**S2 Bayesian model formulation.**

Let **Y***jt* be the average number of deaths (all-cause or malaria-specific) in village *j* at time interval *t*. We assume that **Y***jt* arises from a negative binomial distribution.

where P*jt*, is the proportion of deaths occurring in village *j* at time interval *t* and *r*is the dispersion parameter with,

and.

We modeled the association above between covariates (*X*) and mortality status of individuals by village on the logit, as

, *u=1,2,……k*

where is the number of deaths in each village at time *t*, the total person time contributed by persons in each village as discrete months, the regression coefficients, the village specific spatial effects and the temporal (monthly) random effects.

We assumed that are parameters from a latent spatial process modelled by a Gaussian distribution with covariance matrix quantifying the relation between any pair of villages as a function of their distance irrespective of the direction using an exponential correlation function, that is , where is the spatial variation, is the distance between villages *k* and *l*, and is the rate of correlation decay with increasing distance. The minimum distance at which the spatial variation is less than 5% is called range and can be obtained from the value (49). Temporal effect () was modeled by an autoregressive process of order 2. We specified non-informative normal prior distributions with mean zero and large variance for the *βi* *i*=1,…… regression coefficients, an inverse gamma prior for , an inverse gamma priors for and . A gamma prior for , that is and .

The model was fitted using Markov Chain Monte Carlo (MCMC) simulation algorithm in OpenBugs version 3.1.2 (Imperial College and Medical Council, London, UK) to estimate model parameters (50). We ran a single chain sampler discarding the first 10,000 iterations. Convergence was assessed by Gelman-Rubin diagnostic (51) and attained at 100,000 iterations.