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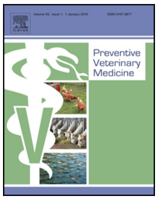

Adapting a scenario tree model for freedom from disease as surveillance progresses: The Canadian notifiable avian influenza model

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ABSTRACT

Scenario tree models with temporal discounting have been applied in four continents to support claims of freedom from animal disease. Recently, a second (new) model was developed for the same population and disease. This is a natural development because surveillance is a dynamic process that needs to adapt to changing circumstances – the difficulty is the justification for, documentation of, presentation of and the acceptance of the changes.

Our objective was to propose a systematic approach to present changes to an existing scenario tree model for freedom from disease. We used the example of how we adapted the deterministic Canadian Notifiable Avian Influenza scenario tree model published in 2011 to a stochastic scenario tree model where the definition of sub-populations and the estimation of probability of introduction of the pathogen were modified.

We found that the standardized approach by Vanderstichel et al. (2013) with modifications provided a systematic approach to make and present changes to an existing scenario tree model. We believe that the new 2013 CanNAISS scenario tree model is a better model than the 2011 model because the 2013 model included more surveillance data. In particular, the new data on Notifiable Avian Influenza in Canada from the last 5 years were used to improve input parameters and model structure.

1. Introduction

Scenario tree models with temporal discounting (Martin et al., 2007a) to support a country's claim of freedom from animal disease have been applied in Europe, Asia, Australia and North America. The models supported claims of freedom from bacterial diseases (TB (Tuberculosis) and Johne's disease), parasites (Trichinella and Echinococcus) and viral diseases (PRRS (Porcine Reproductive and Respiratory Syndrome), CSF (Classical Swine Fever), AI (Avian Influenza), AD (Aujeszky's Disease)) in livestock (swine, cattle, poultry, deer) and wildlife (fox, lemmings, racoon dog, voles, wild boars) (Martin et al., 2007b; Alban et al., 2008; Martin, 2008; Frossling et al., 2009; More et al., 2009, 2012; Schuppers et al., 2010; Wahlström et al., 2010, 2011; Christensen et al., 2011; Goutard et al., 2012; Murphy et al., 2012; Welby et al., 2012; Boklund et al., 2013; Frossling et al., 2013). For simplicity, we refer to this method as the "scenario tree model". Scenario tree models have now been around long enough for us to identify a need to further

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develop, revise or redo an existing scenario tree model. This was recently demonstrated with CSF in Denmark (Martin et al., 2007b; Boklund et al., 2013). This development was expected because surveillance is a dynamic process that needs to adapt to changing circumstances, including the success or failure of surveillance, and new knowledge should be included – the difficulty is in the justification for, documentation of, presentation of and the acceptance by researchers and veterinary authorities of the adaptations to the models (Christensen, 2003a,b, 2012). The justification may be easy to present if new data or new knowledge have been gained or if international standards for surveillance have been changed. The particular challenge for the scenario tree models is the documentation and presentation because the model validation should include: technical validation (*e.g.* same model in different software), biological validation by peer-review and publication in peer-reviewed scientific journals. Thus, having an efficient peer-review process is critical not only when a scenario tree model is developed but also if it is to be adapted. To help in this process a standardized approach to model presentation has been suggested (Vanderstichel et al., 2013) and we propose that this method can also help when a model needs to be adapted, changed or completely redone.

The first Canadian Notifiable Avian Influenza Surveillance System (CanNAISS) scenario tree model was developed and published based on 25 months of surveillance (January 2007 to January 2009) for Notifiable Avian Influenza (NAI) and a history of 4 outbreaks in 60 months (5 years from February 2004 to January 2009) (Christensen et al., 2011). Now in 2013, we have accumulated surveillance data over 5 years and the Canadian history of outbreaks of NAI spans 9 years. We applied these additional data to adapt the CanNAISS scenario tree model.

Our objective was to propose a systematic approach to adapt an existing scenario tree model for freedom from disease. We used the example of how we adapted the deterministic Canadian Notifiable Avian influenza scenario tree model published in 2011 to a stochastic scenario tree model where we modified the definition of sub-populations and the estimation method for the probability of introduction of the pathogen.

In a separate analysis, we assessed if we could change the time period from 1 month to 1 year. However, using 1 year as the time period was not practically useful and therefore the analysis is not included in this manuscript.

2. Materials and methods

2.1. 2011 CanNAISS scenario tree model

The deterministic CanNAISS scenario tree model 2011 was based on existing knowledge about NAI in Canada at the time. In particular, 25 months surveillance (1 January 2007 to 29 January 2009); 4 outbreaks in 60 months from 2004 to 2009; 4 sub-populations (British Columbia (BC), Ontario (ON), Other, Voluntary Enhanced NAI Surveillance); and PrIntro (probability of introduction of the pathogen to the Canadian poultry population) was included as the most likely value with minimum and maximum values applied in a sensitivity analysis (Christensen et al., 2011). For further information see Section 2.5.

Shortly after the publication in 2011, uncertainty was included in the model. We substituted point values with pert distributions for all input parameters with uncertainty (diagnostic test sensitivities (se), probability of introduction (PrIntro), and prior probability of infection (PriorPrInf)). This stochastic version of the 2011 CanNAISS model is the model we set out to change. In the following we simply refer to it as the 2011 CanNAISS model (Table 1).

2.2. New data

The history on Canadian outbreaks from 2004 to 2012 adds to our understanding and knowledge of introduction and spread of NAI in Canada. The reporting of both low and high pathogenic avian Influenza (LPNAI, HPNAI) in Canada has been consistent since 2004 and with each outbreak, we have obtained more detailed data on how quickly outbreaks have been resolved and the size of the reference (or target) population. Therefore, the original 2007 data on the size of the population of chicken and turkey farms from the National Poultry Associations have been improved in completeness: first, with data from BC (647 farms), then with data from Saskatchewan (SK) (68 farms) and finally with data from Manitoba (MB) (598 farms) (Table 2).

Surveillance for NAI in commercial poultry in Canada comprised both passive and active surveillance. The passive surveillance was the early detection of NAI by clinical surveillance and the mandatory reporting of NAI and the active surveillance was the active sampling and testing in CanNAISS. From 2008 to 2012, our active surveillance data included 3085 farms and 32,477 samples and all samples have been tested negative for NAI by at least one of our testing protocols (Table 1 and Christensen et al., 2011). The sampling in CanNAISS was designed to confirm that the passive surveillance was effective and the commercial poultry were free from NAI. Thus, we expected all outbreaks of NAI to be detected by the reporting (passive surveillance) – not by testing in CanNAISS. Over the last 9 years (2004–2012), all 5 NAI outbreaks were detected by passive surveillance. Each outbreak had 1 index farm (an infected farm where contact to an infected farm can be ruled out as the source of infection). In 2 outbreaks, NAI spread to 1 other farm and 1 outbreak included more than 2 farms. An apparent outbreak-farm prevalence >1% (our design prevalence (DP)) was observed only in the first outbreak (BC2004). However, when we calculated the farm prevalence by province, the SK2007 outbreak also had an apparent prevalence >1% (1.5%) (Table 2).

2.3. Literature review

We conducted a literature review with the objective to summarize the methods to estimate the probability of introduction (PrIntro) and justifications provided for case definition (CD), time period (TP), and design prevalence (DP).

A SCOPUS query (ALL(freedom) AND ALL(“scenario tree”)) AND SUBJAREA (mult OR medi OR nurs OR vete OR dent OR heal) AND PUBYEAR > 2006) found 59