

# A Simulation-Based Approach to Determine Sample Sizes in Stochastic Scenario Tree Models for Freedom of Disease

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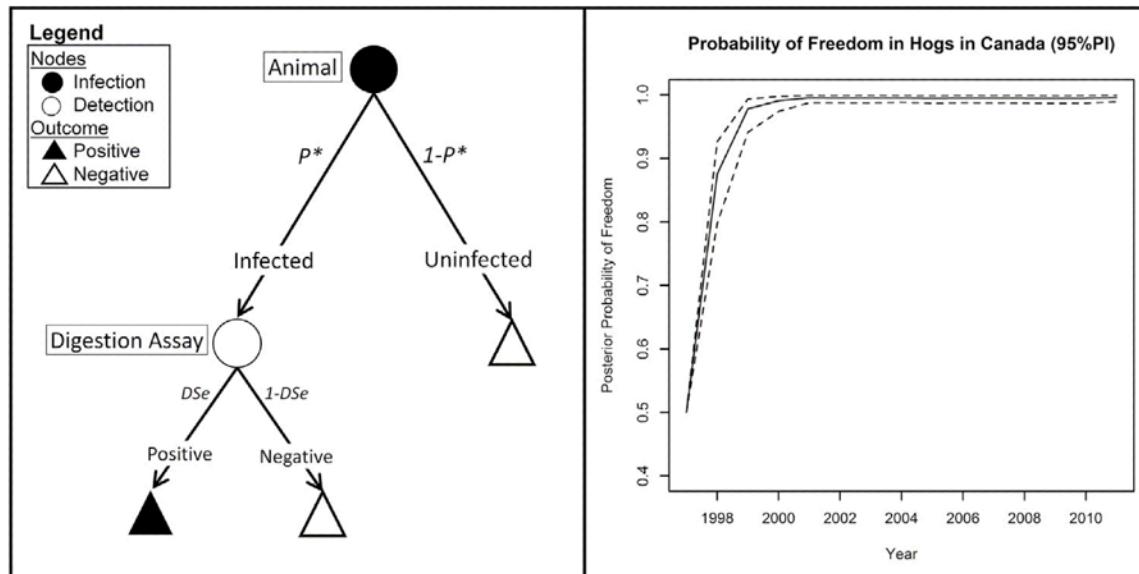
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## SCENARIO TREE MODELS FOR FREEDOM OF DISEASE

- Freedom of disease (in a population)  $\sim$  prevalence below some threshold ( $P^*$ , the “design prevalence”),
- The flow of sampling and testing of animals is organized in a scenario tree,
- When all animals test negative, compute  $\Pr(\text{prevalence} \leq P^*)$ , the “probability of freedom of disease” (PFD) — an important concept e.g. for trade.

Example from  
Vanderstichel  
et al. (2013):  
(*Trichinella  
spiralis*,  
 $P^* = 0.01\%$ )



**Objective (talk):** to outline how sample sizes for stochastic scenario tree models (STMs) can be determined by simulation, and to illustrate the impact of key parameters in STMs.

## KEY PARAMETERS OF SCENARIO TREE MODELS

- **design prevalence**: fixed value set by user/context for “acceptable” low level of disease,
  - \* **1-level model** (“animals”): single value  $P^*$  for population prevalence,
  - \* **2-level model** (“animals within herds”): values  $P_u^*$  and  $P_h^*$  for unit (within-herd) and between-herd prevalences, resp.,
- **probability of “introduction”** ( $P_{in}$ ) of disease from one time step to the next: fixed or stochastic value, possibly time-dependent,
- initial PFD ( $P_0$ , at start-up of sampling/model): fixed or stochastic, sometimes set arbitrarily at 0.5,
- sampling or test parameters, e.g. diagnostic test sensitivity (DSe): fixed or stochastic.

Stochastic nodes/parameters are drawn from probability distributions, e.g. the commonly used **PERT<sup>1</sup> distribution** ( $a, b, c$ ) for values within a bounded range (e.g. probabilities or DSe’s):

- a beta distribution scaled from (0, 1) to an arbitrary interval ( $a, c$ ),
- the two parameters of the beta distribution are restricted to one, the PERT distribution’s most likely value  $b$ , where  $a < b < c$ .

<sup>1</sup> PERT stands for program evaluation and review technique, a project management tool developed in the 1950s and 1960s with a statistical component for the duration of project phases.

## PLANNING A SCENARIO TREE MODEL

... involves to ...

- decide about the **time step** for the model, e.g. yearly updates,
- determine the **sampling design**: which units to be sampled per time step,
- determine the **structure** (e.g., number of levels) and **nodes** of the tree (including any risk nodes) and their **distributions** (or fixed values),
- set values or distributions for the basic model parameters ( $P^*$ ,  $P_{\text{in}}$ ,  $P_0$ ).

**Sample size(s)** are determined to meet a specified criterion, say  $\text{PFD} \geq 0.90$ , but...

- $\text{PFD}$  is random (for a stochastic STM), so need to focus on a **feature of its distribution**, e.g. the mean or a percentile, determined by simulation<sup>2</sup>,
- $\text{PFD}$  is time-dependent (calculated after each time step), so need to decide the **time horizon** for the criterion to be met<sup>3</sup>; **note**: it may be logically infeasible to get a system up to a desired criterion in a single time step.

**Additional consideration**: the sampling will most naturally be designed for two phases:

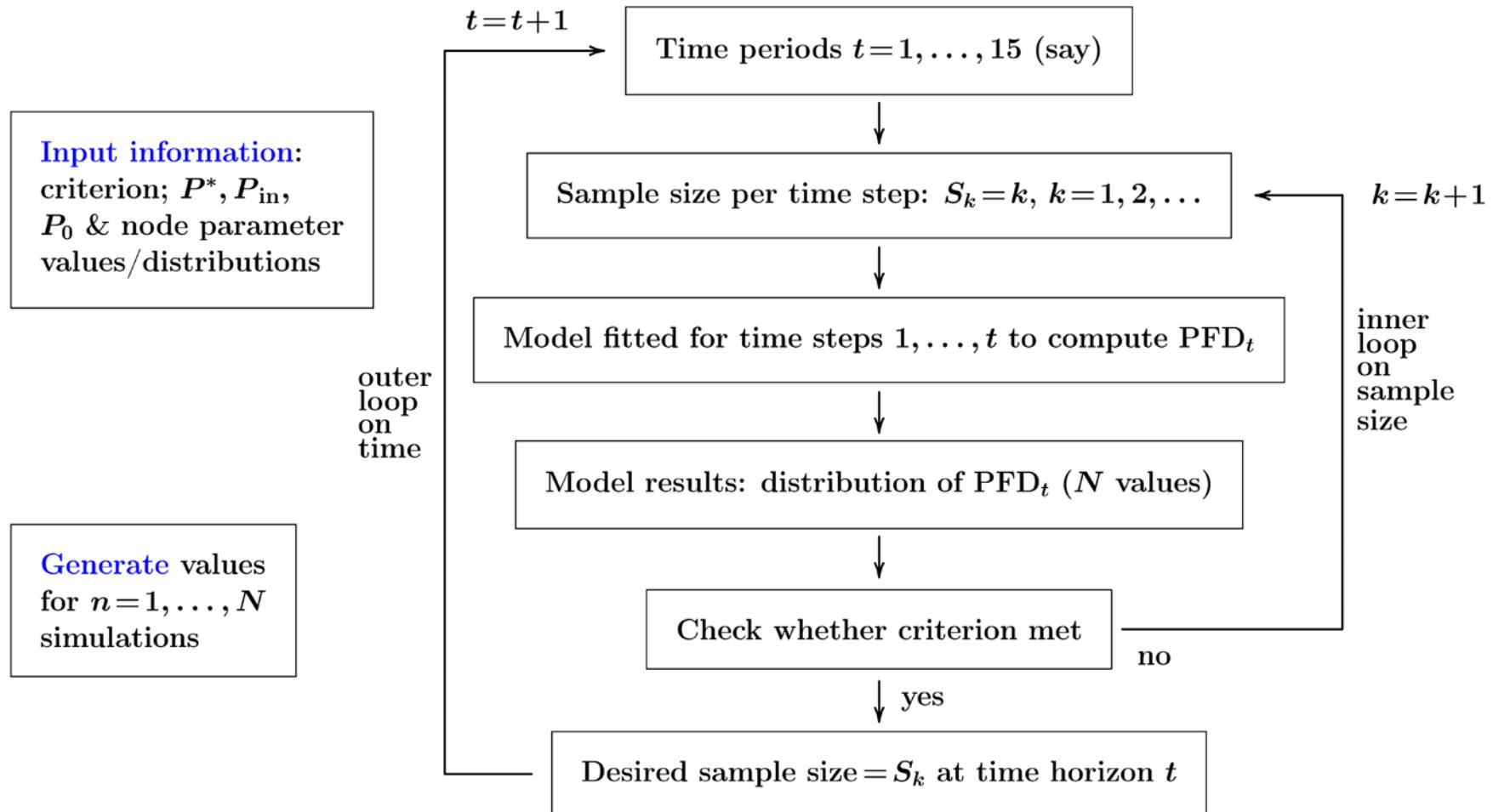
**(i) start-up until criterion is met, (ii) maintenance of criterion.**

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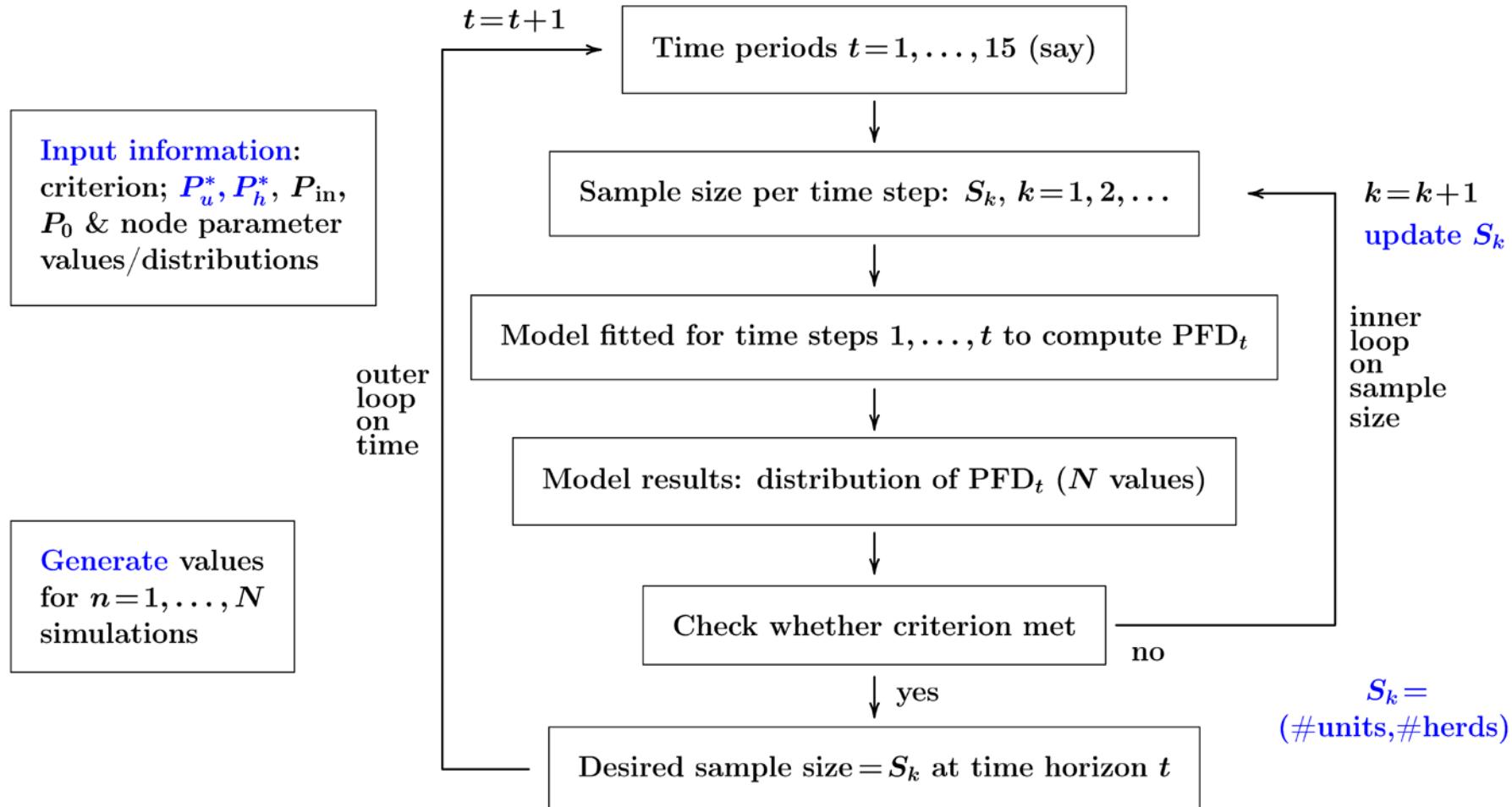
<sup>2</sup> The number of simulations ( $N$ ) will depend on the complexity of the distribution and the feature of interest; e.g., tail percentiles require larger  $N$  than the mean.

<sup>3</sup> If a criterion is to be met immediately (first time step), sample size formula and calculators exist, for both deterministic and simple stochastic trees; e.g., Cameron & Baldock (1998), Cannon (2001), Johnson et al. (2004), and Epitools at the Ausvet website: <https://epitools.ausvet.com.au/samplesize>.

## SAMPLE SIZE ALGORITHM FOR 1-LEVEL STOCHASTIC SCENARIO TREE MODEL



## SAMPLE SIZE ALGORITHM FOR 2-LEVEL STOCHASTIC SCENARIO TREE MODEL



## FIRST RESULTS: PFD VERSUS SAMPLE SIZE (1-LEVEL MODEL)

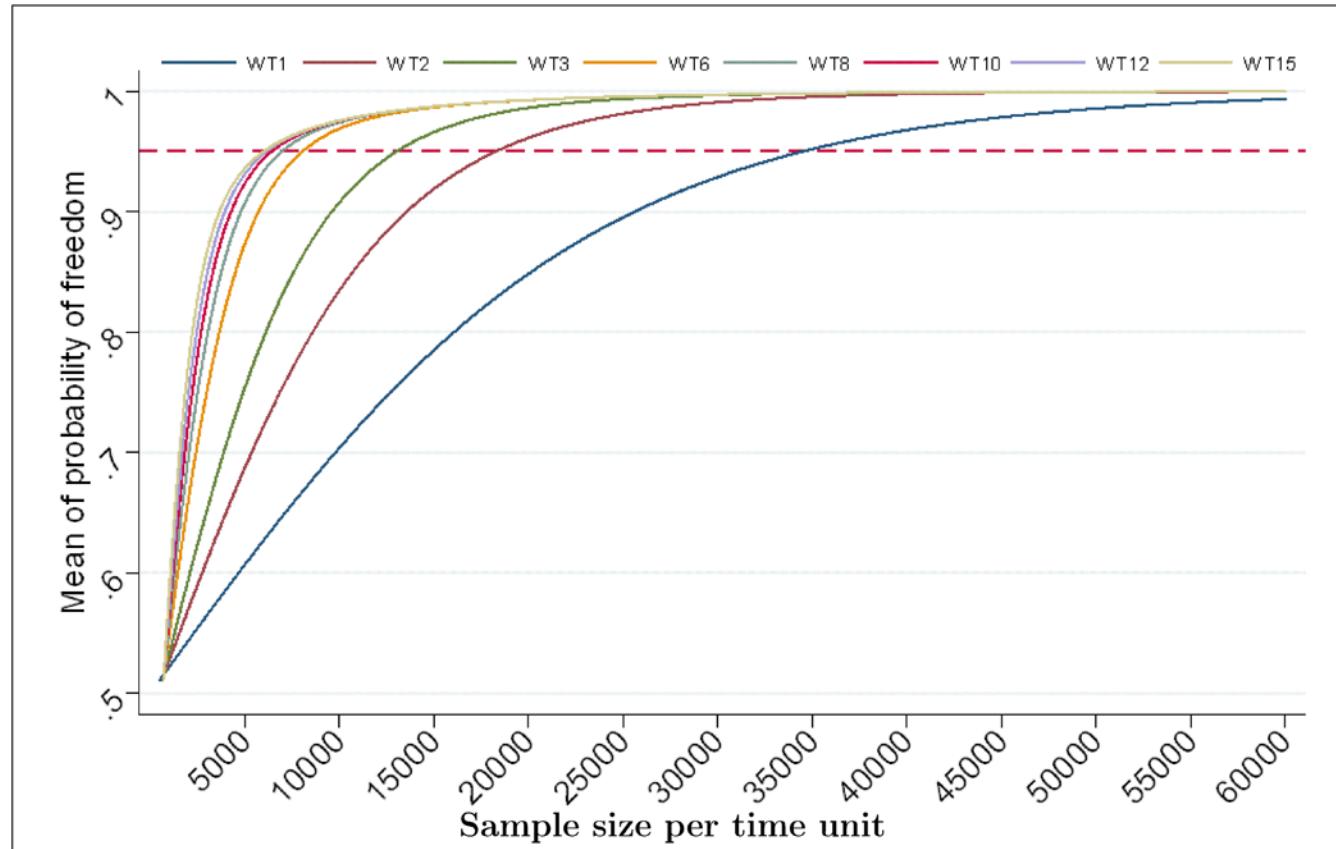
### Model Settings:

$P^* = 0.0001$ ,  $P_0 = 0.5$ ,  $P_{in} \sim \text{PERT}(.001, .03, .07)$ ; test node:  $DSe \sim \text{PERT}(.4, .95, .99)$ .

(WT = waiting time  
for system's PFD)

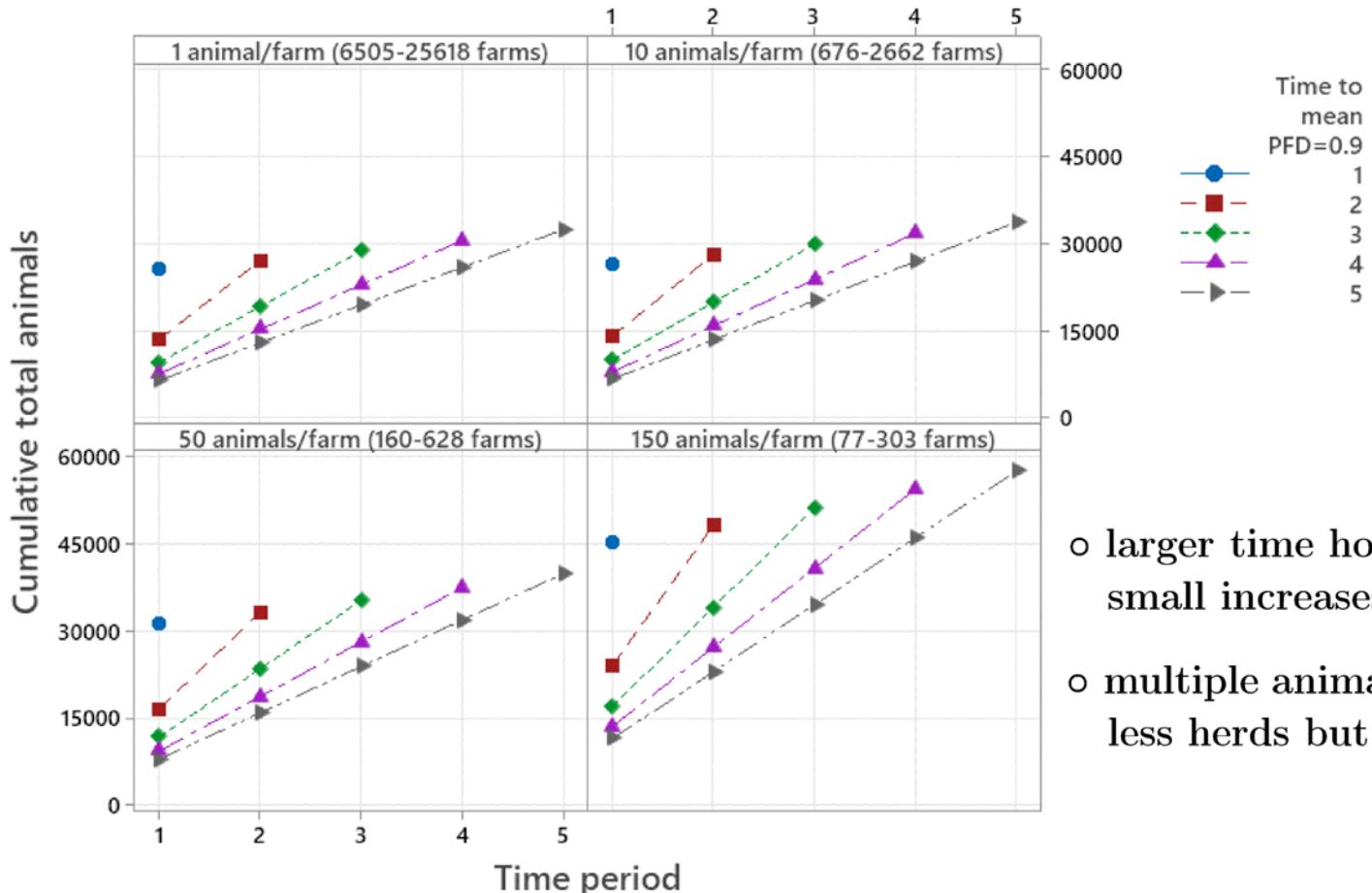
### Findings:

- (mean) PFD increases with sample size and years sampled,
- high PFD may require large number of samples (total).



## NEXT RESULTS: TOTAL ANIMALS REQUIRED (2-LEVEL MODEL)

Model Settings:  $P_u^* = P_h^* = 0.01$ , other settings unchanged.



- larger time horizons  $\Rightarrow$  small increases in # animals
- multiple animals per herd  $\Rightarrow$  less herds but more animals

## ALGORITHM DETAILS

- calculation of PFD used **Bayesian updating** formulas, which are now standard for scenario tree models (e.g., Martin et al., 2007), in particular

$$\text{PFD}_t = \frac{\text{PFD}_t^*}{\text{PFD}_t^* + (1 - \text{PFD}_t^*)(1 - \text{SSe}_t)},$$

where **SSe** is the **system sensitivity**, and  $\text{PFD}_t^*$  is the (posterior)  $\text{PFD}_{t-1}$  from the previous time step updated by the probability of introduction  $P_{\text{in}}$ <sup>4</sup>, now having the role of a **prior probability** for the next time step,

- the **search over sample sizes** for a 1-level model may utilize that larger time horizons require fewer samples per time step,
- the **search over sample sizes** for animals and herds in a 2-level model can be implemented in different ways, e.g. by fixing first the # herds and searching for # animals, or vice versa,<sup>5</sup>
- simulations were based on  $N = 10\,000$  iterations,
- all coding was done in R, using the `mc2d` library.

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<sup>4</sup> This update (also referred to as **temporal discounting**) is a simple multiplication of  $\text{PFD}_{t-1}$  by  $(1 - P_{\text{in}})$ , assuming independence between disease introduction prior to and during the time step.

<sup>5</sup> Note: Some settings with low # herds may not be able to meet the search criterion, regardless of # animals.

## MAINTAINING HIGH PFD; ADAPTIVE SAMPLING

**Fact:** The requirements on sample size to start up a STM surveillance are typically far heavier than for maintaining an ongoing surveillance,<sup>6</sup>

⇒

Also of interest to know required sample sizes for a **running system**:

- **simple approach:** start with high value for  $P_0$  (but ignores uncertainty in PFD distribution),
- **adaptive sample size determination:** for each time step, assume the minimal number of samples to meet the PFD criterion,
  - \* essentially the same algorithm, but the PFD distribution from the previous time steps can be used directly for the next time step,
  - \* two-dimensional searches for (# animals, # herds) may need further assumptions/restrictions on what is desirable.

Some findings for **adaptive sampling** (1-level scenario):

- adaptive sample sizes stabilize, quickly with high  $P_{\text{in}}$  and mean-based criteria,<sup>7</sup>
- adaptive sampling always ( $t > 1$ ) requires more units than fixed horizon sampling.

<sup>6</sup> The trade-off between information from new and past samples is largely controlled by  $P_{\text{in}}$ .

<sup>7</sup> Equilibrium results for PFD exist when  $P_{\text{in}}$  and the system sensitivity are constant.

## CONCLUDING REMARKS

**Main message:** exploring implications of sample sizes is relatively **easy to do** in stochastic scenario tree models once you know how to update such models  
— intuitively because there is no variation in the actual data (all test results are negative).

**Second main message:** the approach is flexible enough to incorporate specific features of the scenario tree to be set up (e.g., its structure, its **time horizon** to meet the PFD criterion, time-varying parameters or sample sizes).

Our results largely confirmed **general rules and expectations** for the system's behaviour (e.g., about the gain of sampling herds relative to animals within herds), but the ability to simulate a system provides quantitative information not otherwise available.

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You Have Just Seen ...

A simulation-based approach to determine sample sizes in stochastic scenario tree models for freedom of disease  
presented by Henrik Stryhn (<http://stryhnstatistics.ca>)

Thank you for your attention!