

Modeling multiple mosquito-borne diseases: A spatio-temporal approach

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Abstract

Mosquitoes are responsible for transmission of a great part of infectious diseases and lead to hundreds of thousands of deaths annually all over the world. In the Americas, for instance, several arboviruses have been co-circulating in the last years, many of them transmitted by the same mosquito species. The seriousness of this situation attracts attention from many experts. In the literature, several studies that explore the evolution of mosquito-borne diseases can be found. However, they usually focus on just one arbovirus at time ignoring a potential autocorrelation between them. In this study, we jointly analyze two diseases, dengue and chikungunya. Our aim is to describe the geographic and temporal patterns of each arbovirus, besides the risk factors to each one. In addition, we seek to identify the high risk areas. To pursue this, we consider a Bayesian hierarchical spatio-temporal model that includes covariates as well as disease-specific and shared spatial and temporal effects. Finally, results are mapped to identify the similarities between diseases.