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Estimating scrapie epidemiological parameters: comparison between a population dynamic model and an individual-based model

Classical scrapie is a transmissible spongiform encephalopathy that affects small ruminants (prion disease) and is submitted to eradication measures. Transmission mechanisms are still incompletely understood and difficult to quantify. Scrapie is characterised in sheep by a genetic susceptibility factor. Its long infectious and undetectable incubation period makes direct data analyses difficult, hence the interest of a modelling approach to estimate the epidemiological parameters.

Two models were developed to represent the spread of the disease within a sheep flock: a realistic structured population model (PDE) and an individual-based model. Both take into account the same epidemiological processes, based on similar assumptions, including seasonality in transmission, genetic and age-dependent susceptibilities, long and variable incubation periods. To focus on the estimation of the epidemiological parameters, demographic processes consisting of seasonal lambings, routine culling and reform, directly derive from the flock data. The data used in this study originate from the Langlade experimental sheep flock (SAGA, INRA, Toulouse, France), in which a natural scrapie outbreak occured.

The criterion implemented to estimate the epidemiological parameters is based on the scrapie incidence observed in the Langlade data and simulated by the two models. As there are quite many parameters to estimate (23, that can be reduced to 11 with simplifying assumptions), an optimisation method based on a random-search minimisation algorithm was chosen.

The parameter values obtained for both models are comparable and realistic, *i.e.* consistent with what is known from the disease and expert opinion. The robustness of these results was tested by a sensitivity analysis, which showed that some parameters are highly sensitive and need to be identified with care.