How do we set the probability of introduction in a scenario tree model to demonstrate freedom from disease?

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SUMMARY

We reviewed how the probability of introduction was defined and estimated in 11 articles where scenario tree models with temporal discounting had been applied. By an example we illustrated the potential impact of the value and distribution of PIntro and we developed a graphical illustration of the relationship between case definition (CD), time period (TP), design prevalence (DP) and probability of introduction (PIntro).

INTRODUCTION

Scenario tree models with temporal discounting [1] has been applied in Europe, Asia, Australia and North America to support claims of freedom from bacterial diseases (tuberculosis (TB) and Johne's disease), parasites (Trichinella and Echinococcus) and virus (Porcine Reproductive Respiratory Syndrome (PRRS), Classical Swine Fever (CSF), Avian Influenza (AI)) in livestock (swine, cattle, poultry, deer) and wildlife. The results have been reported in 11 articles [2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12].

OBJECTIVE

Our objectives were to:

- explore the relationship between case definition (CD), time period (TP) and design prevalence (DP) and how the probability of introduction (PIntro) was set in the 11 published scenario tree models with temporal discounting [2,3,4,5,6,7,8,9,10,11,12]
- describe the relationship between CD, TP, DP & PIntro
- illustrate the potential impact of two methods of estimating PIntro on the posterior probability of freedom

MATERIALS AND METHODS

We extracted information on CD, TP, DP, reference population, and PIntro including how PIntro was estimated from the 11 manuscripts.

We developed a graphical description of the relationship among CD, TP, DP, reference population and PIntro.

We illustrated the potential impact of PIntro in an example where we applied the Canadian Notifiable Avian Influenza Surveillance System (CanNAISS) scenario tree model [3].

RESULTS LITERATURE REVIEW

The DP at the animal level ranged from 1/1 M (no clustering) to 50% (clustering) and from 0.05% to 1% at farm level. The time period was consistently set to 1 year for bacteria and parasites and 1 month for virus. In five papers, the choice of case definition (CD) was justified by reference to EU or OIE regulations. The CD was not always clear from the publication. For livestock (except poultry) the reference populations were described by the number of farms and number of animals in the population but the average number of animals per farm was not reported. The wildlife population sizes were not reported.

The published definitions of PIntro were:

- No introduction; or not provided [2,4,5,9,10]
- Release and exposure; introduction and establishment [1,6,11]
- Introduction (to herd) from contact to local infected animals and importation [8]
- Monthly probability ... CSF will be introduced into Denmark [7]; probability of at least one introduction of NAI, at DPs, into ... flocks during a specific TP [3]

We found three types of approach to estimate PItntro (Figure 1).

Figure 1: Three published approaches to set the value of the probability of introduction

- 1 divided by TPs; outbreaks divided by TPs [2,3,4,9]
- Reference to risk models or risk model included [6,7,8,11*]
- Arbitrarily [5]; No PIntro [10]; Annual prevalence [12*]

Probability of introduction estimation methods (9 manuscripts in peer-reviewed journals)

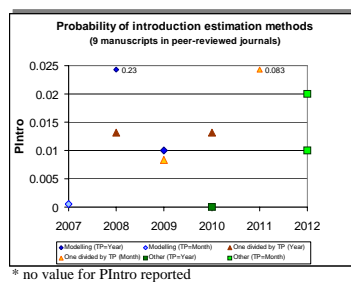* no value for PIntro reported

Figure 2: The relationship between case definition (CD), time period (TP), design prevalence (DP), reference population and probability of introduction (PIntro) with an example from the Canadian Notifiable Avian Influenza Surveillance System (CanNAISS) [3]
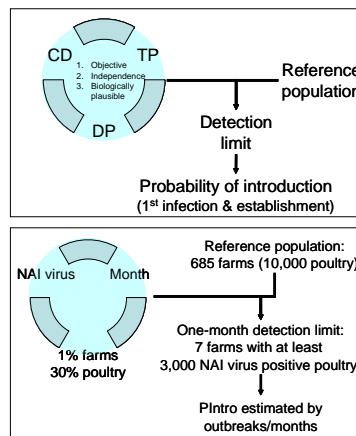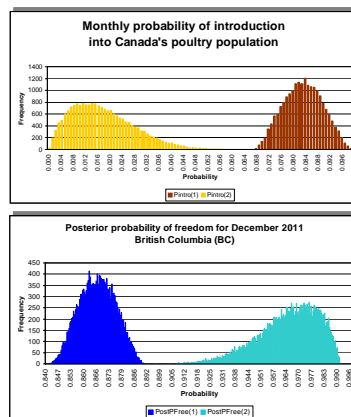

Figure 3: Potential impact of the probability of introduction (CanNAISS example [3])

Monthly probability of introduction into Canada's poultry population

Posterior probability of freedom for December 2011 British Columbia (BC)

RELATIONSHIP between CD, TP, DP and PIntro

To set a value or distribution for PIntro we need to consider the CD, TP, DP and reference population (Figure 2).

The model [1] assumes independence of test results from one TP to the next. This may be achieved by careful consideration of how CD, TP, DP are defined or by designing the surveillance to avoid re-sampling. Therefore, CD, TP and DP are tied together by the objective of the surveillance and a biologically plausible assumption of independence (Figure 2). With the detection limit we understand the number of farms and animals that would be diseased in a TP given the CD, DP and the reference population (Figure 2).

Based on a good understanding of the detection limit we can define PIntro as the probability that a disease (as defined by the CD) enters (or spreads) the reference population and establishes at the level of the DP in one TP.

IMPACT of probability of introduction

We applied the published CanNAISS scenario tree model [3] to illustrate the potential impact of PIntro. Specifically, we compared the outcome distribution (posterior probability of freedom (PostPFree) in December 2011 in British Columbia (BC)) with two different the input distributions (PIntro):

(1) Monthly PIntro(1) = pert(0.067,0.083, 0.1) based on published estimation of PIntro (outbreak/TP)

(2) Monthly PIntro (2) = probability(1st infection) x probability(establishment) = pert (0.04, 0.06, 0.08) x pert(0.001, 0.2, 0.95)

Both PIntro(2) and PostPFree(2) were lower, wider and more skewed than PIntro(1) and PostPFree(2) because the distribution for establishment was wide and skewed. The impact on PostPFree at the end of December 2011 was substantial the mean of the PostPFree increased from 87%, to 96% (Figure 3).

CONCLUSION

- The value or distribution of the probability of introduction can have a substantial impact on the posterior probability of freedom.
- The probability of introduction depends on the detection limit and therefore also on CD, TP, DP and the population.
- The CD, TP and DP need to be set to meet the objective of the surveillance and the assumption of independence of test results from one time period to the next should be biologically plausible.

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