To cull or not to cull: a model-based evaluation of response strategies against Lumpy Skin Disease outbreaks

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Text S1: Details of model transitions.

This section details the equations corresponding to the transitions illustrated in Figure 1. Competing hazards are handled using a two-step process: first drawing the total number of individuals leaving a compartment using a Binomial draw, and then assigning new states using a Multinomial distribution.

Globally, the system is described by the set of equations:

$$S_{t+1,j} = S_{t,j} - n_{S_{t,j}\to E_{t,j}} - n_{S_{t,j}\to V_{t,j}} - n_{S_{t,j}\to C_{t,j}}$$
$$E_{t+1,j} = E_{t,j} + n_{S_{t,j}\to E_{t,j}} - n_{E_{t,j}\to I_{t,j}} - n_{E_{t,j}\to C_{t,j}}$$
$$I_{t+1,j} = I_{t,j} + n_{E_{t,j}\to I_{t,j}} - n_{I_{t,j}\to R_{t,j}} - n_{I_{t,j}\to D_{t,j}} - n_{I_{t,j}\to C_{t,j}}$$
$$R_{t+1,j} = R_{t,j} + n_{I_{t,j}\to R_{t,j}} - n_{R_{t,j}\to C_{t,j}}$$
$$D_{t+1,j} = D_{t,j} + n_{I_{t,j}\to D_{t,j}}$$
$$V_{t+1,j} = V_{t,j} + n_{S_{t,j}\to V_{t,j}} - n_{V_{t,j}\to C_{t,j}}$$
$$C_{t+1,j} = C_{t,j} + n_{S_{t,j}\to C_{t,j}} + n_{E_{t,j}\to C_{t,j}} + n_{I_{t,j}\to C_{t,j}} + n_{R_{t,j}\to C_{t,j}} + n_{V_{t,j}\to C_{t,j}}$$

The number of individuals leaving $S_{t,j}$ is determined as:

$$n_{S_{t,j}\to\bullet} \sim \mathcal{B}(S_{t,j}, 1 - e^{\Lambda_{t,j}+\omega_{t,j}+\xi_{t,j}})$$

Then the number of individuals going from $S_{t,j}$ to $E_{t,j}$, $V_{t,j}$ and $C_{t,j}$ is determined as:

$$(n_{S_{t,j}\to E_{t,j}}, n_{S_{t,j}\to V_{t,j}}, n_{S_{t,j}\to C_{t,j}}) \sim \mathcal{M}(n_{S_{t,j}\to\bullet}, \frac{\Lambda_{t,j}}{\Lambda_{t,j}+\omega_{t,j}+\xi_{t,j}}, \frac{\omega_{t,j}}{\Lambda_{t,j}+\omega_{t,j}+\xi_{t,j}}, \frac{\xi_{t,j}}{\Lambda_{t,j}+\omega_{t,j}+\xi_{t,j}})$$

The number of individuals leaving $E_{t,j}$ is determined as:

$$n_{E_{t,j}\to\bullet} \sim \mathcal{B}(E_{t,j}, 1 - e^{\sigma+\xi_{t,j}})$$

Then the number of individuals going from $E_{t,j}$ to $I_{t,j}$ and $C_{t,j}$ is determined as:

$$(n_{E_{t,j}\to I_{t,j}}, n_{E_{t,j}\to C_{t,j}}) \sim \mathcal{M}(n_{E_{t,j}\to\bullet}, \frac{\sigma}{\sigma+\xi_{t,j}}, \frac{\xi_{t,j}}{\sigma+\xi_{t,j}})$$

The number of individuals leaving $I_{t,j}$ is determined as:

$$n_{I_{t,j}\to\bullet} \sim \mathcal{B}(I_{t,j}, 1 - e^{\gamma+\xi_{t,j}})$$

Then the number of individuals going from $I_{t,j}$ to $R_{t,j}$, $D_{t,j}$ and $C_{t,j}$ is determined using:

$$(n_{I_{t,j}\to R_{t,j}}, n_{I_{t,j}\to D_{t,j}}, n_{I_{t,j}\to C_{t,j}}) \sim \mathcal{M}(n_{I_{t,j}\to\bullet}, \frac{\gamma(1-m)}{\gamma+\xi_{t,j}}, \frac{\gamma m}{\gamma+\xi_{t,j}}, \frac{\xi_{t,j}}{\gamma+\xi_{t,j}})$$

Finally, the number of individuals leaving $V_{t,j}$ and $R_{t,j}$ determined as, respectively:

$$n_{V_{t,j}\to\bullet} \sim \mathcal{B}(V_{t,j}, 1 - e^{\xi_{t,j}})$$
$$n_{R_{t,j}\to\bullet} \sim \mathcal{B}(R_{t,j}, 1 - e^{\xi_{t,j}})$$

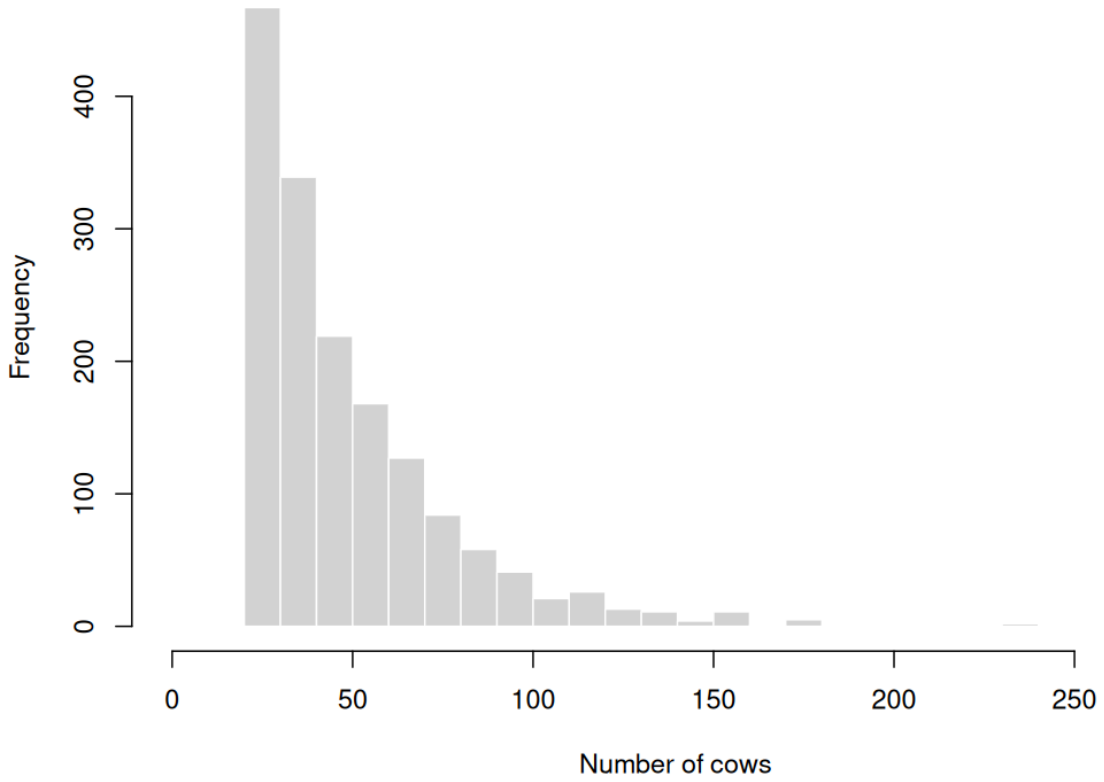

Figure S1: Herd size distribution used in simulated LSD epidemics.
This histogram shows the distribution of herd sizes, defined as the number of cattle living in a farm. It was generated as an exponential distribution with mean 30, with an offset of 20, resulting in an average of 50 cattle per farm.

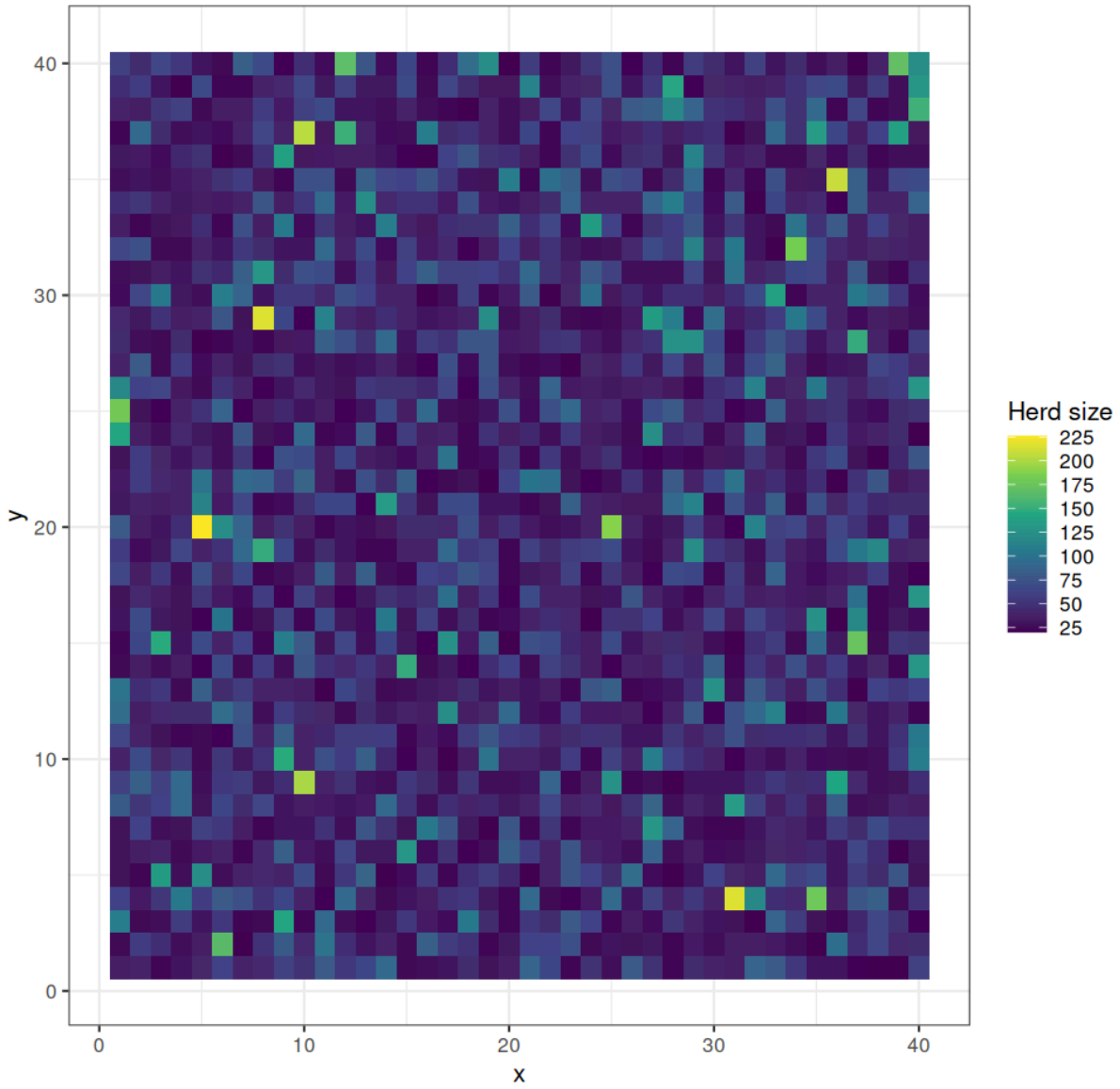

Figure S2: Example of geographic distribution of farms.
This raster illustrates the geographic distribution of one randomly selected meta-population setting amongst the 1,000 used in our simulations. Each pixel represents a simulated farm, colored according to the size of its herd. The x and y axes represent fictitious longitudes and latitudes. Each farm is considered a neighbour to all the farms immediately right, left, up, or down from itself, so that the dispersal network (non-null off-diagonal values of $\delta_{i,j}$) uses rook connectivity.

Table S1: Number of LSD cases in the simulated epidemics.
This table reports, by response scenario, the means, median, 2.5% and 97.5% quantiles of the numbers of cases after a year of simulation, as well as the proportion of simulations with more than 100 cases. See Table 4 (main text) for details of the simulated scenarios.

scenario	mean	median	quantile 2.5%	quantile 97.5%	p(>100 cases)
baseline	25K	25K	1	42K	0.944
cull_quarant_vacc	3	2	1	6	0.000
quarant_vacc	42	37	1	110	0.034
selcull_quarant_vacc	9	8	1	24	0.000
selcull_quarant_vacc_insect	6	5	1	14	0.000
all	2	2	1	6	0.000

Table S2: Number of LSD deaths in the simulated epidemics.
This table reports, by response scenario, the means, median, and 2.5% and 97.5% quantiles of the numbers of deaths after a year of simulation. See Table 4 (main text) for details of the simulated scenarios.

scenario	mean	median	quantile 2.5%	quantile 97.5%
baseline	739	724	0	1K
cull_quarant_vacc	70	56	23	201
quarant_vacc	1	1	0	5
selcull_quarant_vacc	9	8	0	24
selcull_quarant_vacc_insect	6	5	0	14
all	66	54	22	184

Table S3: Attack rates of LSD in the simulated epidemics.
This table reports, by response scenario, the means, median, and 2.5% and 97.5% quantiles of the attack rates of LSD after a year of simulation. See Table 4 (main text) for details of the simulated scenarios.

scenario	mean	median	quantile 2.5%	quantile 97.5%
baseline	0.3196	0.3195	0	0.5383
cull_quarant_vacc	0.0000	0.0000	0	0.0001
quarant_vacc	0.0005	0.0005	0	0.0014
selcull_quarant_vacc	0.0001	0.0001	0	0.0003
selcull_quarant_vacc_insect	0.0001	0.0001	0	0.0002
all	0.0000	0.0000	0	0.0001

Table S4: Number of farms with at least one LSD case in the simulated epidemics.
This table reports, by response scenario, the means, median, and 2.5% and 97.5% quantiles of the numbers of farms affected after a year of simulation. See Table 4 (main text) for details of the simulated scenarios.

scenario	mean	median	quantile 2.5%	quantile 97.5%
baseline	552.55	550	1	920.02
cull_quarant_vacc	1.29	1	1	3.00
quarant_vacc	1.96	2	1	5.00
selcull_quarant_vacc	1.26	1	1	3.00
selcull_quarant_vacc_insect	1.19	1	1	2.00
all	1.23	1	1	3.00