Data-driven stochastic modelling of *Salmonella Dublin* infection in dairy herds

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AIM

To build a within- and between-herd transmission model of *S. Dublin* infection in dairy herds to further evaluate potential suveillance strategies

MOTIVATION

- Around 1% of Swedish dairy herds are infected with *S. Dublin*
- Surveillance and control measures have been in place since 1960s
- Fewer cases were detected over the years → eradication of *S. Dublin* may be possible, but it requires a more sensitive surveillance strategy

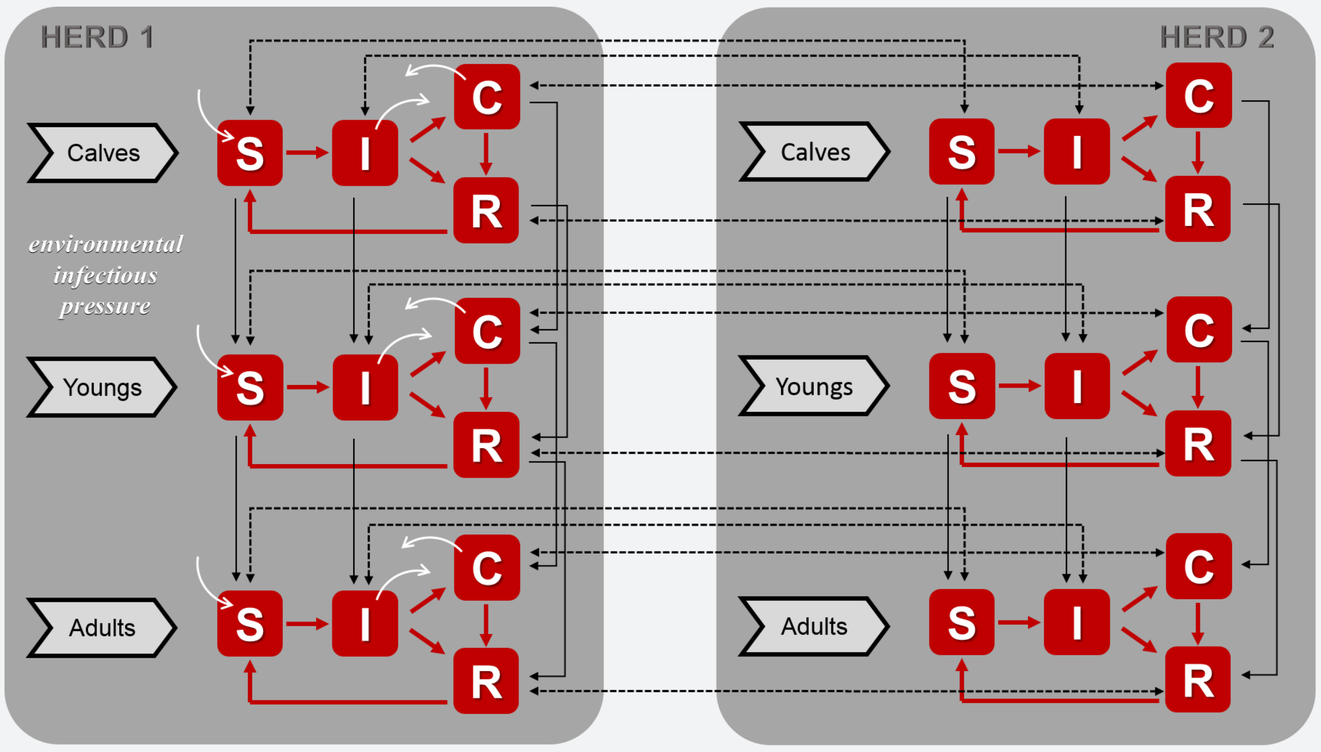
MODEL

WITHIN-HERD INFECTION DYNAMICS

- Stochastic compartmental model based on the Gillespie algorithm (R package *siminf* [1])
- **S**usceptible – **I**nfected – **C**arrier – **R**ecovered
- Age-specific parameters
- Infection probability depending on the environmental infectious pressure

BETWEEN-HERD INFECTION DYNAMICS

- Animals moved between herds according to the Swedish cattle movement registry data
- Same data to determine ageing events, introductions and exits in each herd



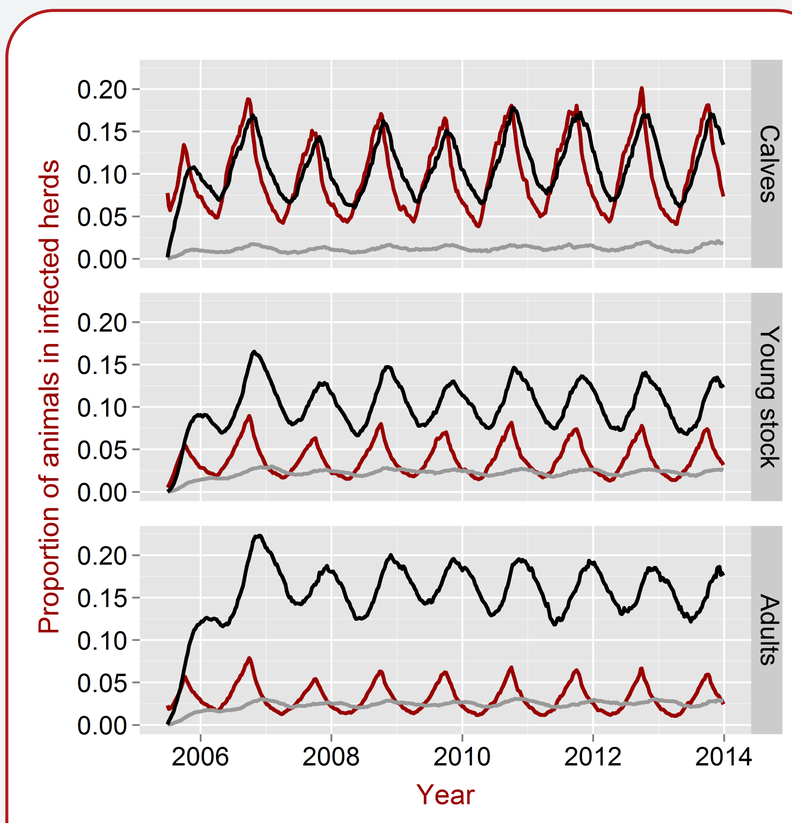


FIG 1. Average within-herd proportion of Infected (–), Carrier (–), and Recovered (–) animals in infected dairy herds, by age group.

DATA

- All cattle movements recorded in Sweden in Jul 2005 – Dec 2013
- 37 000 cattle herds (8400 dairy)
- 1.6 million cattle (900 000 dairy)
- 10.8 million events
  - birth, purchase, death, sale, slaughter, ageing

INITIALIZATION

- 3 age groups
  - calves: < 6 months
  - young stock: 6 – 30 months
  - adults: > 30 months
- Starting point: 420 (5%) randomly selected infected dairy herds, preferentially located in the high-prevalence region.

RESULTS

- Median within-herd prevalence was 9% for calves, 3.5% for young stock and 2.5% for adults (FIG. 1)
- Within-herd prevalence fluctuated around the year (seasonality) but had the same pattern between years
- Seasonality was modelled as different rate of bacterial decay per season → direct (negative) correlation with environmental infectious pressure
- Between-herd prevalence stabilized to around 1% after few years (FIG. 2)
- Results are censored because the model depends on real movement data → sensitive to starting values

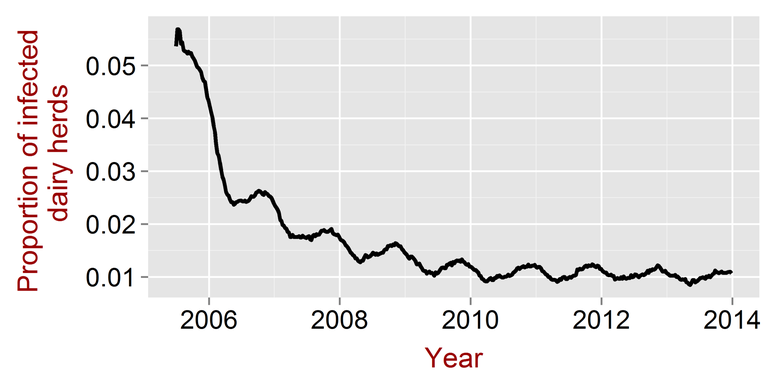


FIG 2. Between-herd prevalence. Proportion of infected dairy herds (i.e. including at least one infectious animal).

DISCUSSION

- Within-herd infection dynamics are driven by the parameters in the model, while between-herd infection dynamics mainly depend on the data
- The model mimics the spread of *S. Dublin* between Swedish dairy cattle herds → influenced by specific herd sizes and pattern of animal movements
- Animal movements include also the control measures applied during the 6 years for any cattle disease → restricted herds = ban of movements
- The model can be useful for evaluating surveillance strategies specific for the disease situation in Sweden

[1] Bauer P, Engblom S, Widgren S – Fast event-based epidemiological simulations on national scales. http://arxiv.org/abs/1502.02908 (submitted manuscript)

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