

Modeling Infant Mortality in Epidemiology Using Bayesian Hierarchical Approach

Rasheed A. Adeyemi¹ and Abiodun D. Obaromi

*Department of Statistics,
Federal University of Technology, Minna, Nigeria*

**¹Corresponding author: Rasheed A. Adeyemi,
Email: rashid.adeyemi@futminna.edu.ng;
Department of Statistics, School of Physical sciences,
Federal University of Technology, Minna - Nigeria.*

Abstract

The study proposed hierarchical Bayesian model to simultaneously capture the over-dispersion due to the effect of varying population sizes across states and spatial auto-correlation inherent in the infant mortality at small-area level in Nigeria. A cross-sectional study among 31842 children were extracted from 2013 Nigeria demographic and Health Survey data. Out of which 2886 children died before reaching the age five years. The standardized mortality ratio (SMR) was estimated and mapped to highlight unusual cluster of the child mortality. Poisson regression model with random effects are formulated to capture spatial heterogeneity of geographical inequalities in child mortality. A full Bayesian framework via Markov chain Monte Carlo (MCMC) simulation was used to estimate model parameters in WinBUGS. The results showed that economically deprived households, 2.088: 95% CI(1.088, 3.165) were significantly associated with childhood mortality, while

unhygienic sanitary and unimproved water source were not significant. The probability maps detected clusters of high prevalence mortality in the northern regions and relatively low prevalence in south-west region of Nigeria. Our approach estimated the geographical variation as well as potential risk factors of infant mortality. The findings can assist relevant agency with information for the initiating public health interventions and child survival.

Keywords: Child mortality, Poisson mixed model, Health Geography, Spatial epidemiology

1 Introduction

Childhood mortality reduction remains a top priority even in the new sustainable development goals. One of the potential threats to the global efforts on child survival is the infant death clustering, which contribute about 38% of under-five mortality. Five countries accounted for half of the global childhood mortality with Nigeria being the third largest contributor to the under-five mortality among the children in sub-Saharan Africa (Blacket *al.* 2003). In 2013, the mortality rates for the five countries stood at: India (24%), Pakistan (10%) Nigeria (9%), the Democratic Republic of Congo (DRC) (4%) and Ethiopia (3%) as reported in You *et al.* (2013). According to a UNICEF/World Bank report, the prevalent of high child mortality is concentrated in four Sub-Saharan African countries of Malawi, Nigeria, Tanzania and Zambia.

The major contributory causes of child mortality could be attributed to individual family poverty level and poor household's environment, which are highly concentrated in rural areas or slums in urban cities (Fotso, 2006; Isunjuet *al.* (2011). The household poverty and poor environment could exacerbate health problems and disease prevalence among children, hence high mortality risks.

The objective of this study is to explore the extent to which the population-level risk factors explain the variation of infant mortality rates and to highlight the high risk

areas by using recently developed statistical methodologies, which incorporate an ecological analysis into Bayesian disease mapping study. The statistical challenges of geographical analysis of health have to deal with methodological uncertainties as well as social and political issues. Methodological uncertainties are caused by the issues of ecological fallacy, scale, the modifiable areal unit problem (MAUP), and spatial autocorrelation (Shaw *et al.* 2001; Wong, 2009). The problems can be inherent in making inference about sub-population or area characteristics as individual within the population. The statistical issues with disease mapping model involved small area estimation of aggregated data over small areas required taking into account local spatial correlation as stated in studies by Ancelet *et al.* (2012) and Wakefield (2006).

This study is therefore motivated using exploratory method via a standardized mortality ratio (SMR) to highlight the unusual clustering and over-dispersion in the count data. The study then proposed Bayesian hierarchical models to identify areas (regions) with an unusual mortality risk and estimate the geographical inequalities in the number of children death across the districts (states) in Nigeria within a full Bayesian framework.

2 Material and Methods

2.1 Study Area and Data

For the purpose of the present study, Figure 1 shows the geographical map of Nigeria showing 36 states and Federal Capital Territory, Abuja Nigeria and comprises of 6 geopolitical regions: North-East, North-West, North-Central, South-East, South-South, and South-West which are sub-divided into 36 administrative states and the Federal Capital Territory (FCT). The population groupings within the geopolitical regions and states are relatively homogeneous. Also, the people's cultural beliefs, demographic characteristics, arid environment and socioeconomic status are considered similar within the geopolitical zones and states.



Figure 1: Map of Nigeria showing 37 districts (36 states and Federal Capital Territory (FCT)-Abuja)

Data

The 2013 NDHS survey conducted by the DHS Measure used a multi-stage cluster design consisting of 40,320 households in 904 clusters, with 372 in urban areas and 532 in rural areas. The data variables extracted from 2013 Nigeria Demographic and Health Survey (NDHS) for the present study include: the number of children born between 2008 and 2013, number of children alive and counts of child deaths at the time of the survey, proportion of poorest and poor households, number of cases (children) with diarrhea two weeks prior to the survey), number of households that used solid cooking fuels such as, coal, charcoal, fire wood, cow dung and agricultural crop residues. The detailed procedure has been reported elsewhere in National Bureau of Statistics (2014) DHS report.

2.2 Model Framework

In disease mapping, the first step is the removal of the effect of the confounding factors on the risk estimate in the study population through distribution standardization according to Woodward (2013).

Consider the infant death counts, Y_k aggregated over a state, k say, index for states 37 ($k = 1, \dots, 37$), where the mother k resides in Nigeria and E_k represents the corresponding expected death count at state, k . In this study, the standardized mortality ratio (or SMR for short) is calculated as

$$SMR = \frac{Y_k}{E_k} \quad (1)$$

and

$$E_k = n_k \left(\frac{\sum_{k=1}^{37} Y_{ik}}{\sum_{k=1}^{37} n_k} \right)$$

where in equation (1), SMR_k is the standardized mortality ratio, which is the ratio of observed number of child death cases to the expected number of cases in the k^{th} state, representing the risk of each k^{th} small area (state). However, this estimate is biased, because it is based only on a sample size of one. Hence, it is not really statistically useful because it is a saturated model. Further readings can be found in Lawson *et al.* (2000) and Clayton and Kaldor (1987).

2.3 Hierarchical Disease Mapping Models

In many epidemiological studies, mortality rates mapping or disease incidence could provide important information for resource allocation and disease management. The models commonly explored are expected to capture the effects of spatial dependence and over-dispersion in the data. The Poisson-Gamma model is often used to model the relative risk of the number of child mortality in a small area, where the relative risk combines the Poisson likelihood function of the death counts and Gamma prior distribution to yield a gamma posterior distribution for the relative risk as details described in Clayton (1992).

Model 1: Poisson Gamma Model

Let y_k and E_k ; $k = 1, \dots, 37$, denote the observed and expected number of death cases in district (state) k . We assume the death count, $y_k \sim \text{Poisson}(E\mathcal{G})$, where \mathcal{G} is the unknown relative risk and Poisson mean μ is modeled as

$$\mu_i = E\mathcal{G}. \quad (2)$$

We assume that \mathcal{G} follows a gamma distribution, i.e. $\mathcal{G} = \text{Gamma}(a, b)$ for $k = 1, \dots, 37$, wherein our study $k=37$ districts (states) in Nigeria. By combining the likelihood and the prior distribution, the posterior mean of the relative risk is obtained as

$$E(\mathcal{G} | a, b, y_k) = \frac{a + y}{b + y} = w_k \text{SMR} + (1 - w_k) \frac{y_k}{E_k} \quad (3)$$

where $w_k = \frac{b}{b + E_k}$ represents the weighted average that indicates on how much the posterior mean shrunk towards the individual expected value E_i as explained in Lawson (2013). One advantage of the Poisson-gamma model is that it provides a simplified way to accommodate over-dispersion in the model. A drawback is that Poisson-gamma model does not permit the inclusion of covariate(s) in the model (Dabney and Wakefield, 2005).

Model 2: Besag, York and Mollie (BYM) Model

BYM model was introduced firstly by Besag (1974) and later extended by Besag and Mollie (1991). The BYM model was then split into two spatial (correlated) random and heterogeneity (uncorrelated) random components, where v_i and u_i are unstructured and structured spatial random effects respectively.

With the infant death counts assume Poisson distribution, i.e. $y_i \sim \text{Poisson}(E\mathcal{G})$ as in equation (2) above, then the log relative risk, \mathcal{G} is modeled via the linear link function as

$$\log(\mu) = \log(E) + \log(\mathcal{G}) = \log(E) + \eta \quad (4)$$

$$\eta = \log(\mathcal{G}) = X'\beta + u_i + v_i$$

$$v_i \sim N(0, \sigma_v^2)$$

$$u_i | u_j, i \neq j, \sim N\left(\sum_j \frac{w_{ij}u_j}{w_{ij}}, \frac{\sigma_u^2}{w_{ij}}\right),$$

Where η is the predictors, $i \neq j$ denotes state i is adjacent to j (neighbours) takes value $w_{ij} = 1$ and zero if they are not. X is a vector of covariates (such as proportion of poor households, unimproved source of drinking water, unprotected toilet, children having diarrhea, proportion of mothers used solid fuels (coal, wood, agricultural residues cow dung etc) as cooking method . The \mathcal{G} reflects the amount of extra Poisson variation in the data as stated in Lawson (2013) and Lawson *et al.* (2000). The precision parameters τ_u^2 and τ_v^2 control the variability of u and v respectively.

The parameter estimation was executed via Bayesian MarkovChain Monte Carlo Convergence of the MCMC was reached at 15000iterations after a burn-in period of 5,000 sample and thinning of every 90th element of the chain. The statistical inference is based on full Bayesian framework and prior distributions were specified for the model parameters. The posterior estimates and 95% credible intervals are used to explain the model results as presented in Table 2 below.

The model performance was investigated via deviance information criterion (DIC) which is due to Spiegelhalter *et al.* (2002) given as $\text{DIC} = D(\hat{\theta}) + \text{pD}$, where D is the posterior mean of the deviance and $\hat{\theta}$ is the vector of model parameters, pD is the number of effective parameters in the model that penalizes the complexity of the model. DIC takes into account both the model fit (summarized by D) and model complexity (captured by PD) when comparing models. Therefore, the model having

smaller value of DIC is the most preferred model as it has achieved a more optimal combination of fit and parsimony.

2.4 Data application and Results

All model parameters are estimated in WinBUGS (Spiegelhalter *et al.*, 2002) and data manipulation was done in R programming (Teem 2014). The parameter estimation was done using Bayesian Markov Chain Monte Carlo via Gibbs Sampling and convergence achieved after 15,000 iterations in a burn-in period of 5,000 samples and thinning of every 90th element of the chain. The hyper-parameter prior distributions assumed for the precision parameters, τ_u^2 , τ_v^2 and τ_β^2 are Gamma distributions as $\tau_u^2 \sim \Gamma(0.05, 0.005)$, $\tau_v^2 \sim \Gamma(0.05, 0.005)$ and $\tau_\beta^2 \sim \Gamma(0.05, 0.01)$ respectively. The regression coefficients of the covariates in the model are assumed to be normally distributed given as, $\beta \sim N(0, 0.005)$.

Table 1 presents the estimates of the parameters and goodness of fit for the hierarchical models discussed in the previous section.

Table 1: Deviance information criteria (DIC) and model goodness of fit based on 2013 Nigeria DHS

Model	Name	$D(\theta)$	pD	DIC
M1	PG	256.885	31.217	288.10
M2	BYM	260.267	25.043	285.31

BYM model each provides important information about clustering of the infant mortality with the incorporation of the relative risk pattern and over dispersion in the model. One would recommend that the BYM was the best fitted model for Nigerian infant mortality data, since it yielded the lowest value of the DIC = 285:310 and with a lower pD = 25.04. However, thus the BYM model is the most preferred model due to its robustness, at the same time one can evaluate the proportion of variation that can

be attributed to spatial dependence (clustering) and the variation due to random heterogeneity effect structure of the mortality prevalence.

The posterior mean and 95 % credible intervals statistics of the fitted hierarchical are presented in Table (2). It can be observed that the posterior mean of Poisson-Gamma model 0.923: 95% CI(0.826, 1.030) is approximately the same as the mean of the standardized mortality ratio, SMR= 0.920(standard deviation sd=0.306) . The overall population parameters, $a = 10.310$; (6.232, 15.970) and $b = 11.20$ CI(6.680; 17.350) from the Poisson Gamma model. The variance component parameters from the BYM model with CAR precision variance, $\tau_u^2 = 56.98$; 95% CI(6.104, 339.0) and $\sigma_u = 0.291$. In other words, the small value of standard deviation, $\sigma_u = 0.291$ of spatial structured random effects, it means that the neighbor are dependent. The uncorrelated random effect of BYM model has precision variance, τ_v^2 , 330.60; 95%CI (23.84, 2101) and $\sigma_v = 0.0991$. One can also deduce that the proportion of the variation that is due to clustering as 69.06% and the proportion of variability attributed to the heterogeneity random effect is 30.93%. The results revealed that the geographic patterns of infant mortality rate in Nigeria exhibits more clustering prevalence by states than the geographical disparities as evidenced from the estimates.

Table 2: Posterior estimates and 95% credible intervals of model parameters and ecological covariate on infant mortality based on 2013 Nigeria DHS.

	M1: PG			M2: BYM		
	Mean	95 % CI		Mean	95 % CI	
β_0	-	-	-	-0.138	-0.196	-0.080
a	10.31	6.23	15.97	-	-	-
b	11.20	6.68	17.35	-	-	-
μ	0.92	0.83	1.03	-	-	-
σ^2	0.09	0.05	0.14	-	-	-
β_1	-	-	-	0.173	-0.372	0.730
β_2	-	-	-	0.353	-0.190	0.851
β_3	-	-	-	-0.226	-0.771	0.333
β_4	-	-	-	2.003	1.101	3.006
β_5	-	-	-	-0.516	-1.591	0.430
τ_u^2	-	-	-	56.98	6.104	339
σ_u	-	-	-	0.221	0.054	0.405
τ_v^2	-	-	-	330.60	23.84	2101
σ_v	-	-	-	0.099	0.022	0.205

(β_1 = Diarrhea, β_2 = proportion of unhygienic toilet /poor sanitary facility, β_3 = proportion of unimproved drinking water,
 β_4 = proportion of poor household and β_5 = cooking sources proportion of population using solid fuels (coal, charcoal, crop residues)

In addition, the covariates estimates are presented along with 95 % credible intervals in Table 2. The results revealed that the estimated overall (intercept) relative risk effect of the models are with model M2: That is $\beta_0 = -0.138$, 95% CI (-0.200, -0.080), indicating that the overall risk was significantly different from zero. The overall relative risk indicates that a decreasing (negative coefficient) relative risk of childhood mortality by keeping the determinant factors constant. Furthermore, the household poverty variables were significant and positive for all the BYM: 2.003, 95% CI (1.101, 3.006). The results showed that a unit increase in household poverty would lead to increase the relative mortality risks among the children who belong to most economically deprived households. Other covariates in the model did not show strong evidence of significant effect on the child mortality. However, the children who suffered from diarrhea and unhygienic toilet/sanitation had higher risk of dying before reaching the age five (i.e. positive association with the under five child mortality), although the association is not significant. Children of mothers, who used solid fuels (such as charcoal/coal/wood or agricultural residues) for cooking and drinking from unprotected water were at lower risk of childhood mortality (negative coefficient), though the effects were not insignificant.

4.4 Geographical disparities and classification of risk regions

The risk map for BYM models analysis is classified into colour intervals of five quintiles range from low (blue) to high (red) prevalence of mortality. The probability risk map displayed in Figure 2 represents smooth map of mortality and the associated exceedance probability of risk value greater than 1. The map indicates that a relatively high prevalence of child mortality is detected in the north regions with clusters of high child mortality found in the North-west and north- East regions, and

in Ebonyi state in south east part of the country. A relatively low prevalence occurred in south western states of the country. The map indicated that there was significantly high prevalence of infant mortality in states. The states with predicted high prevalence are Sokoto, Ebonyi, Bauchi, Kebbi, Jigawa and Zamfara, while a relative low and significant prevalence of infant mortality occurred in 17 states using the 95% credible intervals.

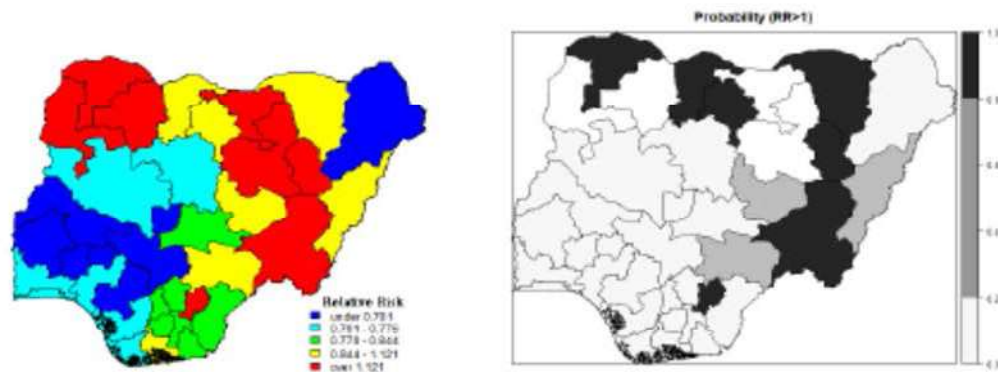


Figure 2: Relative Risk of childhood mortality prevalence and significance probability ($RR > 1.000$) for BYM model based on 2013 Nigeria DHS

5 Discussion

In this study, Bayesian hierarchical model was employed to assess the child mortality risk and potential risk factors such as socio-cultural and environmental factors for the infant mortality in Nigeria. The strength of the approach is the ability to incorporate high over-dispersion, spatial structure and covariates into the models. The usage of Poisson version of generalized Poisson (G-Poisson) distributions in this study was in accordance with empirical studies, although negative binomial models have been used as alternative models for rare disease mapping of count data. The Poisson based models are often used when dealing with rare diseases. Previous studies have explored mixture models. For example, a study conducted by Neyens and Molenberghs (2012), where they had combined convolution model and Poisson-

gamma model to account for both over dispersion and spatial correlation to model the kidney and prostate cancer data.

The result showed that the household poverty was significantly associated with under-five mortality in Nigeria. In other words, an economically deprived household would have higher likelihood of childhood mortality. This finding corroborates what has been established in previous studies by Adeyemi *et al.* (2019). Empirical studies have also shown that people living conditions and household poverty virtually influence the totality of demographic structure and health indices, including life facilities, and even human capital development among others as reported in Adeyemi *et al.* (2019) and González *et al.* (2007). For instance, Adeyemi *et al.* (2009) used DHS data 1990-2008 and found that household wealth had strong association with not only under-five mortality, but the household members' life expectancy, maternal mortality and morbidity, fertility, contraceptive use and use of healthcare.

The results further revealed that unimproved source of drinking water, poor toilet and sanitary conditions were positively associated with childhood mortality, although these factors were not significant. This finding was in agreement with a study conducted by Sherbinin (2011), who investigated biophysical and geographical variables into their model on child malnutrition and found significant correlation between child malnutrition and environmental factors such as drought prevalence, the percentage of households with piped water, and diarrhea disease prevalence. Other studies have identified that inadequate water for food and personal hygiene, and insanitary environments are responsible for about 88 percent of child deaths globally resulting from infectious diseases and diarrhea (Lanata *et al.*, 2013; Cheng *et al.*, 2012;). Our findings were in tandem with a similar study conducted in Ghana by Bodegom *et al.* (2012) detected non-random patterns (clusters) of high child mortality at village level with a large concentration of polygamous population or nuclear family settings, while Dedefo *et al.* (2016) investigated the small area clustering of under five mortality in Ethiopia.

6 Concluding Remarks

The study highlights the social and biological determinants of infant mortality using a Bayesian modeling approach to adjust for inherent correlation between neighbouring sub-nationals (states). The more integrated intervention will assist policy makers in the country with high infant and child mortality burden. The use of Bayesian hierarchical modeling helps to deal with the problems posed by small area estimation such as missing data at the neighbouring states. The usefulness of these findings is further enhanced by the use of advanced geo-mapping of infant mortality risk and the associated risk factors at the small administrative unit. These spatial maps are able to pinpoint areas within a country with higher levels of mortality, as well as explain the most likely reasons for this persistent problem based on attributable factors. This study underscores the need for exploratory and advanced approaches to assess within-country geographic patterns of all-cause infant mortality using national sub-district level ecological data.

The finding of this study can assist the healthcare givers and government agencies in allocation of health recourse and designing interventions.

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