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A global Bayesian approach for Quantitative Risk Assessment (QRA) from farm to illness. Application to campylobacteriosis through broiler

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Abstract

We propose a novel approach to QMRA from farm to illness. The idea is to use Bayesian techniques in two main steps: (1) modelling the process of interest by a Bayesian network based on expert knowledge; (2) extending the model using the data available performing a Bayesian statistical analysis. Unlike the Monte Carlo simulation approach as commonly used in QMRA where data sets are used independently in each module, our approach incorporates information conveyed by data throughout the food chain. It allows in particular "back calculation" in the food chain model, together with the use of data obtained "downstream" in the chain. As an illustration, the estimation of the probability to get a campylobacteriosis originated from broiler contamination in France is attempted.

Keywords: risk assessment, Bayesian network, Bayesian statistics, campylobacteriosis, broiler

Introduction

Quantitative Microbiological Risk Assessment (QMRA) is growing in importance for both public health and trade purpose. A modular approach is often proposed called Process Risk Modelling (PRM; Cassin *et al.*, 1998) or Modular Process Risk Modelling (MPRM; Nauta, 2001) which splits the farm-to-fork chain into modules that logically and sequentially progress in a similar order to that of the food system. The modules needs to be determined by the assessor by means of data or/and expert knowledge. Most models start by modelling confined modules before attempting to link them.

We tackle the problem starting with a global modelling. The model could be improved gradually at certain point while remaining consistent globally. The aim of the approach proposed is to produce a clear framework for an iterative learning process using expert knowledge and data, allowing a statistical model for mutual consolidations of the chain modules. The novel method is built on the definition of a core model based on a Bayesian network, then on the integration of available data by a Bayesian statistical approach.

The methodology proposed is applied to the disease of campylobacteriosis via broiler which is of first concern for most European countries. This simple model from farm to illness in the French context clarifies the principles and properties of the method proposed.

Materials and methods

Campylobacteriosis and broiler chickens

The model presented herewith is a continuation of the expert review carried out by the French Agency for Food Safety (AFSSA) (Mégraud *et al.*, 2004), the main aim of which was to determine the incidence of campylobacteriosis in the French population, with particular emphasis on cases caused by home consumption of chicken meat. The available data come from the AFSSA report on chicken flock and carcass contamination, from purchase data on

raw chicken from the TNS Worldpanel database concerning 4770 households and from an epidemiological study carried out in the United Kingdom which determined the number of campylobacteriosis cases for the equivalent of 4026 person-years (Wheeler *et al.*, 1999).

Bayesian global modelling

The methodology proposed comprises two main successive steps: in step M a stochastic model of the phenomenon under study is defined by constructing a Bayesian network; in step D the model is improved with the help of available data through Bayesian statistics.

Step M: Core model through a Bayesian network

In this first step, data are not introduced, just expert opinions and relevant scientific literature.
M1: Make the inventory of the variates of interest (**vi**) to characterize the system under study.
M2: Link the **vi** by means of conditional dependencies. Most often, extra variates are necessary (complementary and ancestor variates).
M3: Specify the marginal distributions of the ancestor variates and the conditional distributions of the other variates.
M4: Run the model to check that the set of all variates behaves sensibly.

Step D: Incorporating data within a Bayesian paradigm

This second step is devoted to extracting from available data as much information as possible.
D1: Relevant data are linked to the core model by means of new random variates.
D2: The posterior distribution of non observed variates is calculated using MCMC algorithms (Gilks *et al.*, 1996).
D3: A round similar to M4.

Computation

Numerical computations can be performed using Jags (Plummer, 2005), WinBUGS (Spiegelhalter *et al.*, 2003) softwares or programming in R (R Development C. Team, 2004).

Results and discussion

Results

Step M1: The **vi** are listed (see Table 1). Step M2: A directed acyclic graph (DAG; Bishop, 2006) of the model is built (see Figure 1). Step M3: The logical or stochastic links between the variates are defined (for example, $\text{logit}(p_f) \sim N(m_f, s_f)$) and the ancestors marginal distributions on prior knowledge are given (for example, $m_f \sim N(0,0.22)$ and $s_f \sim Uniform(0,0.2)$).

Table 1: Variates of interest (**vi**) in the six modules.

Module	vi	Definition
Chicken farm	p_f	Probability of a chicken flock being contaminated
Broiler production	p_b	Probability of a chicken carcass being contaminated
Consumption	λ_c	Intensity of chicken consumption in a household over a four-week period
Hygiene	p_h	Probability of cross-contamination from a contaminated broiler in a household
Exposure	p_{ey}	Probability of a person being exposed during a period of one year
Illness	p_{ib}	Probability of a person suffering from campylobacteriosis due to broiler meat within one year
Illness	p_{it}	Probability of a person suffering from campylobacteriosis within one year, whatever the source

Step M4: The prior marginal and bivariate distributions of the **vi** are displayed (see Figures 2 and 3) to validate the global behaviour of the model.

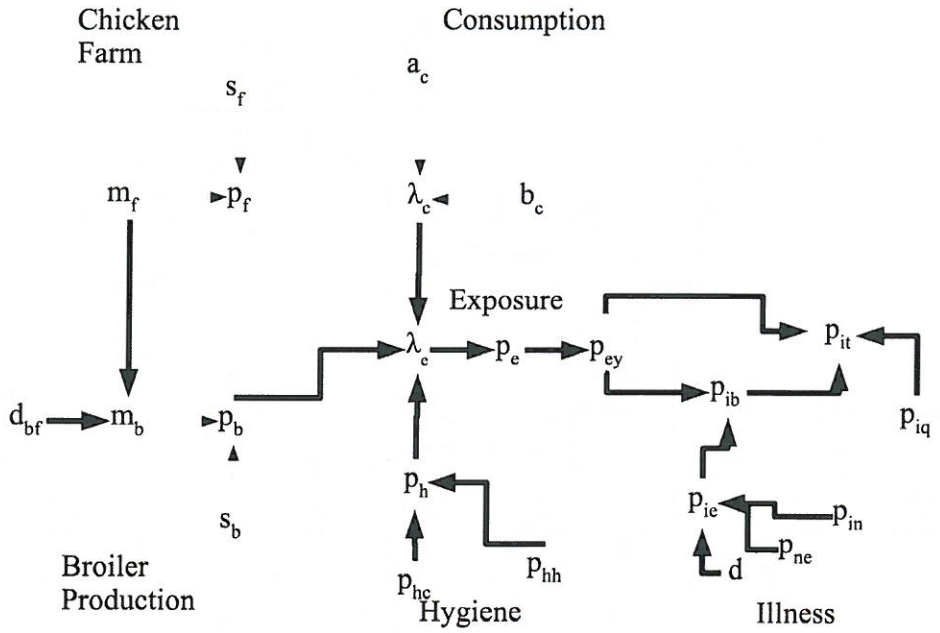

Figure 1: DAG of the core model.

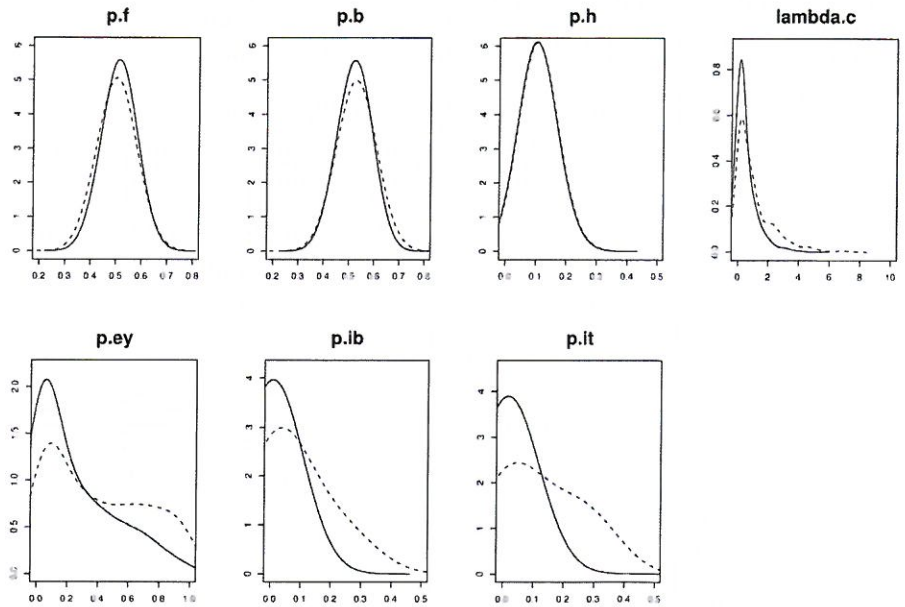

Figure 2: Prior (dotted lines) and posterior (solid lines) marginal densities of the **vi.**

Step D1: The data are incorporated (upstream and downstream) using new random variates. Step D2: The posterior distribution of non observed variates is calculated. Step D3: Comparisons between prior and posterior distributions are done (see Figure 2 and 3). Also, sensitivity analyses have been performed to determine the stability of the results obtained, concerning prior distributions and the inclusion or not of data sets in the model (upstream and downstream).

A second round with experts in the field is now necessary in order to improve the knowledge available on each **vi**. The global model we have proposed for the Campylobacter-broiler problem can be improved in numerous ways. Also, the methodology proposed arises new problems as the assembly of the modules and their interactions which depend a lot of the modelling if insufficient data are available.

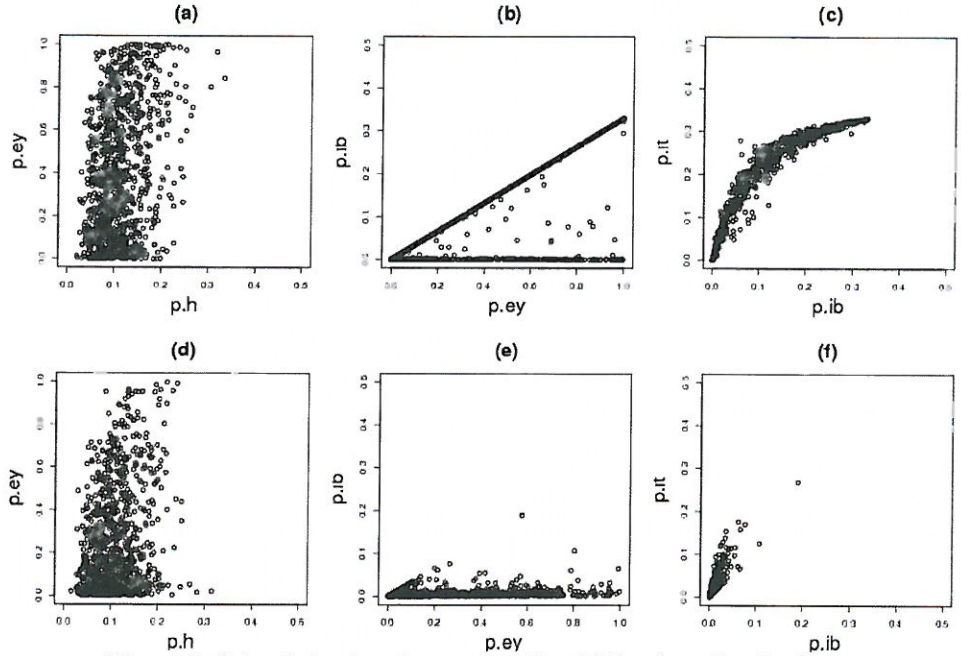

Figure 3: Prior (a-b-c) and posterior (d-e-f) bivariate distributions.

Conclusions

Although the model constructed is oversimplified, it clarifies the principles and properties of the method proposed, it demonstrates its ability to deal with quite complex situations and provides a useful basis for further discussions with different experts of the food chain.

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