A nomogram to calculate output estimates from surveillance models used to



Confirm freedom from infection Vanderstichel R¹ & Caraguel C²



SCHOOL OF ANIMAL AND VETERINARY SCIENCES

THE UNIVERSITY

¹Centre for Veterinary Epidemiological Research, University of Prince Edward Island, Canada ² School of Animal & Veterinary Sciences, The University of Adelaide, Australia

What is a nomogram?

A nomogram is a convenient graphical tool to represent the mathematical relationships between two or more parameters where it is possible to determine values of one or several outcomes by constructing simple lines (see Fig. 1).

What do nomograms have to do with surveillance models?

Surveillance models, used to demonstrate freedom from disease (described by Martin *et al.* 2007), apply Bayes' theorem and rules of probabilities to incorporate historical surveillance data. The complexity of these models makes it difficult for decision-makers to understand the relationship and the impact of the surveillance system sensitivity and the risk of introduction on the confidence of being free. A nomogram that graphically captures these relationships and includes the parameters needed for the model, will help policy-makers to easily explore and understand the impact of model parameters on the outcome.

What is the objective of this nomogram?

To serve as a pedagogical tool to facilitate the understanding of surveillance models by those not actively involved in analytical modeling. We hope this nomogram will be used as a visual link between analysts and those making decisions based on surveillance models.

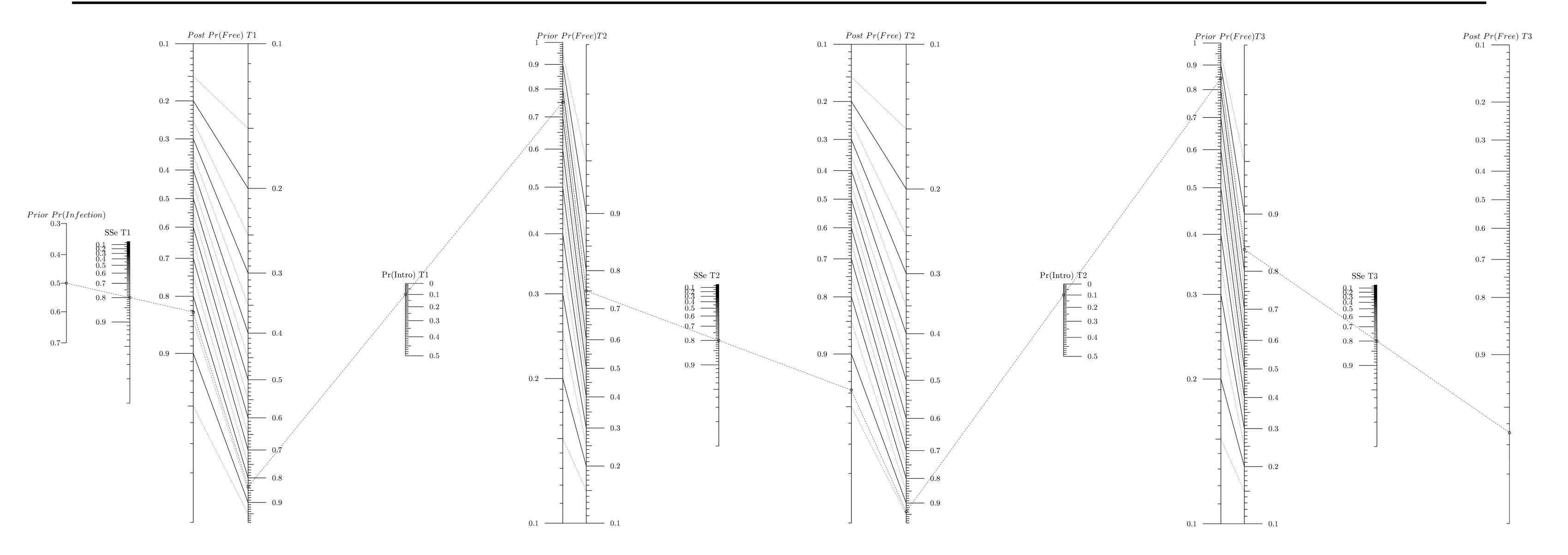


Figure 1. Freedom from infection nomogram. The nomogram estimates output values from surveillance models to confirm freedom from infection, as described by Martin *et al.* 2007. As a demonstration (dotted lines), the prior probability of infection [Prior Pr(Infection)] is set at 0.5, the surveillance system sensitivities [SSe] are the same for each time period (set at 0.8), and the probabilities of introduction [Pr(Intro)] are set at a constant value of 0.1. With these parameter values as an example, the posterior probabilities of freedom [Post Pr(Free)], which is the outcome of interest, continue to increase from time period to time period, thus indicating that the surveillance activities are sufficient to counter balance the probabilities of introduction. Although this nomogram includes only three time periods (T1-T3), surveillance models can include as many time periods as necessary.

How to use the nomogram

Required information

The only two parameters that are required as inputs are the surveillance system sensitivities [SSe] and the probability of introduction [Pr(Intro)] for each time period. In absence of prior information, the prior probability of infection [Prior Pr(Infection)] is traditionally set at 0.5. The SSe can be loosely interpreted as the probability that the surveillance activities would detect the pathogen if it is present in the population – estimating this value is well described by Martin *et al.* 2007, and the model assumes that the surveillance system specificity is perfect.

Getting the outputs

The nomogram is designed as a series of vertical scales starting with the Prior Pr(Infection) [far left]. A line is drawn through the SSe for the first time period, and the intercept indicates the posterior probability of freedom [Post Pr(Free)] for the first time period, after accounting for the surveillance data collected in that time period.

Before the beginning of the second time period, the risk of a pathogen being introduced during the first time period and not detected [Pr(Intro)] must be accounted for. Therefore, the line from the Post Pr(Free)T1 is extended through the Pr(Intro)T1 to determine the Prior Pr(Free) for the second time period. The process is repeated for subsequent time periods. Please note that for illustrative purposes, Fig. 1 has only three time periods – surveillance models could include more time periods.

Reference: Martin, PAJ, Cameron, AR, Greiner, M. 2007. Demonstrating freedom from disease using multiple complex data sources 1: A new methodology based on scenario trees. Prev Vet Med 79:71-97.

The nomogram was created with PyNomo (GNU General Public License, version 0.2.2) www.pynomo.org



dian SwineConseil canadienh Boardde la santé porcine

