

A Bayesian Hierarchical Poisson Model with an Underlying Cluster Structure for the Analysis of Measles in Colombia

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Abstract : In 2016, the Region of the Americas was declared free of measles, a viral disease that can cause severe health problems. However, since 2017, measles has reemerged in Venezuela and has subsequently reached neighboring countries. In 2018, twelve American countries reported confirmed cases of measles. Governmental and health authorities in Colombia, a country that shares the longest land boundary with Venezuela, are aware of the need for a strong response to restrict the expanse of the epidemic. In this work, we apply a Bayesian hierarchical Poisson model with an underlying cluster structure to describe disease incidence in Colombia. Concretely, the proposed methodology provides relative risk estimates at the department level and identifies clusters of disease, which facilitates the implementation of targeted public health interventions. Socio-demographic factors, such as the percentage of migrants, gross domestic product, and entry routes, are included in the model to better describe the incidence of disease. Since the model does not impose any spatial correlation at any level of the model hierarchy, it avoids the spatial confounding problem and provides a suitable framework to estimate the fixed-effect coefficients associated with spatially-structured covariates.

Keywords : Bayesian analysis, cluster identification, disease mapping, risk estimation

Conference Title : ICSRD 2020 : International Conference on Scientific Research and Development

Conference Location : Chicago, United States

Conference Dates : December 12-13, 2020