 3.15 1.55 5.39 33 104320 4.642.51 8.36 4.26 0.97 9.734.332.11 8.43 34 277786 106 4.77 7.584.662.20 4.59 2.66 7.542.96 8.00 35 142946 4.77 4.75 4.67 2.77 7.47 150 2.94 7.67 2.17 8.28 36 2.42 7.653.467.26 3.93 140684 50 4.42 0.972.01 6.9137 88034 56 4.62 2.69 7.71 4.34 1.65 8.22 4.38 2.35 7.67 38 56751 0 4.622.438.47 4.280.79 10.344.322.04 8.57 262337 4.54 3.93 1.39 4.02 41 96 2.55 7.59 7.55 2.18 6.67 42186553 4.752.60 8.41 4.49 1.15 9.854.422.20 8.49 0 5.07 5.28 4.92 8.78 43 79428 56 2.98 8.641.97 10.182.66 496608 3.80 3.30 3.55 44 454 2.51 5.521.95 4.962.325.10 45 114390 54 4.852.91 7.93 4.81 2.06 8.64 4.612.52 7.9946 224356 209 4.93 3.28 7.39 4.94 2.76 7.72 4.83 3.04 7.37 51 79372 151 5.29 3.34 8.365.572.78 9.305.253.23 8.26 7.40 52 420214 627 7.11 5.62 9.025.68 9.34 7.09 5.40 9.14 53 249153 293 5.85 4.24 8.10 6.12 4.11 8.51 5.72 3.85 8.25 54 4.56 4.22 4.302.38 70016 97 2.637.641.57 8.05 7.2255 174142 187 6.86 4.82 9.96 7.414.70 10.77 6.80 4.47 10.24 56 146253 181 4.39 2.606.99 3.81 1.77 6.524.012.326.3257 140673 201 4.60 2.93 7.06 4.43 2.31 7.174.43 2.71 6.82 61 100543 5.39 3.57 5.57 3.07 4.872.71 8.48 548.18 8.7962 584398 618 4.866.674.82 3.23 6.714.793.46 6.41 3.52 63 266334 454 5.18 3.76 7.125.24 3.51 7.295.113.60 7.05 64 68767 100 4.46 2.48 7.463.47 1.16 6.783.772.02 6.233.59 71 399 3.95 2.75 5.55 2.29 5.175.54 384503 3.84 2.51 72 220231 154 4.16 2.22 7.18 2.53 0.62 5.53 3.20 1.68 5.29 73 105190051 4.56 2.70 4.09 4.262.41 7.03 7.431.67 7.50 52301 5.28 5.39 5.17 3.27 81 210 3.53 7.88 3.08 8.32 7.87 41103 82 260 4.182.556.513.581.76 5.983.822.325.81 83 50911 307 6.21 4.48 8.69 6.52 4.31 9.18 6.18 4.248.80 84 55743 309 3.82 2.20 6.09 2.711.22 4.733.20 1.88 4.91 48692 212 5.04 2.68 4.93 3.07 7.56 85 3.25 7.745.06 8.15 91 100298 4.88 1.24 4.522.24 8.66 2.66 8.62 4.67 10.12294 92 283793 4.272.94 6.053.99 2.515.78 4.172.656.16 61733 134 4.492.717.08 4.03 1.89 6.87 4.232.41 6.82

Table 10: Predicted asthma prevalences by district in Belgium using the 2001 Belgian Health Interview Survey. \hat{p}_k : point estimate; ll: lower limit of the 95% credible interval; ul: upper limit of the 95% credible interval.

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District	Population	Sample		ES		_	M1-RV	V		M2-RW	I
index	size	size	\hat{p}_k	11	ul	\hat{p}_k	11	ul	\hat{p}_k	11	ul
11	931567	895	3.09	2.11	4.27	3.37	2.43	4.60	3.37	2.46	4.54
12	306413	202	4.46	2.91	6.56	4.07	2.58	6.19	4.07	2.55	6.14
13	407672	200	3.89	2.33	6.02	4.04	2.52	6.35	4.03	2.57	6.27
21	811076	2949	5.86	5.06	6.74	6.01	5.21	6.91	6.00	5.23	6.86
23	560138	337	5.24	3.65	7.32	5.02	3.50	7.11	5.01	3.52	7.19
24	458265	250	3.97	2.35	6.12	4.48	2.91	6.71	4.47	2.93	6.58
25	352018	290	7.75	5.50	10.80	7.23	5.03	10.40	7.21	5.16	10.20
31	271437	199	5.24	3.43	7.85	5.18	3.34	7.84	5.18	3.36	7.90
32	48082	103	3.47	2.87	4.14	3.39	1.77	5.55	3.38	1.77	5.56
33	104320	0	4.46	2.37	8.16	4.52	2.23	8.13	4.51	2.38	8.45
34	277786	106	4.66	2.82	7.40	4.60	2.83	7.55	4.59	2.79	7.39
35	142946	150	4.68	2.79	7.52	5.34	3.43	8.35	5.34	3.41	8.63
36	140684	50	4.14	2.26	7.01	4.14	2.24	7.27	4.14	2.24	6.98
37	88034	56	4.48	2.56	7.46	4.38	2.50	7.51	4.37	2.43	7.35
38	56751	0	4.45	2.30	8.28	4.52	2.26	8.41	4.51	2.35	8.52
41	262337	96	4.31	2.42	7.10	4.51	2.62	7.48	4.51	2.68	7.26
42	186553	0	4.55	2.45	8.21	4.54	2.49	8.33	4.53	2.41	8.05
43	79428	56	4.91	2.76	8.51	5.07	2.91	8.85	5.06	2.96	8.96
44	496608	454	3.68	2.44	5.20	3.69	2.52	5.37	3.69	2.48	5.24
45	114390	54	4.71	2.76	7.72	4.49	2.50	7.35	4.48	2.54	7.62
46	224356	209	4.84	3.13	7.27	4.81	3.23	7.27	4.81	3.12	7.25
51	79372	151	5.17	3.15	8.23	6.24	4.13	9.76	6.23	3.98	9.72
52	420214	627	7.08	5.48	8.99	6.22	4.70	8.22	6.21	4.72	8.13
53	249153	293	5.80	4.09	8.02	4.75	3.18	6.88	4.74	3.22	6.92
54	70016	97	4.42	2.51	7.35	4.73	2.91	7.65	4.73	2.77	7.74
55	174142	187	6.69	4.50	9.92	6.38	4.31	9.48	6.37	4.32	9.72
56	146253	181	4.20	2.50	6.48	4.16	2.56	6.45	4.15	2.51	6.34
57	140673	201	4.51	2.83	6.83	4.56	2.97	6.96	4.56	2.92	7.08
61	100543	54	5.27	3.37	8.06	4.17	2.25	7.00	4.17	2.28	7.04
62	584398	618	4.81	3.42	6.55	5.66	4.29	7.48	5.65	4.33	7.46
63	266334	454	5.13	3.64	7.02	5.12	3.68	7.15	5.10	3.65	7.02
64	68767	100	4.15	2.32	6.76	4.16	2.41	6.69	4.15	2.35	6.65
71	384503	399	3.87	2.68	5.33	3.37	2.12	4.97	3.37	2.14	4.95
72	220231	154	3.75	2.02	6.20	3.79	2.20	5.91	3.78	2.18	5.86
73	190051	105	4.40	2.57	7.12	4.58	2.77	7.43	4.57	2.78	7.33
81	52301	210	5.18	3.35	7.76	5.12	3.38	7.70	5.11	3.35	7.54
82	41103	260	4.02	2.46	6.08	4.25	2.78	6.22	4.24	2.76	6.47
83	50911	307	6.12	4.27	8.63	6.02	4.26	8.53	6.01	4.28	8.67
84	55743	309	3.51	2.08	5.34	3.60	2.21	5.38	3.59	2.26	5.38
85	48692	212	4.94	3.09	7.57	5.34	3.53	8.09	5.33	3.53	8.07
91	100298	0	4.67	2.50	8.39	4.58	2.44	8.16	4.57	2.46	7.86
92	283793	294	4.18	2.86	5.82	3.53	2.18	5.33	3.52	2.17	5.24
93	61733	134	4.33	2.60	6.69	4.09	2.38	6.37	4.09	2.43	6.63

Table 11: Predicted as thma prevalences by district in Belgium using the 2001 Belgian Health Interview Survey. \hat{p}_k : point estimate; ll: lower limit of the 95% credible interval; ul: upper limit of the 95% credible interval.

District	Population	Sample	vai.	M1-PS			M2-PS	!
index	size	size	\hat{p}_k	ll	ul	\hat{p}_k	ll	ul
11	931567	895	$\frac{p_k}{3.32}$	2.40	4.45	$\frac{p_k}{3.34}$	2.41	4.55
12	306413	202	3.94	$\frac{2.40}{2.43}$	6.10	4.03	2.56	6.20
13	407672	202	3.96	2.39	6.10	3.98	2.48	6.11
21	811076	2949	5.93	5.15	6.83	5.96	5.20	6.88
23	560138	337	4.96	3.43	7.15	4.98	3.47	7.01
24	458265	250	4.39	2.87	6.40	4.43	2.89	6.79
25	352018	290	7.04	5.00	9.98	7.10	5.10	10.04
31	271437	199	5.11	3.43	7.83	5.13	3.40	7.67
32	48082	103	3.36	1.69	5.51	3.38	1.78	5.57
33	104320	0	4.43	2.38	8.07	4.47	2.40	8.17
34	277786	106	4.52	2.78	7.43	4.55	2.85	7.30
35	142946	150	5.21	3.38	8.29	5.29	3.37	8.25
36	140684	50	4.09	2.15	6.92	4.11	2.21	6.75
37	88034	56	4.26	2.30	7.12	4.30	2.43	7.28
38	56751	0	4.44	2.29	8.15	4.47	2.32	8.36
41	262337	96	4.36	2.50	7.09	4.49	2.70	7.30
42	186553	0	4.46	2.25	8.30	4.50	2.46	8.31
43	79428	56	4.95	2.82	8.37	4.97	2.83	8.69
44	496608	454	3.62	2.45	5.16	3.64	2.46	5.18
45	114390	54	4.37	2.46	7.41	4.41	2.56	7.29
46	224356	209	4.73	3.12	7.13	4.77	3.11	7.20
51	79372	151	6.12	3.95	9.72	6.14	4.10	9.73
52	420214	627	6.13	4.72	8.03	6.15	4.65	8.14
53	249153	293	4.65	3.12	6.89	4.69	3.10	6.99
54	70016	97	4.65	2.82	7.58	4.67	2.79	7.63
55	174142	187	6.25	4.23	9.50	6.25	4.28	9.56
56	146253	181	4.10	2.43	6.32	4.10	2.49	6.44
57	140673	201	4.50	2.90	6.92	4.51	2.91	6.82
61	100543	54	4.14	2.24	6.80	4.18	2.29	6.90
62	584398	618	5.52	4.16	7.38	5.58	4.24	7.49
63	266334	454	4.99	3.59	7.01	5.02	3.57	7.00
64	68767	100	4.02	2.42	6.62	4.08	2.42	6.58
71	384503	399	3.33	2.10	4.97	3.34	2.11	4.96
72	220231	154	3.73	2.11	5.96	3.76	2.20	5.98
73	190051	105	4.54	2.80	7.22	4.55	2.67	7.21
81	52301	210	5.02	3.28	7.76	5.04	3.36	7.82
82 83	41103 50911	260	4.15 5.89	$2.66 \\ 4.15$	$6.10 \\ 8.68$	4.18 5.93	$\frac{2.69}{4.20}$	$6.20 \\ 8.52$
83 84	50911 55743	$\frac{307}{309}$	3.51	$\frac{4.15}{2.20}$	5.23	3.53	$\frac{4.20}{2.24}$	$\frac{8.52}{5.31}$
84 85	48692	$\frac{309}{212}$	5.21	$\frac{2.20}{3.43}$	$\frac{5.23}{7.96}$	5.22	$\frac{2.24}{3.51}$	$\frac{5.31}{7.94}$
85 91	$\frac{48092}{100298}$	0	$\frac{5.21}{4.50}$	$\frac{3.43}{2.33}$	8.11	4.53	$\frac{3.51}{2.44}$	7.94 8.41
91	283793	$\frac{0}{294}$	$\frac{4.50}{3.45}$	$\frac{2.33}{2.11}$	5.20	$\frac{4.53}{3.50}$	$\frac{2.44}{2.14}$	5.33
93	61733	134	$\frac{3.45}{4.05}$	$\frac{2.11}{2.34}$	6.46	4.08	$\frac{2.14}{2.44}$	5.55 6.61
90	01199	104	4.00	4.94	0.40	4.00	2.44	0.01

10. Application: Estimated Cell Probabilities for RW1 model

In Figure 9 we present the estimated cell probabilities obtained via model (13) with RW1 together with the 95% credible intervals. It can be observed that the result is quite different with the estimated cell probabilities obtained via (13) with PS (Figure 4 in the manuscript). The RW1 is much less able to capture the non-linear trend. The estimate under RW1 is smaller near 0 and approaches a constant value around 0.07 after a small initial drop.

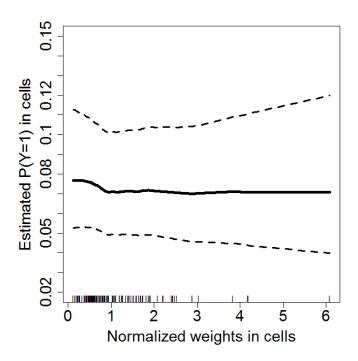


Figure 9: Estimated cell probabilities obtained via (13) with RW1 together with the 95% credible intervals.

11. Application: Sensitivity to Prior Distributions

We also investigate the sensitivity with respect to the choice of prior distributions on the results obtained in the real data application in Section 5 of the manuscript. We vary the prior distributions in a similar manner as described in Section 7 of the Supplementary Materials. We again use the averaged squared deviation to quantify the difference between the results obtained by different prior choices. The results are presented in Table 12.

Table 12: The averaged squared deviations of small area prevalence estimates of modified prior settings with the original prior settings for σ_u , σ_v and σ_w . Results are for the application described in Section 5 of the manuscript.

prior for σ_u^{-2}	prior for σ_v^{-2}	prior for $\sigma_w^{-2}/\sigma_\alpha^{-2}$	M1-RW	M1-RW M2-RW M1-PS M2-PS	M1-PS	M2-PS
Gamma(0.5,0.008)	Gamma(0.5,0.008)	Gamma(1.0,0.01)	0.0	0.0	0.0	0.0
Gamma(0.5,0.008)	Gamma(2.0,0.4)	$\operatorname{Gamma}(1.0,0.01)$	2.1e - 6	4.8e - 6	1.6e - 6	4.7e-6
Gamma(0.5,0.008)	Gamma(0.3,0.001)	Gamma(1.0,0.01)	5.3e - 8	9.4e - 7	5.1e - 8	9.4e - 8
Gamma(2.0,0.4)	Gamma(0.5,0.008)	Gamma(1.0,0.01)	2.6e - 6	5.0e - 7	2.6e - 6	4.9e-6
Gamma(2.0,0.4)	Gamma $(2.0,0.4)$	Gamma(1.0,0.01)	6.6e - 6	2.4e - 6	6.2e - 6	2.4e-7
Gamma(2.0,0.4)	Gamma(0.3,0.001)	$\operatorname{Gamma}(1.0,0.01)$	2.4e - 6	6.7e - 6	2.3e - 6	
Gamma(0.3,0.001)	Gamma(0.5, 0.008)	$\operatorname{Gamma}(1.0,0.01)$	8.9e - 9	6.4e - 7	1.0e - 8	6.4e - 7
Gamma(0.3,0.001)	Gamma(2.0,0.4)	Gamma(1.0,0.01)	2.1e - 6	5.9e - 6	1.8e - 6	5.9e - 6
Gamma(0.3,0.001)	Gamma(0.3,0.001)	Gamma(1.0,0.01)	5.4e - 8	4.9e - 8	5.1e - 8	4.8e - 8
Gamma(0.5,0.008)	Gamma(0.5, 0.008)	$\operatorname{Gamma}(2.0,0.4)$	6.8e - 7	7.5e - 6	2.9e - 8	7.5e - 7
Gamma(0.5,0.008)	Gamma(0.5, 0.008)	Gamma(0.3,0.001)	6.7e - 7	$8.7e{-7}$	4.4e - 9	$8.7e{-7}$
flat prior on $\log(\sigma_u^{-2})$	Gamma(0.5, 0.008)	Gamma(1.0,0.01)	1.5e - 6	1.6e - 6	4.3e - 7	3.5e - 7
Gamma(0.5,0.008)	flat prior on $\log(\sigma_v^{-2})$	$\operatorname{Gamma}(1.0,0.01)$	9.3e - 7	4.2e - 6	6.6e - 7	3.8e - 7
Gamma(0.5,0.008)	Gamma(0.5, 0.008)	flat prior on $\log(\sigma_v^{-2})$	$8.1e{-7}$	1.9e - 7	3.9e-7 $6.1e-7$	6.1e-7

12. Application: Model Checking

We assessed the fit of the model to the data using posterior predictive checks (Gelman et al., 1996). We found no significant evidence against the model, indicating the model fitting performs well. The procedure we followed is outlined below.

For all 12,003 individuals, we generate replicated data y^{rep} from their posterior predictive distribution. A test statistics $T(y^{rep})$ is calculated based on this replicated data. This test statistic is also calculated for the original data y, namely T(y). Here, the test statistics used is the sample total $y_{(k)}$ of responses in area k (thus the sum of the binary responses). We restrict to those areas where $y_{(k)} > 0$. Model fitting is assessed by calculating the posterior predictive p-values $\Pr[T(y^{rep}) \geq T(y)]$ per area k. If the posterior predictive p-value is close to 0 or 1 (say 0.05 or 0.95), then it suggests that our observed data has an extreme test statistic and that something in our model may be inadequate. The posterior predictive p-value is calculated as

$$\frac{1}{L} \sum_{l=1}^{L} I(y_{(k)}^{rep} \ge y_{(k)})$$

for each area $k=1,\ldots,K$. $I(\cdot)$ is the indicator function and L denotes the number of posterior samples. We take L=2,500. In the application study, for Model 1 using penalized splines the posterior predictive p-values range between 0.1348 to 0.7880. The average of the posterior predictive p-values over all areas is 0.4503. The p-values do not provide significant evidence against the model, indicating the model fitting performs well. Results for Model 1 using the random walk of order one and Model 2 are qualitatively similar.

13. Application: Additional Covariate

We investigate whether the addition of an extra covariate to model (13) has an effect on the result obtained in the application of the described methods to the Belgian Health Interview Survey. We add the age variable as a covariate to model (13). The linear component of the model used is thus given by

$$\eta_{ik} = \beta_0 + \beta_a \operatorname{age}_{ik} + f(\tilde{w}_{ik}) + u_k + v_k, \tag{10}$$

where age_{ik} denotes the age indicator of individual i living in district k ($x_a = 1$ for 0-4 year-olds, $x_a = 2$ for 5-9 year-olds,..., $x_a = 18$ 85+ year-olds). We present the results for the model using the penalized splines here.

In Figure 10 we present the estimated cell probabilities obtained via (10) for the district of Nivelles for different age groups. We observe that the estimated probabilities are very similar as those obtained without the age

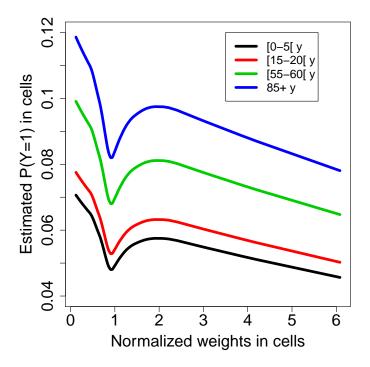


Figure 10: Estimated cell probabilities obtained via (10) for the district of Nivelles for different age groups.

covariate (see Figure 4 in the manuscript). A map with the predicted prevalences is presented in Figure 11.

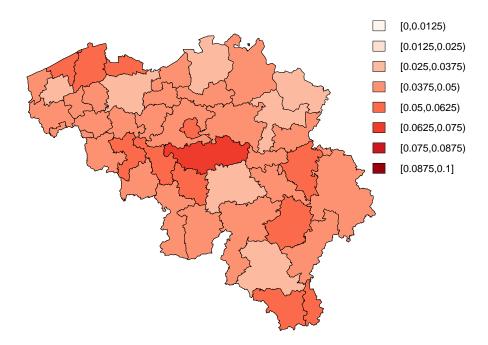


Figure 11: Predicted prevalences using the model (10) with a penalized spline model.

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