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Quantifying Multivariate Spatiotemporal Dynamics of Malaria Risk Using Graph-Based Optimization in Southern Ethiopia

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Abstract : Background: Although malaria incidence has substantially fallen sharply over the past few years, the rate of decline varies by district, time, and malaria type. Despite this turn-down, malaria remains a major public health threat in various districts of Ethiopia. Consequently, the present study is aimed at developing a predictive model that helps to identify the spatio-temporal variation in malaria risk by multiple plasmodium species. Methods: We propose a multivariate spatio-temporal Bayesian model to obtain a more coherent picture of the temporally varying spatial variation in disease risk. The spatial autocorrelation in such a data set is typically modeled by a set of random effects that assign a conditional autoregressive prior distribution. However, the autocorrelation considered in such cases depends on a binary neighborhood matrix specified through the border-sharing rule. Over here, we propose a graph-based optimization algorithm for estimating the neighborhood matrix that merely represents the spatial correlation by exploring the areal units as the vertices of a graph and the neighbor relations as the series of edges. Furthermore, we used aggregated malaria count in southern Ethiopia from August 2013 to May 2019. Results: We recognized that precipitation, temperature, and humidity are positively associated with the malaria threat in the area. On the other hand, enhanced vegetation index, nighttime light (NTL), and distance from coastal areas are negatively associated. Moreover, nonlinear relationships were observed between malaria incidence and precipitation, temperature, and NTL. Additionally, lagged effects of temperature and humidity have a significant effect on malaria risk by either species. More elevated risk of P. falciparum was observed following the rainy season, and unstable transmission of P. vivax was observed in the area. Finally, P. vivax risks are less sensitive to environmental factors than those of P. falciparum. Conclusion: The improved inference was gained by employing the proposed approach in comparison to the commonly used border-sharing rule. Additionally, different covariates are identified, including delayed effects, and elevated risks of either of the cases were observed in districts found in the central and western regions. As malaria transmission operates in a spatially continuous manner, a spatially continuous model should be employed when it is computationally feasible.

Keywords : disease mapping, MSTCAR, graph-based optimization algorithm, P. falciparum, P. vivax, waiting matrix
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