**Appendix I. Spatial-statistical analysis approach**

Let denote the number infants infected with HIV in district and time out of children at risk, and . We assumed that has a Poisson distribution with a risk of infection . That is, , where denotes the expected number of infants infected with HIV in district and time . We model the risk of HIV infection using Hierarchical spatial Poisson regression models that accounts for excess heterogeneity and similarity over space and time. A class models were fitted to the data to assess the effects of selected covariates on the outcome of interest. These were based on a variant of the [Knorr-Held[[1]](#footnote-2)](#_ENREF_2)  formulation expressed as:

where ’s are unknown functions of the covariates , the ’s represent the linear effect of covariates s are spatial unstructured components, which are independent and identically distributed with zero mean and unknown precision, ; and s is spatially structured component which is assumed to vary smoothly from region to region. To account for such smoothness s are modelled as an intrinsic Gaussian Markov random field with unknown precision, *τ**s*. In this formulation, represents temporally unstructured components which are independent and identically distributed with zero mean and unknown precision, ; and is the temporally structured effect, modelled dynamically using a random walk through the following structure:

Estimation of parameters was carried out using the Integrated Nested Laplace approximation approach. The latent Gaussian field for the model was with hyperparameter vector . Vague independent Gamma priors are assigned to each of the elements in *ϑ*.

The model was also expanded to include an interaction between space and time as follows:

Where

1. Knorr-Held, L., *Bayesian modelling of inseparable space-time variation in disease risk.* Statistics in medicine, 2000. **19**(17-18): p. 2555-2567 [↑](#footnote-ref-2)