

Space-time clustering of Swiss Bovine Spongiform Encephalopathy (BSE) cases

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Cases of bovine spongiform encephalopathy (BSE) have been diagnosed in Switzerland since 1990. Until February 28, 2003, a total of 433 cases were detected. Of these, 189 were born after the ban on feeding mammalian meat-and-bone meal (MBM) became effective in December 1990. As in 1999 visual evidence pointed towards clustering in at least two geographic regions, a cluster analysis was performed. Exact co-ordinates of farms where BSE cases had spent their first year of live (farms of putative exposure) and of farms without a reported BSE case (control farms) were acquired. We also acquired exact co-ordinates of all farms and feed mills in Switzerland.

Clustering of cases was tested with tests for global clustering. Detailed statistical testing for clustering was carried out using the SaTScan-statistic (Kulldorf, 1997) and a Bayesian approach (Knorr-Held and Rasser, 2000). Odds ratios (OR) were calculated with NCSS (Kaysville, Utah 84037, USA).

Global clustering was shown for all BSE cases born after the feed ban (BAB cases). Two statistically significant clusters were identified in the analysis of the BAB cases, whereas no clustering was detected for cases borne before the feed ban. The two clusters appeared in distinct time periods, indicating different time intervals of exposure to the BSE agent. Interestingly, if the analysis was extended to detect space-time clusters, only one of the clusters of BAB cases came up significant. In contrast, there was a strong time cluster and some significant space-time clusters for cases borne before the feed ban in December 1990. Clusters resulting from a focussed analysis, where location of feed mills was provided as starting point for cluster detection, were almost identical to the clusters identified before.

Further analysis of the cluster regions showed high cattle and pig density and also a high proportion of farms with both species. Farms with a reported BSE case had an OR of 1.7 to have pigs on the farm if compared with farms without a reported BSE case. The OR to have pigs on the farm was 2.0 for farms with a BAB case if compared with farms without a reported BSE case. If BAB cases inside the cluster regions were compared with BAB cases outside these regions, the OR to have pigs on the farms was 3.8 for farms inside the cluster regions.

No significant difference in the reporting of BSE-suspect animals between regions inside and outside the clusters was found.

With the Bayesian approach the posterior relative risk for occurrence of BAB cases in a region could be identified. Regions with a higher posterior relative risk resembled well the regions identified as clusters with the SaTScan-test. However, with the Bayesian approach results for areas without a prior information should be interpreted with caution

The facts that purely spatial clustering of BSE cases was only shown for BAB cases and these clusters were located in regions with high pig density and a high proportion of mixed farms supports the hypothesis that contamination of cattle feed

with feed for other species (containing MBM) may have caused these BAB cases. The occurrence of the clusters in different time periods, as well as the results of the focussed analysis using location of feed mills as starting points, provided evidence for the hypothesis that clustering may be linked to the source of feed used on the farm of putative exposure.

Knorr-Held, L. & Rasser, G. (2000) Bayesian Detection of Clusters and Discontinuities in Disease Maps. *Biometrics*, 56, 13-21

Kulldorff M. (1997) A spatial scan statistic. *Communications in Statistics: Theory and Methods*, 26, 1481-1496