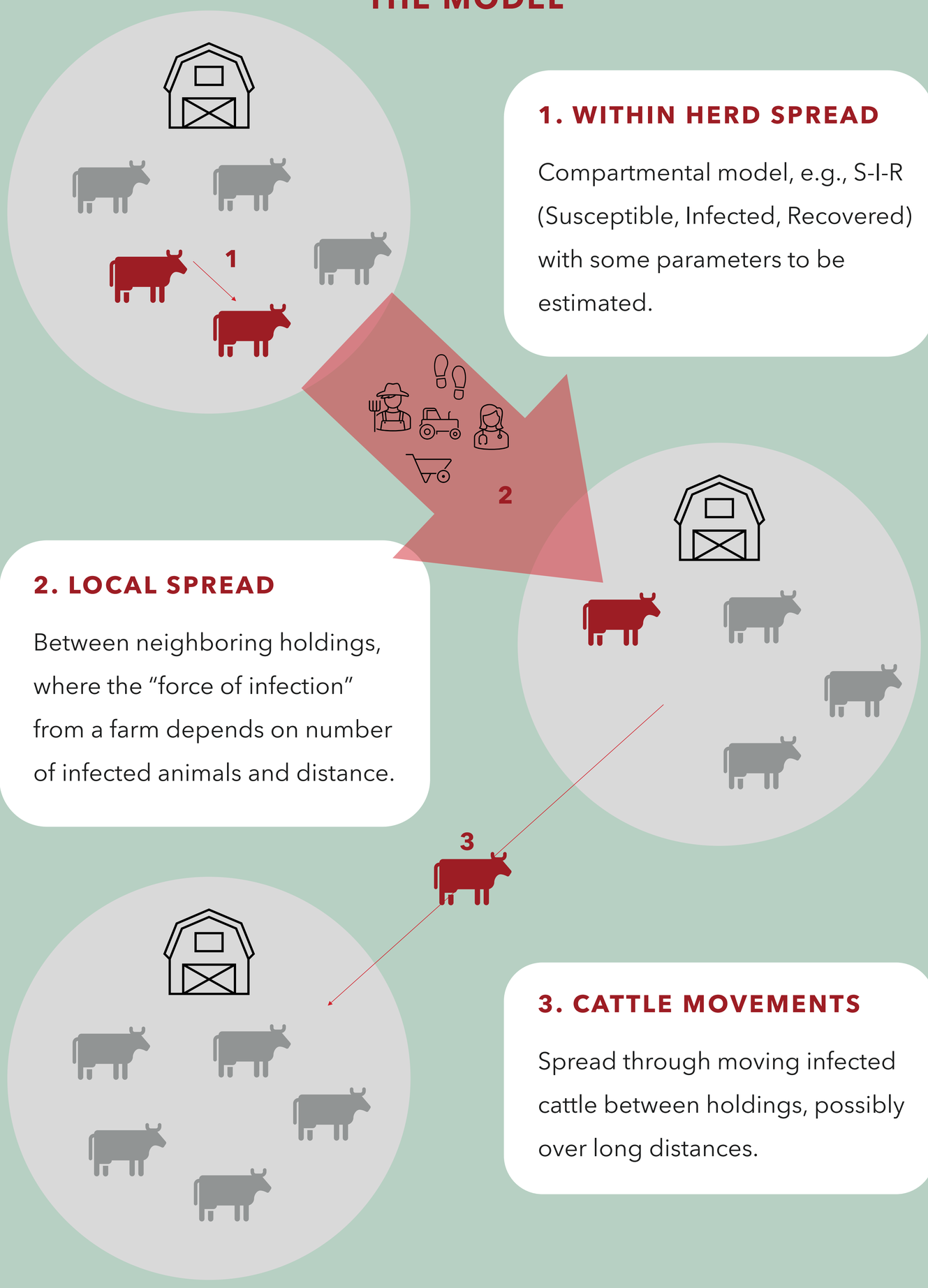
SVEPM 2026 London, UK

STEFAN WIDGREN & **IVANA R. EWERLÖF**
irewe.github.io | ivana.ewerlof@sva.se

MODELLING DISEASE SPREAD IN THE SWEDISH CATTLE POPULATION USING SIMINF & BAYESIAN METHODS

THE MODEL



1. WITHIN HERD SPREAD

Compartmental model, e.g., S-I-R (Susceptible, Infected, Recovered) with some parameters to be estimated.

2. LOCAL SPREAD

Between neighboring holdings, where the "force of infection" from a farm depends on number of infected animals and distance.

3. CATTLE MOVEMENTS

Spread through moving infected cattle between holdings, possibly over long distances.

SIMINF

SimInf

A flexible and efficient framework for data-driven stochastic disease spread simulations.

Available at CRAN

CONTEXT

A disease spread model fitted to data:

- Helps to understand the epidemiology of a pathogen
- Can simulate and evaluate how control measures affect spread
- Improves the basis for decision-making to mitigate disease spread

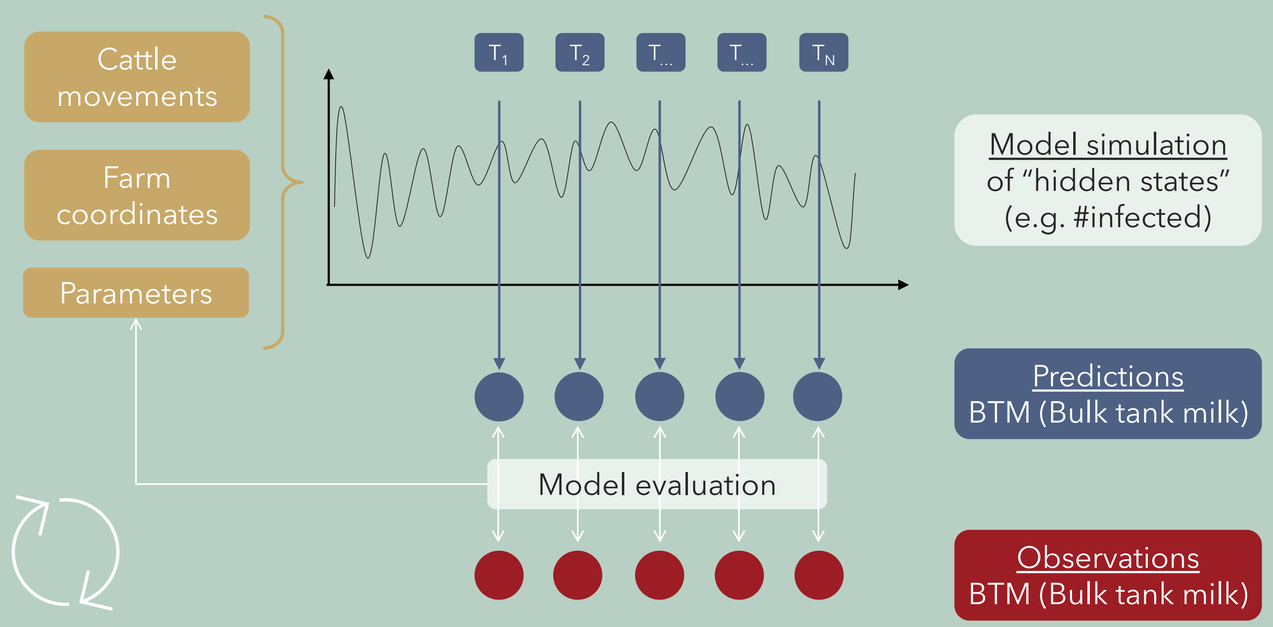
APPLICATION

With few modifications, this method can be applied on various pathogens.

Currently used in Sweden for:

- *Salmonella* Dublin
- *Mycoplasma Bovis*

MODEL PARAMETERISATION



PARTICLE MARKOV CHAIN MONTE CARLO

PMCMC [1,2] is a Bayesian method that was used for parameter inference. It is well suited for stochastic models with time-dependent outcomes that are not directly observable.

[1] Andrieu, C., Doucet, A., Holenstein, R., 2010. *Particle Markov Chain Monte Carlo Methods.* J. R. Stat. Soc. Ser. B Stat. Methodol. 72, 269–342.

[2] Endo, A., Van Leeuwen, E., Baguelin, M., 2019. *Introduction to particle Markov-chain Monte Carlo for disease dynamics modellers.* Epidemics 29, 100363.

MycoModel

FUNDED BY FORMAS

CO-FUNDED BY EUP AH&W

SLU VÄXA SVA SWEDISH VETERINARY AGENCY