Bayesian multinomial modeling of spatial patterns of childhood diseases co-morbidity in Nigeria and Tanzania

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Abstract

Comorbidity is associated with worse health outcomes, more complex clinical management, and increased health care costs. We explore multinomial models to analyze the co-morbidity with conditions such as fever, diarrhea and pneumonia among under five children in Sub-Saharan Africa. However, little is known about geographical variations of these illness. In addition to the statistical relevance, its spatial overlapping would enhance the understanding of the epidemiology of the diseases for efficient management and cost-effective control. Using self-reported illness data from 2013 NDHS and 2010 TDHS, we applied a random effect multinomial model to assess the risk factor of childhood co-morbidity and estimate the spatial effects. In the built model, we simultaneously quantify the effects of different kinds of covariates in a unified framework. The spatial structure effect was modeled using two dimensional P-spline. We run several Bayesian models via Markov Chain Monte Carlos(MCMC)simulation techniques and the models were compared using Deviance information criteria(DIC). We found the spatial variation in childhood co-morbidly and the determinants of the each category separately. We found that the risk factors associated with childhood co-morbidity determinants include child's age,place of residence, maternal poverty index, undernutrition, vitamin A, and geopolitical zones. Higher residual risk were identified in Northern-central for Nigeria and South eastern for Tanzania. In addition to the statistical significance of the research output, the spatial maps of the identified hot-spot can assist government and developing partners to target scarce health resources.

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