

# Extending Comparisons Beyond Time and Space: Looking for Similarities Between Diseases

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## BACKGROUND

Early detection of new diseases such as bovine spongiform encephalopathy is the subject of great interest (Gibbens et al., 2008). Understanding whether a disease is infectious or sporadic becomes essential for the application of control measures. Consistent and robust ways to the assessment of temporal trends are required to help in the elucidation of this question. Clustering of cases in space, or time and space, is also relevant in the understanding of the aetiology of a new disease. This paper presents a third approach: knowledge by comparison, either of diseases, surveillance sources or both. We applied this approach to the current debate about the nature of atypical scrapie, a fatal neurological animal disease, by comparing the spatial distribution of this form of scrapie with that of classical scrapie. A similar spatio-temporal distribution of these two diseases would indicate shared environmental disease determinants and help in the generation of hypotheses about the aetiology of atypical scrapie.

## METHODS

We applied Bayesian Hierarchical Models (BHM) to the test results from four surveillance sources, two sample-based and two exhaustive lists, on classical and atypical scrapie collected in Wales in the period 2002 to 2006. Covariate information on the premises where confirmed disease was traced was collected from population-based data sources.

More specifically, we jointly modeled the variation of scrapie risk for the two groups of combined datasets sharing a latent spatial field with a possible different risk gradient. In a second phase, we explored whether previous models could be improved by adding holding-specific covariates. Models were built on those of Knorr-Held and Best (2001) and were implemented in WinBUGS and R.

## RESULTS

Comparison of the risk maps for classical and atypical scrapie suggests that there was little agreement between them. For classical scrapie, the risk gradient between the combinations of surveillance sources was significantly different indicating an increased sensitivity of those sources targeting clinical disease vs. those targeting infection.

For atypical scrapie the two combinations of sources returned a similar risk gradient. This finding supports the hypothesis of reduced mortality associated with the atypical form. Furthermore, the risk of classical scrapie produced a stronger spatial signal, as expected from an infectious condition, than that of the atypical form. The joint spatial regression model to assess the association between covariates and disease risks returned different significant variables for each disease. The inclusion of the covariates produced flatter risk surfaces for both conditions indicating that some of the geographical variation was explained by the covariates. This effect was stronger for classical scrapie.

## CONCLUSIONS

Our results suggest that classical and atypical scrapie differ in their spatial patterns and disease determinants. Considering the well-known infectious nature of the classical form, a discrepancy from its distribution would be suggestive of a non-infectious aetiology, or one based on very different disease determinants, for atypical scrapie.

This methodology is appealing in the syndromic surveillance context. Via the incorporation of time-space, disease-space and disease-time interaction terms in our models we could account for the presence of aberrations in time and space (Richardson et al., 2006). A seemingly obvious application of these methods would compare a particular syndrome, e.g nervous, with the spatio-temporal distribution of known nervous diseases to assess any shared patterns. Together with the incorporation of the above interactions, such an approach would provide more information, including the occurrence of shared environmental and/or surveillance-related patterns, than the mere identification of clusters of disease.

## REFERENCES

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