

Modelling Bluetongue Outbreaks and Control Using a Deterministic Model

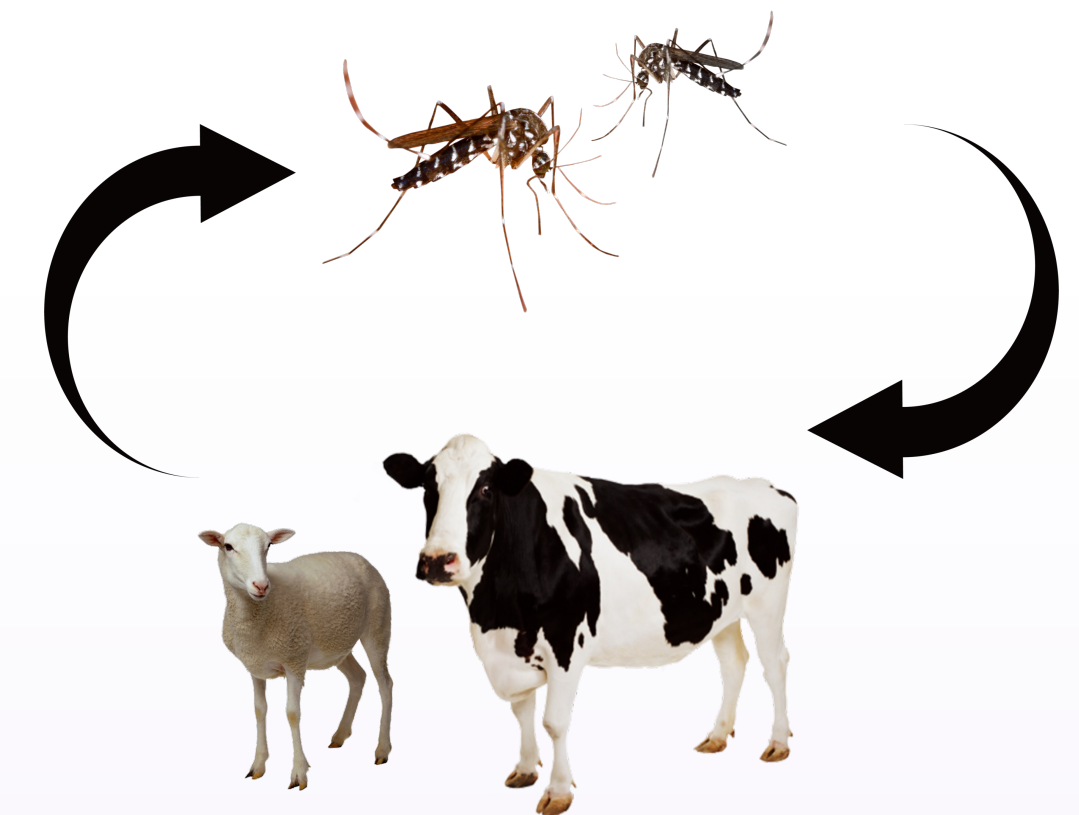
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INTRODUCTION

- Bluetongue (BT) is a virus spread by *Culicoides* biting midges to livestock and wildlife, in particular, sheep and cattle.
- To date there are 36 known serotypes, however many are considered to be putative (serotypes 27-36).¹
- BT results in severe economic consequences, through direct losses, such as clinically ill animals and decreased production, and indirect losses, such as trade restrictions and quarantine.²



METHODOLOGY

- A two-host/-vector, ordinary differential equation model was developed, which could be adapted for any region of the world.
- It was parameterised using a PRISMA systematic literature review.³
 - 652 studies published between 1957 and 2023.
 - 90 studies contributing data towards the analysis.
- The ODE model was simulated with updated parameters, using data from the Western Cape, in South Africa, as cattle and sheep populations, local environmental parameters, and *Culicoides spp.* presence data were known.
- Latin hypercube sampling and distance correlation were undertaken to explore how the parameters affected the outbreak dynamics:
 - Total number of animals affected, time to peak infection, outbreak length, number of animals infected at the peak.

RESULTS

Figure 3: Boxplots showing the difference between sheep and cattle parameters based on data extracted from the literature review

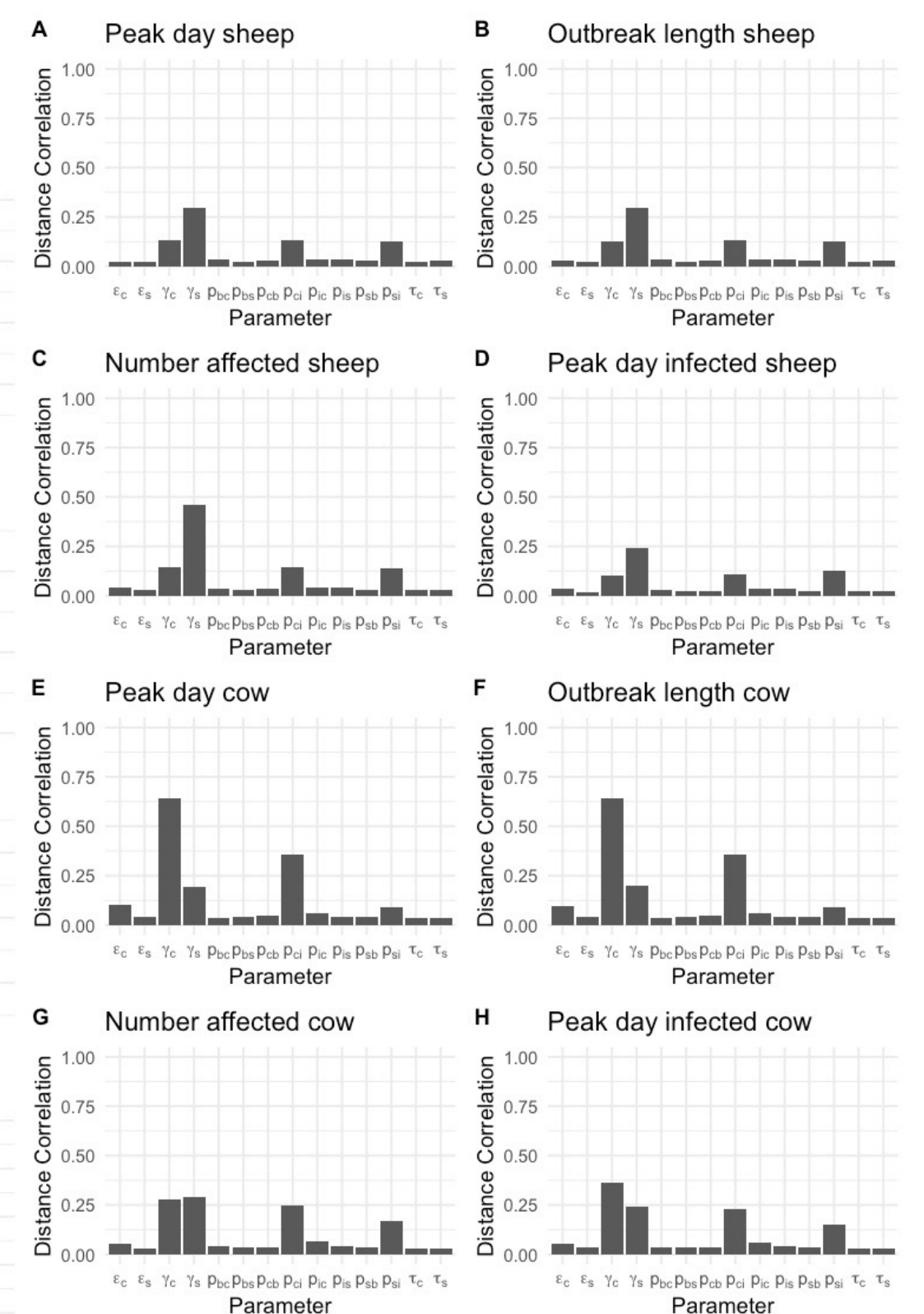
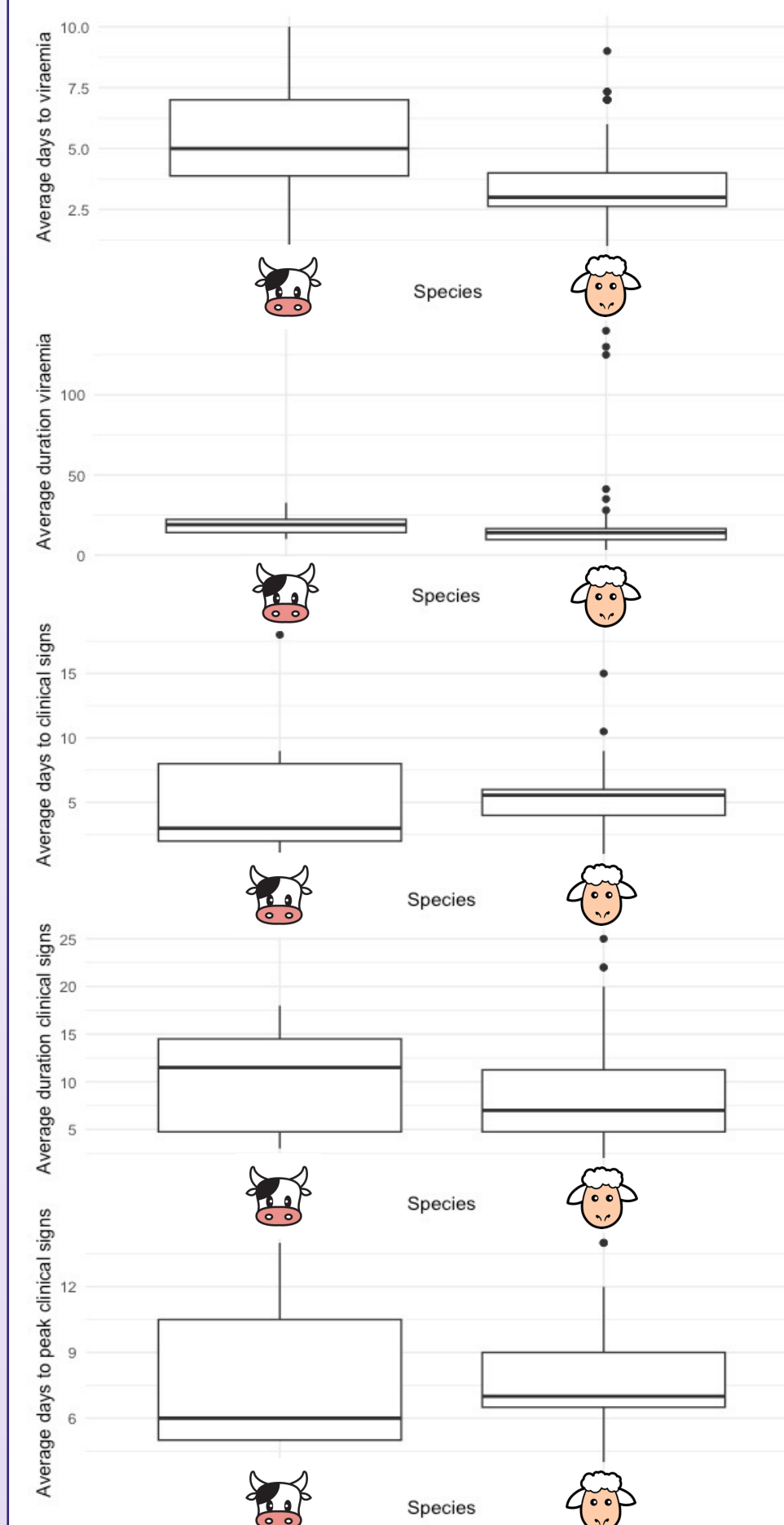


Figure 4: Bar chart displaying the results of the sensitivity analysis after Latin hypercube sampling. Recovery rates and transmission from hosts to vectors had the greatest correlation with the recorded outbreak dynamics, whereas protection factor of the vaccine and transmission rate from vectors to hosts made very little impact.

THE MODEL

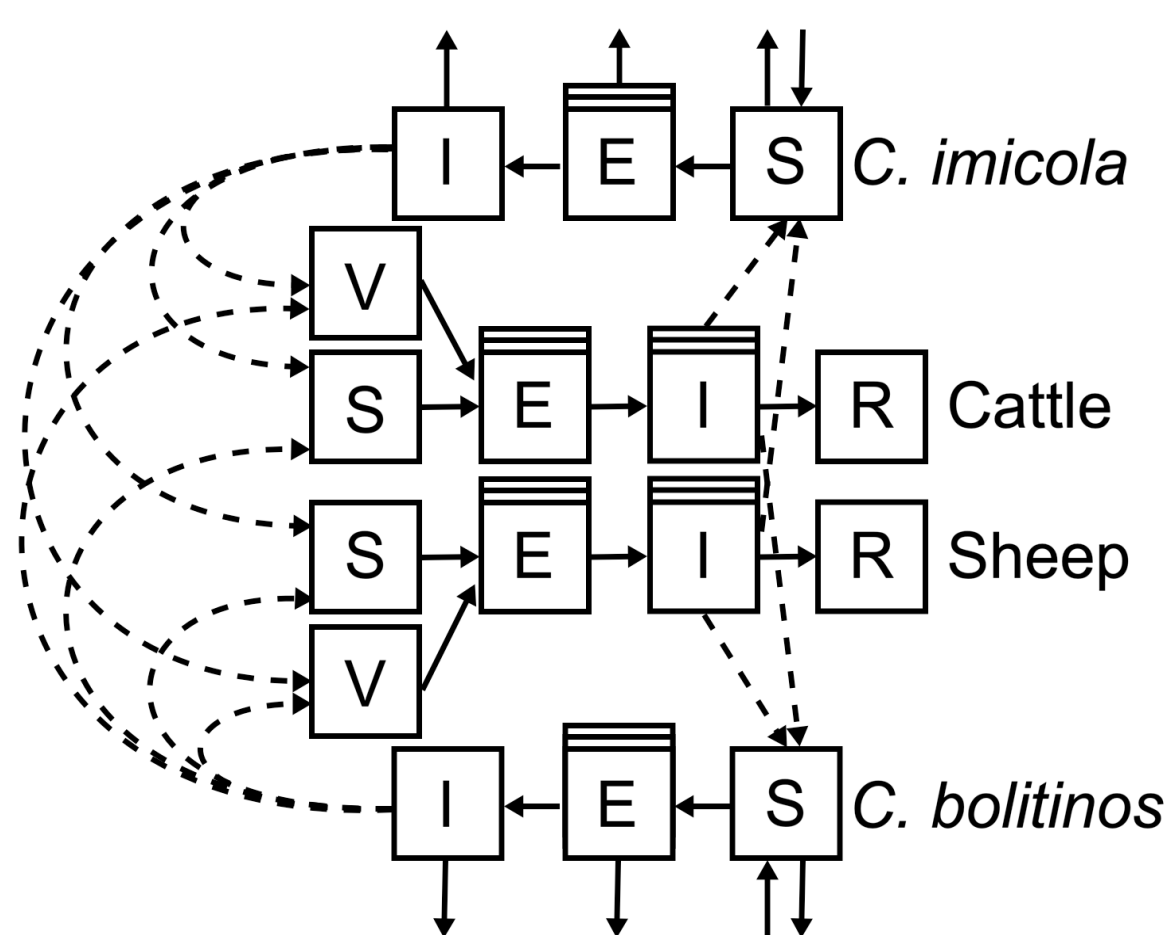


Figure 1: A flow diagram demonstrating the movement of hosts and vectors through the simulation. Compartments were susceptible (S), vaccinated (V), exposed (E), infected (I) or removed (R). Vectors also experienced mortality in all compartments and new births into the susceptible compartments. Viral transmission from host to vector or vector to host is represented with dotted lines.

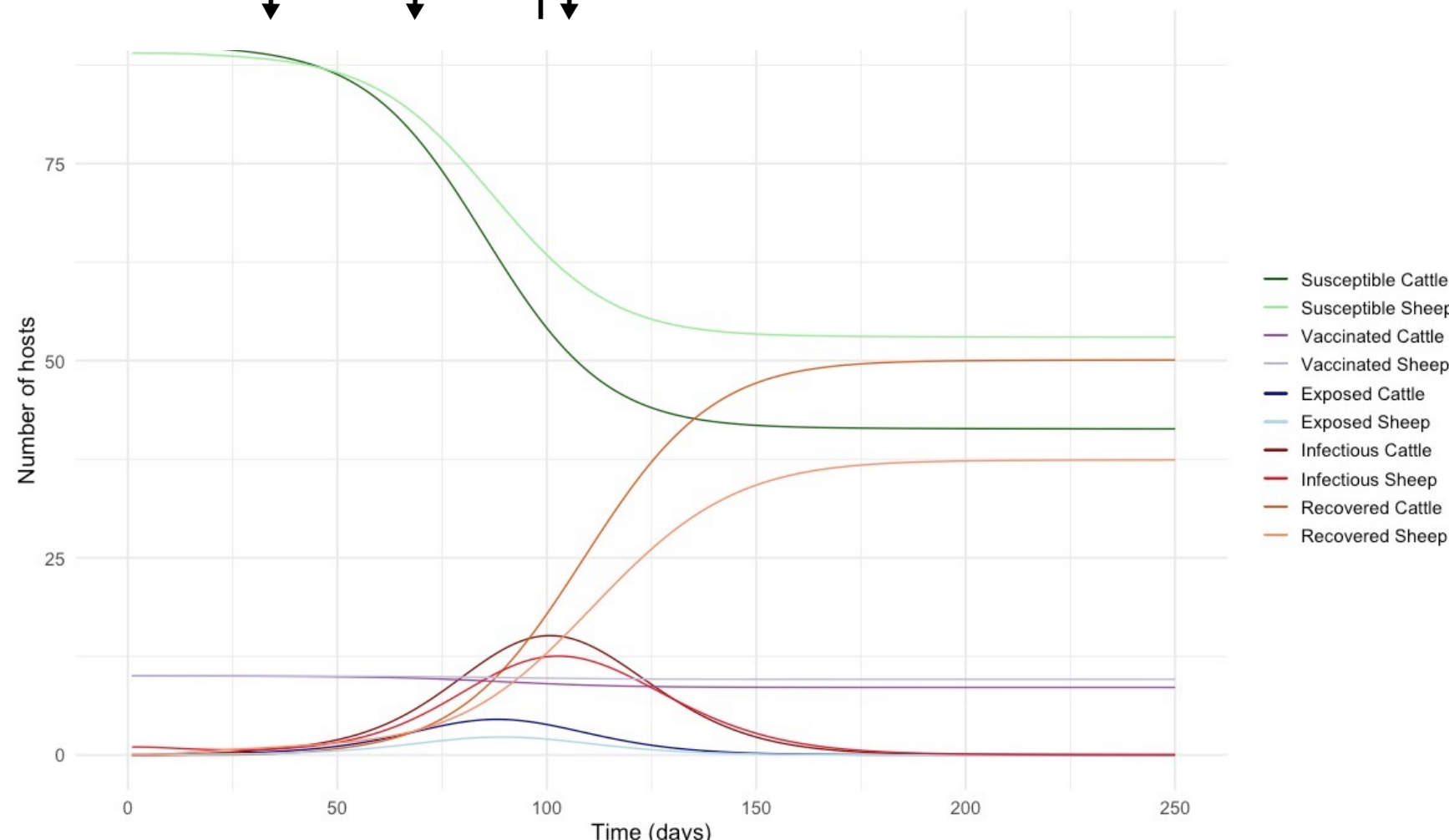


Figure 2: Host simulation over 250 days, with a starting population of 90 susceptible cows, 10 vaccinated cows, 89 susceptible sheep, 10 vaccinated sheep and 1 infected sheep.

DISCUSSION

- The model and sensitivity analysis identified that the recovery rates for sheep (γ_s) and cows (γ_c) had the greatest correlation with the outbreak dynamics, closely followed by transmission rates from cows (p_{ci}) and sheep (p_{si}) to *C. imicola* midges. This knowledge could aid in the development of control measures.
- Further work is needed to explore how vaccination reduces the transmission from hosts to midges, since this parameter was identified as considerably contributing to outcomes.
- In the future, the model can be run starting in different months of the year, to understand if the same parameters, thereby influencing control measures, are significantly correlated with outbreak dynamics year-round.



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