# Bayesian Hierarchical Models for the Evaluation and Design of Surveillance Systems: an Application to Scrapie Surveillance in Great Britain

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## Abstract

**OBJECTIVE**

We have developed a flexible model which can evaluate surveillance strategies at different hierarchical levels. It identifies key elements in the performance of the surveillance and recommends optimal sampling designs.

**BACKGROUND**

There is a need for regular evaluation of surveillance strategies. The emergence of new diagnostic tests and new sources of data, changes in the spatio-temporal distribution of diseases and other factors must be periodically assessed to guarantee that the objectives of the surveillance effort are met. Underlying this evaluation process is the need to increase the efficient use of resources.

Active surveillance remains the primary target of evaluation exercises due to the ability to introduce measurable modifications. The cost of the active surveillance of scrapie, a fatal neurological disease of small ruminants, since its implementation in 2002, has exceeded 1.18 billion dollars across the EU. In this paper, we have evaluated the scrapie active surveillance in Great Britain. More specifically, whether the current sampling strategy returns the most efficient detection capability.

**METHODS**

Our interest was to evaluate the efficacy rate, defined as the ratio between the apparent prevalence and the true simulated prevalence at the holding level. The need to account for the clustering of animals within holdings together with the presence of uncertainty for several parameters has been previously modeled to inform sampling regimes by means of Bayesian Hierarchical Models (BHM)[1]. In this study, we applied BHM to the results of the two active surveillance sources targeting scrapie in GB. We expanded on previous models by means of incorporating further levels of aggregation identified as important in the epidemiology of the disease (spatial variation, holding size). Several scenarios were simulated to investigate the impact of changing assumptions on within-holding sampling, within-county sampling and varying sampling across the categories of holding size.

The input parameters of the model comprised information about the population size, previous estimates of the holding and within holding prevalence, "true" prevalence figures to simulate the "real" population, percentage of holdings sampled within each county, percentage of animals sampled within the selected holdings, percentage of animals selected by each source , and sensitivity and specificity of the diagnostic test in both surveillance sources. Efficacy estimates for the two surveillance sources were obtained and compared across the simulated scenarios to evaluate the surveillance programme.

**RESULTS**

Our results showed the efficacy could be improved if we test more animals within a holding rather than testing few animals in many holdings. We also demonstrated the positive impact on the sensitivity of targeting large holdings and the effectiveness of the different active surveillance programmes. The application of this model may return savings whilst increasing the sensitivity of the surveillance system.

**CONCLUSIONS**

The challenging nature of the study tested the flexibility of the model, demonstrating that the model can be adapted to evaluate and optimize additional surveillance strategies; For example, the model can be easily updated to include new evidence that reflect changing trends in disease. This could also be a valuable tool for implementing targeted surveillance as high risk areas and risk dependent on holding size can be specified.

**REFERENCES**

1.Branscum,A.J., Johnson,W.O., Gardner I.A. Sample size calculations for disease freedom and prevalence estimation surveys. Statistics in Medicine 2006;25:2658-2674.