

Introduction: Vector borne diseases are a continuing global threat to both animal and human health. The ability of vectors such as mosquitoes to cover large distances and cross country borders undetected provide an ever present threat of introduction to other countries. Many diseases can infect multiple vector species, such that even if the climate is not hospitable for a new invasive species, local species may be susceptible and one incursion event could lead to disease establishment in these species. Here we present a model to simulate the potential outbreaks of vector borne diseases in the UK, simulating both within herd dynamics, and between herd spread. We use Rift Valley Fever (RVF) as a case study to parameterise this model.

Model Design: The model will initially seed a farm with a given number of infected mosquitoes. The location of the farm and time of year for this seeding is based on previous work on the populations of suitable mosquitoes to harbour the RVF virus. Then to simulate spread, we combine a within herd model, and a between herd model.

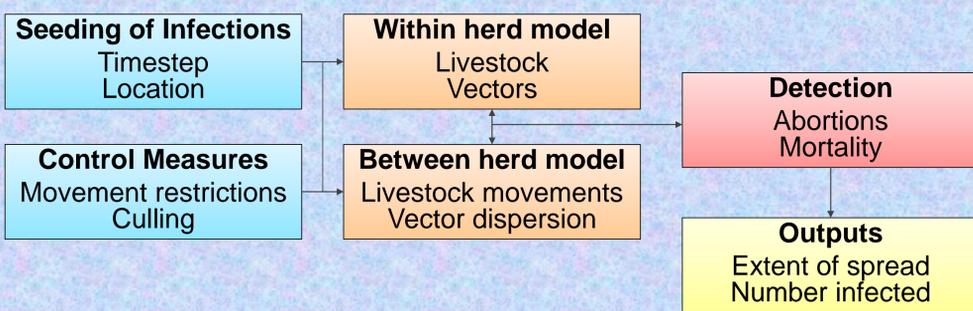


Figure 1: Framework for the model, detailing initial inputs and outputs of the model.

Within Herd Model Features:

- SEIR Model
- Species: Sheep (S), Cattle (C), Vectors (V).
- Infection states: Susceptible (S), Latent (L), Infected (I), and Recovered (R)
- Vector population split into Dormant (DV) and Biting (BV)
- Vectors become dormant after biting, and return to biting after a period of dormancy

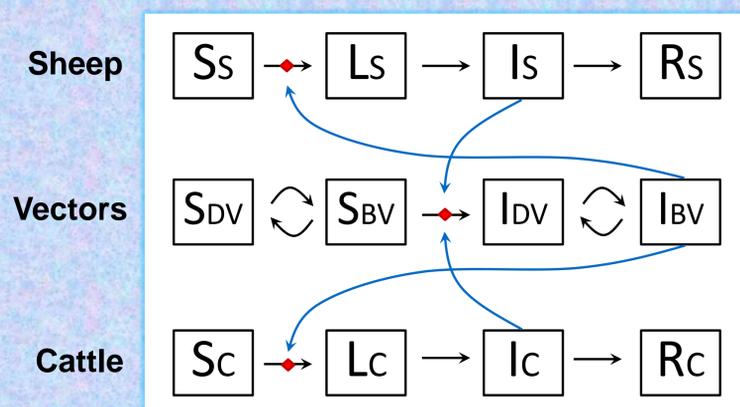


Figure 2: Summary of the within herd spread model. Blue arrows represent the spread of infection, with black arrows showing changes of state.

The within herd model allows us to track the spread of infection on single farms. This allows us to quantify the number of animals infected in an outbreak. We are also able to track individual farms to examine how the infection spreads on a single farm level, as seen in Figure 3.

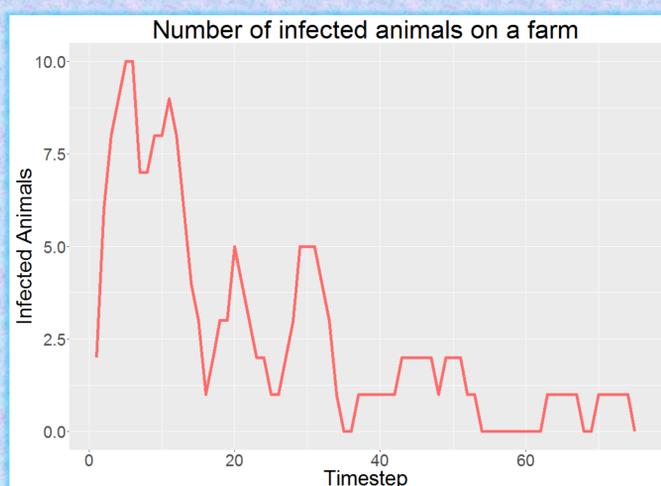


Figure 3: Example of the levels of infection on a single farm, showing the change in number of infected animals over time (assuming a recovery period of 5 days).

Conclusions:

- Detailed model, simulating complex interactions between livestock and mosquitoes.
- Can examine outbreaks on individual farm, and national levels.

Between herd model Features:

- Between herd spread by both local spread and animal movements.
- Local spread via dispersion of vectors.
- Mosquitoes have a chance of moving to another close farm depending on distance
- Movement of infected animals can spread disease over longer distances
- Model replays cattle and sheep movements from UK data

The between herd model allows us to track how large an infection becomes. In particular, we can see how many farms could be infected in a specific scenario. By including animal movements, we can examine how often outbreaks are worsened by animal movements. Figure 4 shows farms infected by cattle and sheep movements across 582 iterations. These iterations started with 100 infected mosquitoes. We see that there are more infections through sheep movements than cattle movements, and a high concentration of infections in Wales.

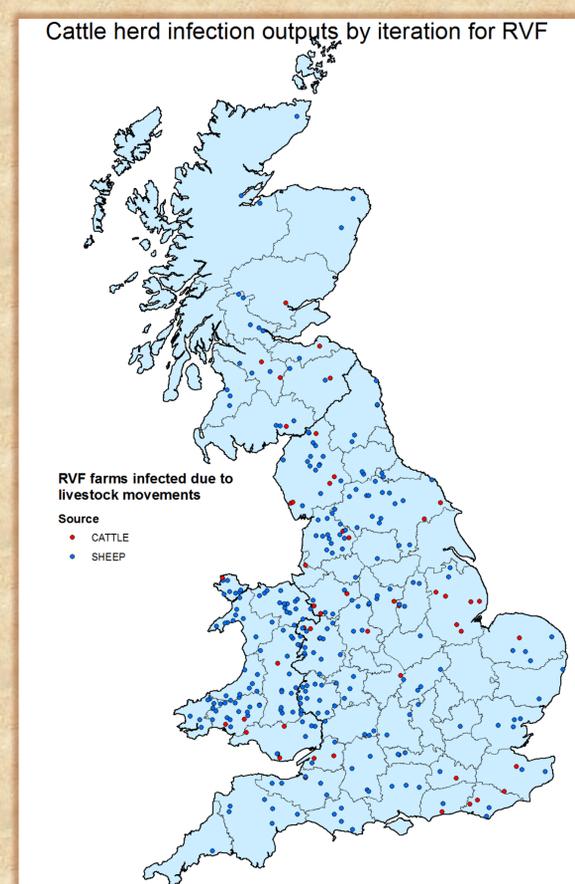


Figure 4: Farms infected by animal movement in a batch of 582 iterations. Red dots are from cattle movements, and blue dots from sheep movements.

Caveats:

- Model only runs for one year, ending in October when mosquitoes hibernate. As seen in Figure 5, there are sometimes still mosquitoes present at the end of the model, and there is a possibility of these mosquitoes overwintering and infecting new animals at the beginning on the next year.
- Uncertainty regarding the probability of mosquitoes spreading between farms.
- Model does not assess probability of disease introduction, only spread if an outbreak occurs.

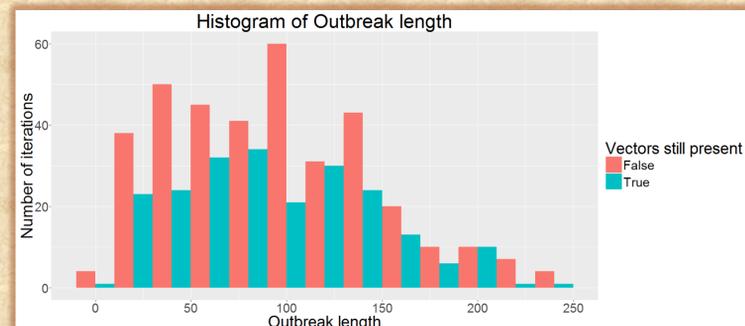


Figure 5: Length of outbreaks per iteration. Red bars represent iterations in which there were still infected mosquitoes at the end of the simulation. We see there is a large number of such outbreaks.

- Possible to simulate the effects of movement restrictions on spread.
- Can identify regions of the UK where (if there was an outbreak of RVF), there would be a high chance of disease spreading.
- Leads to locations where surveillance would be of particular use.