Multivariate spatially structured variability of ovine parasitic infections

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Abstract: We take advantage of a Veterinary Epidemiology survey in the Campania region (Italy), 2004-2005, to develop a Bayesian approach to analyze the multivariate geographical distribution of four different sheep parasites. We specified a series of Multivariate hierarchical Zero Inflated Poisson models. The results were consistent with theoretical knowledge, quantified impact of common intermediate hosts (*Fasciola hepatica* and *Paramphistomidae* share the same species) and supported evidence of previously unknown ecological components (*Dicrocoelium dendriticum* was correlated to *Fasciola* and *Haemonchus contortus* was not found spatially associated with the previous parasites).

Keywords: Hierarchical Bayesian Models; Multivariate Disease Mapping; Veterinary Epidemiology; Parasitic infections

1 Introduction

Multivariate disease mapping has been introduced in the context of hierarchical Bayesian modeling. The interest is in estimating any shared component of the risk surface, and relating it to underlying prevalence of exposure. Examples were in cancer epidemiology (see Knorr-Held and Best, 2001). Veterinary parasitic diseases offer sensible applications. Parasites are strongly dependent on environment characteristics and ecological analysis can address relevant scientific questions. We develop a Bayesian model for Multivariate Zero Inflated Poisson counts and study the degree of spatial correlation among four parasites accounting for known hosts ecology.

2 Data

A cross-sectional coprological survey was conducted to evaluate liver fluke (*Fasciola hepatica*), lancet fluke (*Dicrocoelium dendriticum*), rumen fluke (*Paramphistomidae*), and abomaso's parasite *Haemonchus contortus* infections in pastured sheep from the Campania region, Italy, 2004-2005. All sheep farms were geo-referenced and systematically sampled on a grid of 134 10 × 10 km quadrants. The closest farm to the quadrant centroid with more than 50 animals was selected, resulting in 121 over 134 potential farms. On each sampled farm faecal specimens were collected from 15 adult and 5 young sheep and pooled into 4 composites. Laboratory coprological examination of the composites followed (FLOTAC) (Cringoli, 2004).

3 Statistical methods

The data likelihood is a mixture of two distinct processes governing presence and extent of parasite infection. The first is Bernoulli and the second, conditionally on being positive, is truncated Poisson, the extent of infection measured by eggs/oocists count per gram of feces (EPG). The likelihood is re-parameterized as a mixture of two Poisson random variables. Following Lambert (1992):

$$L(Y_{ik}) = \pi_{ik} f_1 + (1 - \pi_{ik}) f_2$$

where i=1, ..., 121 indexes farm and $k = 1, \ldots, 4$ parasite, f_1 is discrete with mass point at zero, f_2 is Poisson(μ_{ik}) with mixing probability $1 - \pi_{ik}$. In the second layer of the hierarchical model we specify a spatially structured random Markov field. For the Bernoulli process the logit of the probability of being positive is modelled as a convolution of two random effects, spatially structured (clustering) and unstructured (heterogeneity). The spatially structured terms are assumed conditionally autoregressive based on the adjacency matrix:

$$\text{logit}(\pi_{ik}) = \alpha_k^1 + u_{ik}^1 + v_{ik}^1$$

For the Poisson process the log intensity is modelled as a convolution of two random effects, as before:

$$\log(\mu_{ik}) = \text{offset} + \alpha_k^2 + u_{ik}^2 + v_{ik}^2$$

in which the offset specifies the by design number of composites (1 for *Haemonchus contortus* and 4 for the others).

Prior information on the parasite biology maps into the hierarchical model as follows. Two flukes (liver and rumen) were relatively rare, 12% - 14% of positive farms, and we specified spatially structured random terms in the Bernoulli process. Lancet fluke was more frequent, 61% of positive farms, and we specified spatially structured terms in the truncated Poisson process. *Haemonchus contortus* was very common (more than 90% of positive farms) and we fixed $\pi_{ik} = 0$. Spatially structured terms were specified in the Poisson process.

3.1 Statistical inference

We aim to assess the extent of spatial co-variation among the risk of different parasite infections. Liver and rumen flukes share the species of intermediate hosts, amphibious snails. We expect a strong spatial correlation among the two processes. Lancet fluke has like intermediate hosts a black aunt and a terrestrial snail. We expect absence of correlation with the two previous parasites. *Haemonchus contortus* has no intermediate hosts. Three different larvae live in the external environment and we are interested in looking at possible correlation with the other parasites. To address those hypotheses we specified common and shared clustering components as follow:

1- a decomposable model, clustering and heterogeneity parasite specific terms;
2- as before but with common clustering terms for liver and rumen flukes;
3- as before but with shared clustering terms between *Haemonchus contortus*, liver and rumen flukes;
4- as model 2 but with shared clustering terms between lancet fluke and *Haemonchus contortus*.

Comparing model 1 vs model 2 we can assess how strong is the effect of a common species of intermediate hosts. Comparing model 3 vs model 2 we evaluate the importance of wet environment and water in the transmission of *Haemonchus contortus* and comparing model 4 vs model 2 we could conclude for the importance of drier environment.

4 Results

A total of 121 farms were visited and a sample of 2420 animals underwent coprological examinations. Over the 121 farms 15 was positive to liver fluke, 17 to rumen fluke, 81 to lancet fluke and 109 of *Haemonchus contortus* with an average extent of parasite infection of 4.20, 3.51, 33.08, 79.01 EPG, respectively. The surfaces for the spatially structured terms are displayed in Figure 1. It emerges a strong spatial gradient very similar for liver fluke and rumen fluke, as expected. The surface for lancet fluke shows a spatial pattern surprisingly close to *Fasciola hepatica*. Both flukes affect liver but have different seasonal pattern which could explain coexistence in a common environment of intermediate hosts (Asanji and Williams, 1984). *Haemonchus contortus* infection shows higher prevalence along the coastal region and no correlation with rumen fluke. Model comparison confirms this findings.

5 Conclusions

Multivariate disease mapping can be helpful to test hypothesis on ecological patterns of disease risk. We developed a Bayesian approach to Multivariate

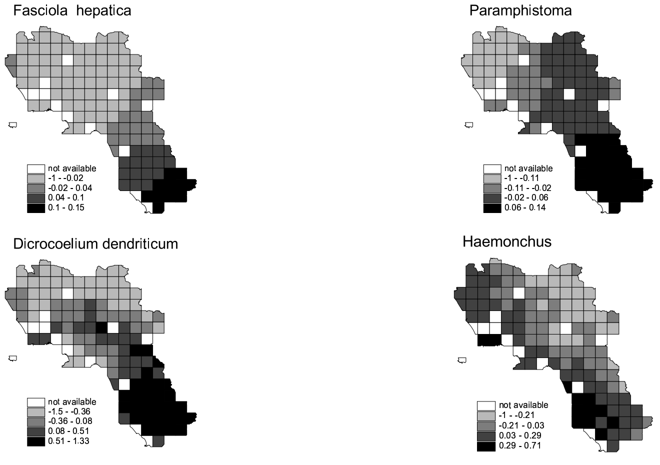

FIGURE 1. Spatially structured random terms.

Zero-inflated Poisson processes in the context of Veterinary Parasitology. Spatially structured terms are introduced at the second layer of the models. Based on parasite ecology, spatially structured variability is specified for the probability of being positive or for the count of parasite eggs/oocists. For two flukes results are consistent with theoretical expectation, for a third (*Haemonchus contortus*), the findings suggest coastal environmental factors in the transmission of the infection. Lancet fluke showed a structure similar to liver fluke, while the baseline prevalence was very different.

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