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### Modelling for epidemiology: goals and methods

M. A. Dubois

Rather than an introduction to modelling for epidemiology, we here give a short user's notice to modelling and modellers in epidemiology. We emphasize the necessity to know in advance what one really seeks: understanding or prediction? Because the tools are usually not the same.

### The use of modelling in animal epidemiology

P. Sabatier, D. J. Bicout, B. Durand & M. A. Dubois

Mathematical modelling in epidemiology was pioneered, at the end of the eighteenth century, in a work demonstrating the effectiveness of the technique of variolisation against smallpox [Bernoulli, 1760]. In spite of the remarkable progress of the biology of the contagious diseases, which brought numerous tools allowing to quantify the distribution (broadcasting) of the infectious agents within the populations, the veterinarian environment (middle, and medical generally) remained for a long time reluctant to the use of mathematical models. Today, the emergence and the persistence of numerous infectious diseases, ask practical and theoretical questions which cannot be approached without a mathematical study of the natural, and/or controlled, dynamics of the infections within the concerned populations. To take the example of the emergence of Rift Valley Fever in sub-Saharan Africa, we show that the modelling of the infectious processes allows developing tools of epidemiological forecast and early warning, answering to the recommendations of OIE, FAO and WHO [S2E, 2001].

### Modelling vector-borne diseases

Annelise Tran, Fabienne Biteau-Coroller, Hélène Guis & F. Roger

Vector-borne diseases present complex epidemiologic cycles because of their indirect transmission mode which includes an arthropod called vector. These diseases are of major importance for human and animal health, because of the morbidity and mortality that they imply. In order to improve the understanding and control of these vector-borne diseases, different kinds of models can be developed. In this paper we present two main types of models that can be carried out for vector-borne diseases: geographic models, which describe the vector distribution based on environmental conditions, and epidemiologic models based on the calculation of the vector capacity and the disease basic reproductive ratio (R0). For each of these models, we give an example of application with the case of the bluetongue disease. Objectives, data, results, limits and the complementarities of the two approaches are discussed.

### Design and evaluation of the fox rabies control strategy in France: help of modelling

M. Artois

The paper reviews rabies epidemiological models published since 1973. It focuses on the control of fox rabies in Europe. It is suggested that models can help the understanding of the

complex interactions between the ecology of the reservoir and the transmission of the infection. Such models should be used to analyse results of disease control and forecast outcomes of new programmes.

**About usage of deterministic and stochastic models in infectious disease epidemiology: example of the Puumala hantavirus**

F. Sauvage & D. Pontier

Beyond the main factors of infectious disease emergence, it is crucial to understand mechanisms of the host-parasite relationships. We studied here the bank vole-Puumala hantavirus system through mathematical modelling. Puumala is the agent of a human nephropathy representative of several emergent rodent-borne zoonosis. Two main patterns exist for the reservoir population dynamics: a seasonal one and a multi-annual one. Human cases take place only in the multi-annual pattern area. The models reveal the importance that the vole infection through the contaminated litter can have on Puumala spread and persistence. The endemic area of the nephropathy and the simultaneity of the epidemics in the two species, revealed by field data, rest on the synergy of dynamics of both vole populations and viral shedding. The synergy is likely to extend geographically under the effect of the environmental modifications.

**Use of models for a cost/benefit study of Paratuberculosis in France**

Barbara Dufour, B. Durand & R. Pouillot

To the request of Association for certification in animal health (ACERSA) a cost/benefice analysis of paratuberculosis certification was conducted in France. This analysis required the construction of two models: A herd dynamics infection model which was exploited in a deterministic way and in a stochastic way, and an economic model. The parameters used for the dynamic model were taken in the literature or, failing this, near experts. The stochastic model was used like helps to experts and the deterministic model was useful for the economic analysis. The hypotheses and the results of these models are presented. This example illustrates the simple use of models to concretely answer questions in the field.

## COMMUNICATIONS

**Erratic canine rabies in Europe: epizootic risk?**

D. J. Bicout & M. Artois

Sporadic cases of imported canine rabies have frequently occurred in Europe in countries yet free of other "terrestrial" forms of the disease. Case study shows that most of these rabid cases result from illegal introductions of dogs in incubating period. We have employed an analysis based on the theory of epidemic processes and stochastic simulations to assess the probability of occurrence of a rabies outbreak in a region caused by an imported index case in incubating period. The treatment costs associated to the affected human population post exposition are estimated and strategies to control the epizootics are tested. It follows from this first analysis that, early clinical detection followed by culling turns out to be more efficient to decrease the outbreak probability than quarantine.

**Modelling horizontal transmission of a pathogen: hypotheses related to the chosen function and influence on simulated results**

T. Hoch, Christine Fourichon & H. Seegers

The horizontal transmission of a pathogen represents a major process when studying the spread of this pathogen in a herd and plays an important role in the dynamics of epidemiological models. This paper aims at testing the influence of different mathematical formulations encountered in the literature for the transmission function on the results of a classical SIR type model. Simulations underline that great' differences in the behaviour of the models, each of these using a different transmission function, appear when the population size varies. They also show that two main types of transmission function may be distinguished: density- and frequency-dependence. The choice of the transmission function must be based on the knowledge of the biology of the modelled pathogen-host couple and/or on experimental data.

**Estimation of the true BSE prevalence in Belgium during 2002 and 2003**

Julie Penders, N. Praet, D. Berkvens, C. Saegerman, M. Dispas, Sonja Verbraecken, S. Roels & E. Thiry

In 2002 and 2003, the mean apparent prevalence of bovine spongiform encephalopathy (BSE) in Belgium was of $6.29 \cdot 10^{-5}$. Since 2001, the detection system of this zoonosis has been based mainly on the use of a "rapid" test. The only rapid test in use in Belgium at that time was the Platelia® test, commercialized by Bio-Rad. At the development of the test, its sensitivity and specificity were estimated at 100% [95 % confidence interval (95% CI): 99%- 100%] and 100% [95% CI: 99.7% - 100%] as the ability to accurately identify a non-infected animal. However, this test has generally been used in order to screen non-clinical populations. Under these conditions, the sensibility and specificity of the test could differ from the initially calculated values, and the true prevalence of BSE could diverge from the apparent prevalence. The sensibility and specificity of the rapid test, as well as the true prevalence of BSE in Belgium, have thus been estimated by Bayesian methods for the years 2002 and 2003. Prior distributions were obtained from expert opinion, and likelihood was based on data from tested animals. The posterior distribution of the true BSE prevalence used Markov Chain Monte Carlo Gibbs sampling. In 2002 and 2003, the true BSE prevalence in Belgium is situated in a credibility interval (CI) going from approximately $10^{-7}$ to $10^{-5}$. The specificity and sensitivity of the rapid test were estimated at 99.99% [CI: 99.99 100%] and 91.23% [CI: 81.69 - 91.64%] respectively. This study shows the importance of a critical study of the sensitivity and specificity of BSE diagnostic tests, as well as the apparent prevalence of this zoonosis, as their discrepancy with initial values could have important consequences for active and passive epidemiosurveillance of BSE.

**Trends in age-at-detection in Bovine Spongiforme Enceohalopathy cases: a useful indicator of the epidemic curve in Belgium**

C. Saegerman, N. Speybroeck, E. Vanopdenbosch, J. Wilesmith, Karen Vereecken & D. Berkvens

There were 118 BSE cases in Belgium before 1 January 2004. The trends in age at time of detection of the BSE cases were analysed. This parameter was used as a predictor tool for the

current stadium of the BSE epidemic curve in a country. The following indicator variables were considered: date of birth, breed, date of detection, mode of detection, monthly number and age of animals slaughtered and rendered. The trend in age at detection in function of date of birth is a very poor epidemiological indicator. The increasing of the average age of BSE cases at the time of detection is due to the decrease of cases. That appears to be a reliable indicator of the onset of a decrease in the epidemic curve in Belgium. By means of simulations using fictitious data sets compared to real data from Great Britain, a relation between the trends of age distribution at the time of detection and the stage of the epidemic curve was demonstrated. Trend in age at the time of detection of the BSE cases may be of use in those situations where absolute numbers of BSE cases cannot be determined accurately; that constitutes the originality of this epidemiological indicator.

**Study of the space distribution of cases of bovine spongiform encephalopathy (ESB) in Galicia (2000-2004)**

A. Allepuz, G. Fernandez, Anna Alba & J. Casal

The main hypothesis for BSE infection is the feeding of cattle with meat and bone meals (MBM). In 1994, the use of MBM for ruminant feeding was banned on Spain. In this work, we describe the spatial pattern of affected animals born after MBM ban. The analysis was done in Galicia (NW of Spain). In this region, 183 cases have been detected until December 2004 of which 173 were born after 1994. Using a hierarchical Bayesian model, we estimate that the risk of infection in the parishes of the central and SE areas of Galicia had a risk 2-4 times higher than those in the other parts of the region. A significant cluster was detected by SatScan software in the central part of Galicia. That cluster is situated in an area with a high pig density. These findings could support the hypothesis of the role of cross contamination between mono-gastric feeding and ruminant feeding to explain the BSE cases of animals born after MBM ban.