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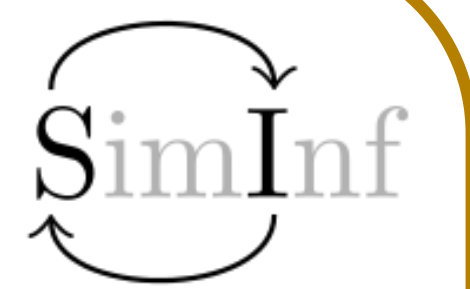
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MODELLING THE SPREAD OF *MYCOPLASMA BOVIS* IN SWEDEN USING THE SIMINF FRAMEWORK

BACKGROUND

- *M. Bovis* causes severe infections in cattle
- Negative impact on animal welfare and production
- Difficult to treat, no efficient vaccine
- Prevalence in Sweden is increasing

SIMINF

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

Available at CRAN

METHODS

MODEL

A data-driven within- and between-herd spread model will be developed in SimInf (Widgren et al., 2019).

Farm scale
Compartmental model

Regional scale
Local spread and spatial properties

National scale
Between-herd movements

SUSCEPTIBLE		INFECTIOUS
S_t	$\beta \frac{E(t)}{N} S_t$ / αI_t	I_t

φI_t

ENVIRONMENT
$E(t)$	$\mu E(t)$

Figure 1. A plausible compartmental model for M. Bovis is a SIS model with an environmental compartment. Transition between compartments depends on the values of parameters $\beta, \alpha, \varphi, \mu$, the environmental contamination E(t), as well as no. of individuals in the population (N) and in the different compartments.
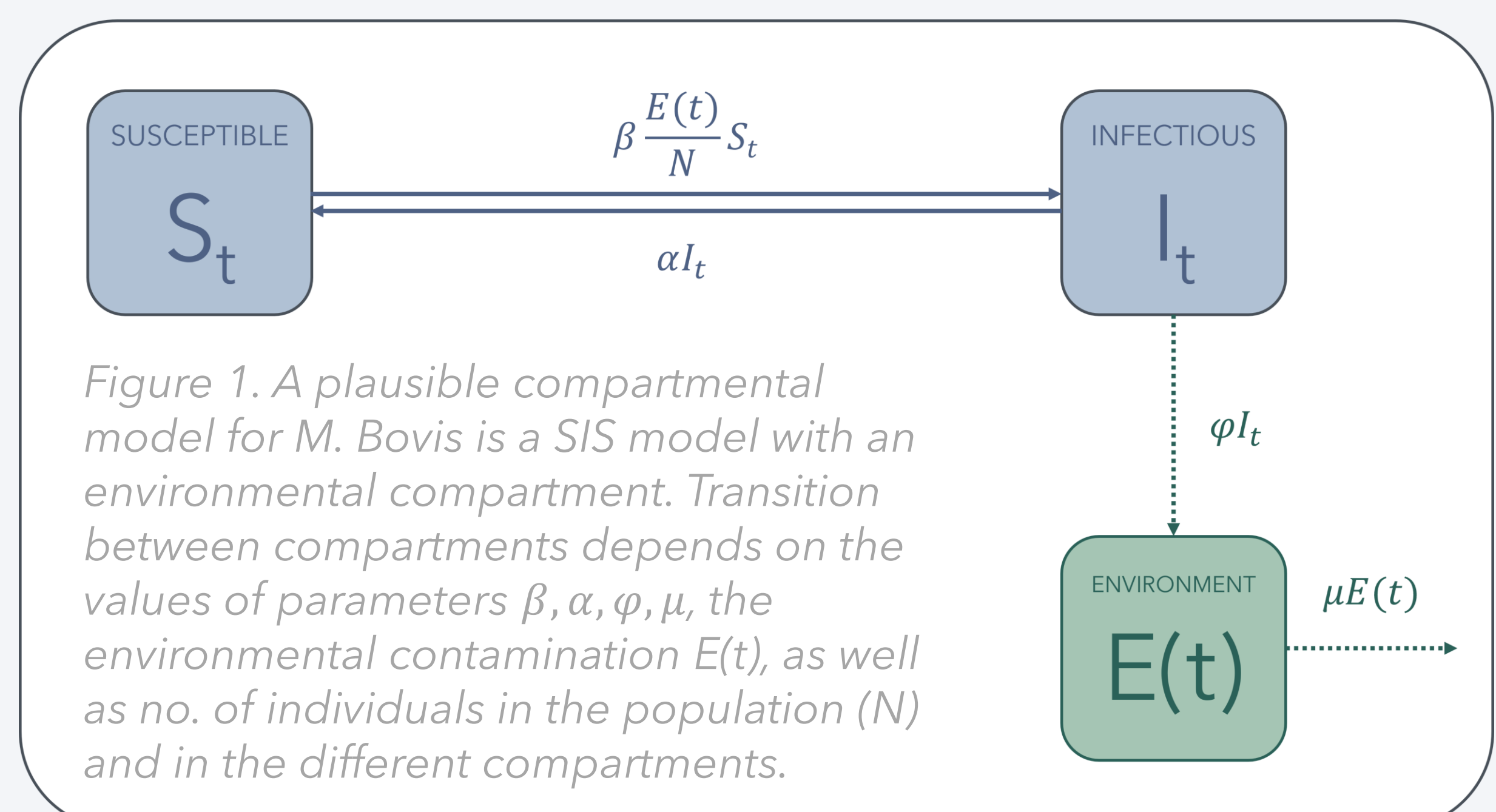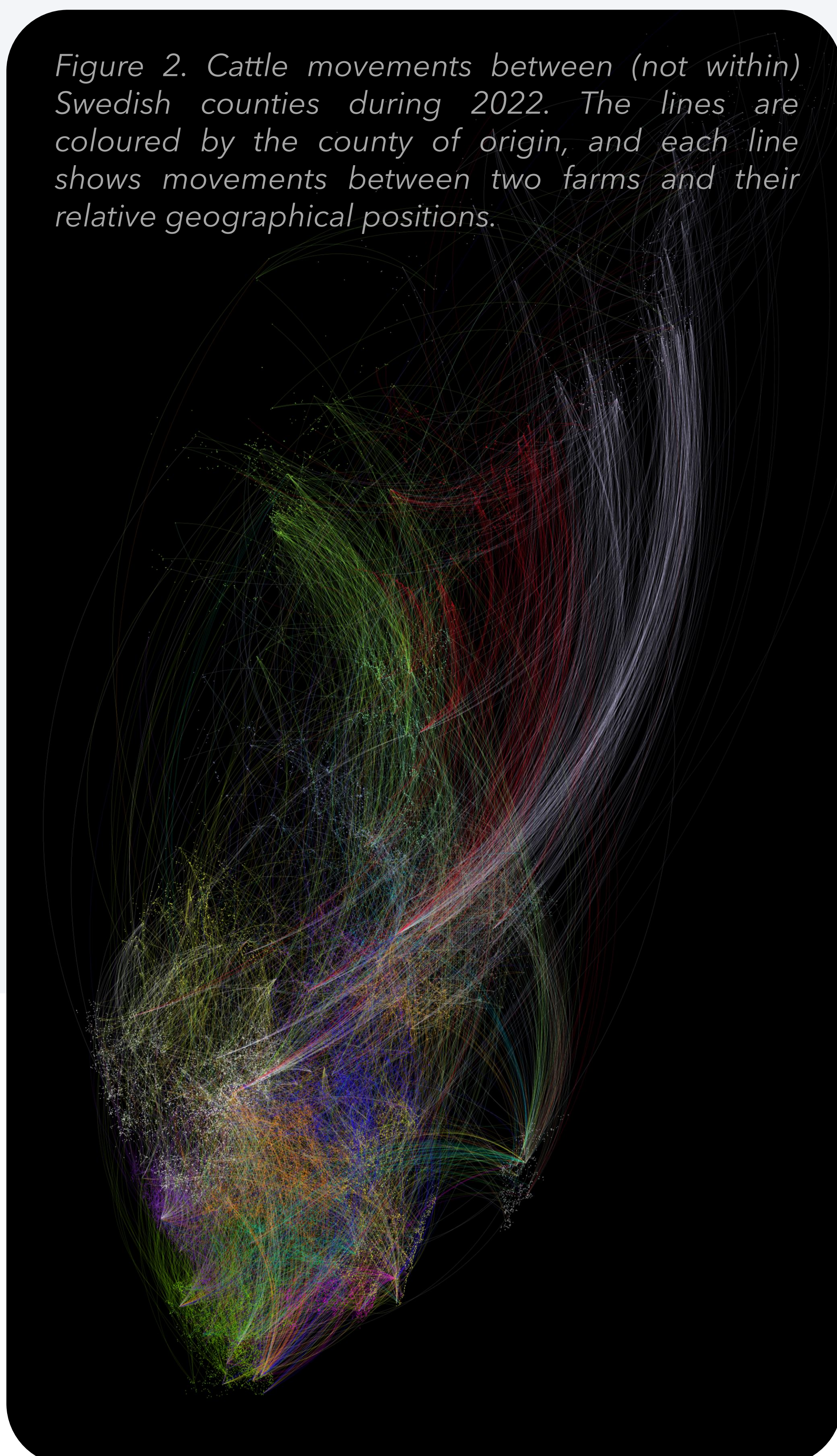
Figure 2. Cattle movements between (not within) Swedish counties during 2022. The lines are coloured by the county of origin, and each line shows movements between two farms and their relative geographical positions.

DATA

- Longitudinal sampling of *M. Bovis*
- All registered births, deaths, and between-herd movements of cattle, since 2005
- Composition (no. of individuals and age) at each farm at every time step
- Geographical location of farms

APPROXIMATE BAYESIAN COMPUTATION

will be used to find a model and parameters that best match the observations from the *M. Bovis* sampling.

EXPECTED RESULTS

The developed model can be used to simulate various control strategies and how they impact the prevalence and spread over time. The results will be valuable for farmers, veterinarians and decision makers.