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Estimating block level malaria fever risk zones of West Bengal in India using space-time conditional autoregressive model

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Malaria, a prominent Vector Borne Diseases (VBD) causing over a million annual deaths worldwide, predominantly affects vulnerable populations in the least developed regions. Despite the increase in malaria control and elimination efforts, climatic and non-climatic factors continue to serve as important drivers of malaria transmission, which is highly variable in space and time. A vital aspect of disease management lies in identifying associated risk factors in space and time. This study aimed to investigate the spatiotemporal heterogeneity of two malaria species, i.e. Plasmodium vivax and falciparum, as well as the effect of covariate risk factors and health inequalities within the targeted population at the block level in West Bengal, India. Different space-time conditional autoregression (STCAR) models were applied to quantify how P. vivax and P. falciparum malaria fever risk is influenced by lag and without lag-affected climatic and associated non-climatic factors. Statistical inference was performed in a Bayesian setting using Markov chain Monte Carlo (MCMC) simulation. Combining the seasonally lagged climatic variables with the spatial covariates, the results provide thorough insights about spatial heterogeneity and associated risk factors at the block level over the period. Whereas the trend of health inequalities is decreasing narrowly across time, which signifies the regions are still experiencing a greater burden of malaria species. Our space-time models are capable of investigating geographical heterogeneity for both malaria species, emphasizing the need for tailored approaches. Addressing the determinants of malaria transmission, as well as estimating health inequities, necessitates regional collaboration and strategic plans, which are critical steps towards overcoming the remaining hurdles in malaria eradication.

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