

Application of Spatial Analytical Methods for Determining Optimal Prevention Strategies for Rift Valley Fever in Senegalese Livestock

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RVF is an insect-borne viral disease that affects a range of livestock species as well as man. RVF is included in the Office International des Epizooties (OIE) List A, meaning it is an important socioeconomic, public health and international trade constraint. Epidemics have been reported in countries throughout Africa, as well as the Arabian peninsula. Epidemics in Sub-Saharan Africa have been associated with periods of above-average rainfall, resulting in rapid expansion of the vector insect population. Attempts have been made to predict RVF epidemics in Africa using satellite-generated rainfall and vegetation cover data, ocean temperature anomalies and the Southern Oscillation Index for the El Niño phenomenon (Linthicum and others, 1987; Linthicum and others, 1991; Linthicum and others 1999).

The main objective of this project is to conduct a spatial risk assessment of Rift Valley fever (RVF) in livestock in Senegal to facilitate allocation of resources to potential disease interventions, such as the control of vectors or the use of preventive vaccines.

Serological data for RVF were collated by staff at the Food and Agriculture Organisation of the United Nations (FAO) from herds sampled in two separate studies. These included bovine, ovine and caprine sentinel herds that were selected due to their location within perceived high-risk areas of the country (mainly along the northern border with Mauritania) and herds that were targeted during the Pan African Rinderpest Campaign (PARC), which were randomly selected from all bovine herds in the country. Cases were defined on the basis of serological status using the virus neutralisation test. Potential predictor variables, including cattle density, distance from perennial and non-perennial lakes and rivers, land-use, elevation and vegetation, were identified. Epidemiological data and predictor variables were aggregated in raster grid cells with dimensions of 0.05 decimal degrees squared.

This paper outlines the process of exploratory data analysis, including analysis of clusters using SaTScan version 2.1.3 (National Cancer Institute, Bethesda, MD, USA), investigation of first-order trends using fixed-effects Poisson regression and Bayesian methods, identification and quantification of spatial autocorrelation, and the development of mixed-effects spatial models. The geographical information system (GIS) ArcView 3.2 (ESRI, Redlands, CA, USA) was used for the management of the spatial predictor variables and to develop predicted disease risk maps. Bayesian analyses were performed using WinBugs 1.3 software (MRC Biostatistics Unit, Cambridge, UK). The above data-driven modeling approaches are compared to multiple criteria decision making models, developed using the GIS IDRISI 32 for Windows (Clark Labs, Worcester, MA, USA).

The results are considered in terms of how they may assist national policy-makers in forming decisions about the control and prevention of RVF. The main focus of this body of work is on the methodological application of spatial techniques to the problems of animal health. Integration of multiple techniques leads to better utilisation of existing knowledge. Exploratory data analysis may suggest areas where more detailed spatial analysis may be required. Spatially referenced serological data can be combined with climatic, topographic and management-related predictor variables to determine maps of disease risk. These maps can be combined with economic information to plan the optimal geographical distribution of financial resources for potential disease interventions. Systematic review and meta-analysis of data from peer-reviewed and grey literature sources can also provide valuable information. Further utilisation of existing knowledge with methods such as MCDM can add value to this information. Geographical information can also be used to develop maps of disease probability with MCDM methods.

A number of potential problems are associated with combining data from different sources. These may include differing definitions of serological status, different sampling strategies, and different sampling times in relation to season. These issues must be addressed when collating data, whether it be via a systematic review, a meta-analysis, or collation of serological data from different studies for predictive mapping of disease risk.

Bayes theorem, the basis of Bayesian inference, is that the joint probability of two events is the product of one event and the conditional probability of the second event given the first event. This contrasts with traditional statistical inference, which is based on hypothesis testing using measures such as confidence intervals and p-values. Data collected in economic or epidemiological studies is often patchy and incomplete. Application of Bayesian methodology is one way to make predictions for spatial units for which there is no outcome data, using prior information from surrounding units and from predictor variables that exist for that unit. Bayesian methodology also provides an avenue for dealing with the problem that heterogeneity displayed in maps of disease frequency can be misleading as raw measures can also reflect differences in size of underlying populations (e.g. relative risks are likely to have more extreme values in areas with small populations) (Clayton and Kaldor, 1987; Langford, 1994). Bayesian methods allow for weighting of the contribution of the observed data (relative to the prior information) to a posterior distribution according to the number of samples obtained from each spatial unit.

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