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Bayesian hierarchical modelling to enhance the epidemiological value of abattoir surveys for bovine fasciolosis

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Abstract

Four classes of Bayesian hierarchical models were evaluated using an historical dataset from an abattoir survey for fasciolosis conducted in Victoria, Australia. The purpose of this analysis was to identify areas of high prevalence and to explain these in terms of environmental covariates. The simplest of the Bayesian models, with a single random effect, validated the use of smoothed maps for cartographic display when the sample sizes vary. The model was then extended to partition the random effect into spatially structured and unstructured components, thus allowing for spatial autocorrelation. Rainfall, irrigation, temperature-adjusted rainfall and a remotely sensed surrogate for rainfall, the normalised difference vegetation index (NDVI), were then introduced into the models as explanatory variables. The variable that best explained the observed distribution was irrigation. Associations between prevalence and both rainfall and NDVI that were significant in fixed effects models were shown to be due to spatial confounding. Nevertheless, provided they are used cautiously, confounded variables may be valid predictors for the prevalence of disease.

Keywords: *Fasciola hepatica*; *Fasciola gigantica*; GIS; Liver fluke; NDVI; Bayesian statistics; Hierarchical models; Ecological correlation; Abattoir survey

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1. Introduction

Bovine fasciolosis, caused by the liver flukes *Fasciola hepatica* and *Fasciola gigantica,* is a worldwide disease of immense clinical and economic importance to the livestock industry (Torgerson and Claxton, 1999). Accordingly, considerable efforts have been expended to assess the prevalence and severity of infection, and for this purpose abattoir surveys have played a major role. Both the flukes and/or the pathognomic liver damage they cause are detected readily during routine meat inspection, thus enabling surveys to be undertaken with minimal disruption to the killing chain. Although such surveys can determine only the prevalence of the disease in the age class of animals sent to an abattoir for slaughter, the estimate frequently is extrapolated to the wider population of cattle due to the chronic nature of the disease (Behm and Sangster, 1999; Radostits et al., 2000). Accordingly abattoir examination remains an efficient method of surveillance even though reliable and sensitive in vivo tests exist which could permit farm level surveys of high accuracy and precision.

Most authors of the large number of published abattoir surveys of fasciolosis report the overall prevalence of affected livers, along with supporting data such as severity according to age and sex classes. More recently, with better data handling permitting the identification of the origin of the slaughtered animals, the focus has shifted to identifying locations with higher than expected apparent prevalence. Occasionally this trace-back has been to the actual source farm, but more generally it is reported for the region or local administrative area from which the cattle originated. Several authors have presented their results as choropleth maps of crude prevalence (Baldock and Arthur, 1985; Froyd, 1975; Mzembe and Chaudhry, 1981; Tembely et al., 1988; Watt, 1980). With the widespread adoption of geographical information systems (GIS), the use of maps to display the results of abattoir surveys for fasciolosis is likely to become the norm.

A commonly stated reason for exploring spatial variability of fascioliasis is to relate prevalence to climate, because of the latter's overwhelming importance in the epidemiology of the disease (Ollerenshaw, 1958; Radostits et al., 2000; Torgerson and Claxton, 1999). This importance principally is because of the requirement of the snail intermediate host for water, but also because of temperature constraints in cooler areas. The strength of the disease–climate relationship has enabled the development of predictive risk models, the most sophisticated of which have been explicitly spatial and several researchers have used remote sensing to provide covariate information over wide areas (Malone and Yilma, 1999). Of the remotely sensed variables, the normalised difference vegetation index (NDVI), a measure of vegetation greenness, has attracted considerable interest. This is because it integrates a number of different environmental factors (land cover, temperature, rainfall, vapour pressure, etc.) into a single variable and thus simplifies analysis (Hay et al., 1997).

A limitation to the studies that have mapped spatial variability in the prevalence of fasciolosis and/or attempted to relate this variability to environment determinants has been in their statistical analysis. Mostly, the analyses have been absent or very crude, using tests such as the χ^2-test for association, the Spearman rank–order correlation or linear regression. The essential problem with such tests is that they ignore any spatial correlation between adjacent areas, and invariably result in biased parameter estimates. The practical