

# A Bayesian model with an underlying cluster structure for Disease Mapping

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Recent developments in disease mapping studies have enable to accurately explore geographic disease variation in terms of underlying spatially-varying risk factors. Most of the models proposed in the literature provide small-area relative risks estimates taking into account the neighborhood structure, so that neighboring areas have similar risks. However, there are situations where this assumption may not be appropriate.

We present here an alternative approach where small areas relative risks are assigned to underlying risks. A novelty of our model formulation is that the areas in each cluster share the same risk of disease but do not necessarily share common borders. Hence, the proposed model incorporates ideas from mixture models, clustering models and models with latent structure. To illustrate the accuracy of our procedure, we show the main results obtained in a simulation study. We estimate the parameters of our model using MCMC simulation techniques implemented in R. Some partial conclusions are: The estimated risks with our model recover quite well the true model. Besides, by studying the final distribution of the number of clusters we are able to obtain an estimate of that number close to the real one.

**Keywords:** Bayesian approach, disease mapping, underlying cluster structure.

**AMS:** AMS classification. (Optional)