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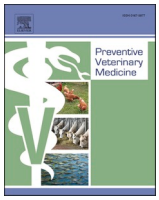

# Incorporating heterogeneity in farmer disease control behaviour into a livestock disease transmission model

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ABSTRACT

Human behaviour is critical to effective responses to livestock disease outbreaks, especially with respect to vaccination uptake. Traditionally, mathematical models used to inform this behaviour have not taken heterogeneity in farmer behaviour into account. We address this by exploring how heterogeneity in farmers vaccination behaviour can be incorporated to inform mathematical models. We developed and used a graphical user interface to elicit farmers (n = 60) vaccination decisions to an unfolding fast-spreading epidemic and linked this to their psychosocial and behavioural profiles. We identified, via cluster analysis, robust patterns of heterogeneity in vaccination behaviour. By incorporating these vaccination behavioural groupings into a mathematical model for a fast-spreading livestock infection, using computational simulation we explored how the inclusion of heterogeneity in farmer disease control behaviour may impact epidemiological and economic focused outcomes. When assuming homogeneity in farmer behaviour versus configurations informed by the psychosocial profile cluster estimates, the modelled scenarios revealed a disconnect in projected distributions and threshold statistics across outbreak size, outbreak duration and economic metrics.

## 1. Introduction

The actions of farmers are fundamental to disease control in their livestock, with the disease management behaviours they enact in their own herds contributing to the success of wide-scale disease control. For example, (i) it is necessary for UK-wide farmer engagement with bovine viral diarrhoea testing practices for the goal of bovine viral diarrhoea eradication by 2031, however, engaging with bovine viral diarrhoea testing is presently (as of August 2023) voluntary in England and Wales (Armstrong and Gow, 2021; Ruminant Health & Welfare, 2021), (ii) risky cattle purchasing behaviour by individual farmers is associated with new bovine tuberculosis herd breakdowns, with implications for both regional and national bovine tuberculosis control (Vial et al., 2015), and (iii) willingness of farmers to report the presence of disease on their farm is important for the control of many epidemics (Hernández-Jover et al., 2016). Farmer heterogeneity towards disease management, therefore, warrants consideration when establishing veterinary health policies. That being said, analytical approaches that can contribute useful insights to the formulation of livestock disease control plans, such as mathematical modelling, traditionally treat farmers as passive bystanders and omit the observed variation in disease management behaviours. Multiple methodological developments are consequently required to overcome these deficiencies.

People are well known to show different behaviours with respect to disease control; for example people can be mutually cooperative (acting for the benefit of both the self and other people), or show parasitism (gain benefit from other people taking action) (Bshary and Bergmüller, 2008). This is seen for human infections where there is considerable variability in the uptake of vaccine or the decision to vaccinate children (Cellini et al., 2022; Dolby et al., 2022), and this concept translates to

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farmers with the decision to protect their livestock. The heterogeneity in farmer behaviour for disease control is in part due to psychosocial and behaviour factors. Trust is a key component underlying cooperation (Kuipers, 2022) and trust in other farmers improves willingness to join disease control schemes (Heffernan et al., 2016; Shortall et al., 2016). However, trust in other farmers is also associated with farmers not controlling specific diseases such as bovine viral diarrhoea (Prosser et al., 2022). Increased trust means that farmers are more likely to believe that purchased animals will be disease-free. Trust also has implications for sources of advice, with farmers preferring to trust veterinary rather than Government advice (Bard et al., 2019; Brennan and Christley, 2013; Fisher, 2013). Related to trust is psychological proximity (closeness) to others. Psychological proximity includes close feelings and behaviours, and connection, interdependence and similarities with the other person (Aron et al., 1992). Psychological proximity has implications for human health behaviour (Shamloo et al., 2023; Thiessen et al., 2021; Tu et al., 2021) but to date has received little investigation in farmer behaviour for controlling livestock disease. Farmers with high psychological proximity to their veterinarian are more likely to control bovine viral diarrhoea in their herd (Prosser et al., 2022). Behaviour is also influenced by capability, opportunity and motivation which are theorised in the COM-B behaviour change framework (Michie et al., 2011). Capability is the physical ability (physical capability) and the knowledge and understanding (psychological capability) required to perform a behaviour. Opportunity is the time and money (physical opportunity) and the support from others (social opportunity) that enable a behaviour. Finally, motivation is decision-making and goals (reflective motivation) and habits and emotions (automatic motivation). Factors that make up this framework are often investigated in isolation in the context of disease control and use of the entire COM-B framework in livestock disease is rare. One study that used the COM-B framework found that farmers with high automatic and reflective motivation, high psychological capability and high physical opportunity were more likely to control disease in their herds (Prosser et al., 2022).

There has been a growing interest in the incorporation of psychosocial factors and behavioural heterogeneity into disease transmission models (Bedson et al., 2021), which will allow improved model predictions for successful disease control. A fundamental component of delivering these methodological advances is having appropriate, well-informed behavioural data available to parameterise models and enhance the robustness of model outputs. One previous example of such data collection activities includes Merrill et al. (2019), who conducted an experimental simulation game to quantitatively explore the effect of interventions that would increase information sharing among stakeholders. Nevertheless, a known challenge of fusing livestock infectious disease models and dynamic human behavioural change is a dearth of quantitative behavioural data (and behavioural data collection methodologies) that can capture relationships between psychosocial factors and the heterogeneity in behavioural response for a given context (Hidano et al., 2018).

Through an interdisciplinary approach, we strive to form a methodological pipeline that can generate novel quantitative data on farmer beliefs and hone epidemiological-behavioural models so the gathered data is amenable for direct usage (and equally, a pipeline where model outputs can inform what attributes may require particular focus in future data collection). To make initial advancements in this emerging research space - establishing a proof-of-concept - requires a well-defined scenario to make elicitation feasible. In this study, we investigated farmer behaviour in a fast, spatially spreading disease outbreak scenario by creating a graphical user interface (GUI) to dynamically show farmers the progress of the epidemic and elicit when they would each use a vaccine that was available to them. This is an important scenario to consider as a pathogen spreading rapidly between farms has the potential to cause substantial negative impacts, albeit a rare occurrence in Great Britain, and would likely need a concerted effort by farmers to control. We chose vaccination as an intervention response because the types of heterogeneity observed in vaccination behaviour and attitudes has been well documented (Böhm et al., 2016; Dudley et al., 2020; Weiss et al., 2016).

Using multiple validated measures, we studied how trust, psychological proximity and COM-B factors were associated with farmer vaccination behaviour in the face of the disease outbreak. We then used the attained behavioural groups within an infectious disease model to explore, through computational simulation, the impact on anticipated epidemiological outcomes (outbreak size, outbreak duration) and economic metrics (associated with cost-effectiveness) when making specific assumptions regarding heterogeneity in behaviour towards disease management. It is revealed how omitting heterogeneity in farmers' disease management of livestock infections can result in ill-judged assessments of the likely projected distributions and threshold statistics associated with outbreak size, outbreak duration and health economic measures.

## 2. Methods

The approach to conduct our analyses consisted of four methodological stages: (i) design of a GUI to act as a core, interactive component of the interview exercise; (ii) development and usage of an interview script to elicit farmer disease vaccination behaviours; (iii) grouping of farmer vaccination behaviour in the elicitation exercise into classes; (iv) incorporation of these vaccination behaviours into an epidemiological model for a fast-spreading livestock infection to compare modelled scenarios with and without inclusion of behavioural heterogeneity.

### 2.1. GUI

We created a graphical user interface (GUI) to dynamically illustrate the spread of an epidemic disease of cattle and used the GUI to investigate farmer behaviour during a simulated disease epidemic. The GUI showed a series of maps, with infected herds plotted, week by week. The outbreak started in southern-central France (epidemic stage 1), was introduced to Great Britain (epidemic stage 2), then spread throughout Great Britain (epidemic stages 3–8). The GUI presented a common outbreak experience at each stage of the epidemic, in terms of distance to the nearest infected farm, for each participating farmer regardless of the location of their farm. An example screenshot from the GUI can be seen in Supplementary Fig. 1 and the GUI can be accessed online (https://feed.warwick.ac.uk/map.html).

### 2.2. Elicitation exercise (farmer interviews)

For the second phase of our study, we conducted interactive online interviews with cattle farmers in Great Britain. The interactive online interviews consisted of three parts: (i) demographic questions, (ii) hypothetical disease scenario using the GUI and (iii) online questionnaire of validated psychosocial and behaviour change measures. The interview script (i and ii) and the online survey (iii) are in Supplementary Text 1 and Supplementary Text 2, respectively. For the disease scenario, we gave farmers a detailed description of the hypothetical disease and a vaccine that was available to them. The vaccine cost £ 50 per animal, had to be given to all cattle on the same day and was 100 % protective after five days. The disease description and parameters were loosely based on foot-and-mouth disease, a historic and potential future disease epidemic concern in the UK, however our aim was to investigate uptake of an effective but costly intervention in a general but plausible epidemic scenario.

The farmers then proceeded with the scenario using the GUI and were asked at weekly intervals whether they would vaccinate or do any other preventative measures. Farmers answered the questions in the online questionnaire directly after the disease scenario, which used validated measures to investigate trust in others, psychological

proximity to others and the COM-B behaviour change framework. Trust in others was measured using five-point Likert-scale statements (from strongly disagree to strongly agree) which investigated both general trust and trust in the context of infectious disease control in other farmers, veterinarians and government (Ferguson et al., 2022; Prosser et al., 2022). The responses to each Likert scale were converted to a numerical response (1 = strongly disagree, 2 = disagree, 3 = neither agree nor disagree, 4 = agree, 5 = strongly agree). Psychological proximity to their cows, other farmers, veterinarians and government was measured using the Inclusion of Other in the Self (IOS) scale on a 1–7 score, with higher scores representing feeling closer to the specific 'other' (Aron et al., 1992; Mashek et al., 2007). The COM-B factors were investigated using Likert-scale statements (using the same scale used to investigate trust) that investigated aspects of each COM-B factor in the context of infectious disease control (Michie et al., 2011, 2014). The mean of the scores for a farmer for the Likert statements within a COM-B factor were taken as that factor score. The questions used to investigate trust, psychological proximity and the COM-B factors are in Supplementary Text 2. The survey web page generated an individual code for each respondent, which was used to anonymously link the responses with the interview responses once all interviews were completed.

We pilot tested the GUI, interview and online questionnaire on three dairy farmers from three counties and two countries in Great Britain. For the research interviews, we then recruited cattle farmers in Great Britain from two sources: (i) farmers who took part in previous research (Prosser et al., 2022), and (ii) via advertisement through multiple cattle interest organisations. The interviews were conducted by the same author (NP), lasted up to one hour, were online (Microsoft Teams) and farmers received a £ 40 voucher for their time.

### 2.3. Analysis of elicitation data

We analysed the interview results using R statistical software v4.2.1 (R Core Team, 2022). To investigate associations between a farmer being an Early (epidemic stages 1–2), Mid (epidemic stages 3–5) or Late (epidemic stages 6–8 or never) vaccinator and their psychosocial and COM-B factor scores, we used a multinomial logistic regression model, which investigated how the trust, psychological proximity, COM-B and demographic factors, were associated with the outcome of a farmer being an Early, Mid or Late vaccinator.

We fit the regression model in the following way. Starting at the null model, each candidate covariate was tested in the model separately and the covariate with the lowest p-value (if less than 0.05) was retained. Each remaining covariate was separately tested in the updated model and the process of testing and retaining the covariate with the lowest p-value was repeated until no further covariates had a p-value of less than 0.05 when included in the model. Every time a new covariate was retained in the model, any covariates with a p-value greater than 0.05 in the updated model were omitted and added to the list of candidate covariates to test in the model.

To mitigate overfitting, we fit the model to 500 bootstrapped datasets and assessed the stability of the model covariates. Bootstrapping was implemented by randomly selecting farmers from the dataset 60 times with replacement. This was repeated 500 times to result in 500 slightly different datasets, though all with data obtained from the 60 interviewed farmers.

The covariates selected by a higher proportion of the models were more likely to be truly associated with when farmers vaccinated (Green et al., 2021; Hyde et al., 2022; Lima et al., 2021). We calculated the stability of each covariate (the proportion of multinomial logistic regression models fit to the 500 bootstrapped datasets that selected the covariate) to mitigate overfitting in this wide dataset (Lima et al., 2021). We calculated stability thresholds for different probabilities of a variable being a true positive using the methods by Green et al. (2021) and Hyde et al. (2022). Selected covariates had a stability higher than a threshold where covariates had a 15 % probability of not being associated with when farmers vaccinated. We calculated odds ratios of the stable covariates by refitting the model to the bootstrapped datasets with the candidate covariates limited to those above the stability threshold and taking the mean of the coefficients. Finally, model fit was assessed by fitting the multinomial logistic regression model to the original dataset and comparing the observed and expected data using a Hosmer-Lemeshow goodness-of-fit test and decile plots (Fagerland and Hosmer, 2012), and by comparing predicted vaccination class from the full and 10 × 10-fold cross validated models.

Using k-means clustering (Hartigan and Wong, 1979), we grouped farmers based on their scores for the covariates selected by stability thresholds for a 10 % and 15 % probability of not being associated with when farmers vaccinated respectively. We used visual inspection of a plot of total within-cluster sum of squares against number of clusters to determine the number of clusters that gave the best fit, where there was the greatest reduction in total within-cluster sum of squares compared to the total within-cluster sum of squares for one fewer clusters (Supplementary Fig. 3). These psychosocial groupings were incorporated into the mathematical livestock disease transmission model.

### 2.4. Mathematical transmission model of infectious livestock disease

For the final portion of our investigation, we sought to ascertain the impact of differing population compositions with regards to behavioural stances on intervention usage on an emergent outbreak of a fast-spreading pathogen. To inform this problem, we used a mathematical transmission model to simulate a livestock disease epidemic process in Great Britain amongst holdings with cattle. Within this subsection we overview: (i) the data sources used to inform cattle demography, (ii) the epidemiological model framework that was conceptually based on a swift, locally spreading pathogen with no long-range movement of animals, (iii) our implementation of vaccination, (iv) expanded details on the eight behavioural configurations and (v) the simulation protocol used to compare scenarios with and without inclusion of behavioural heterogeneity.

#### 2.4.1. Livestock data description

We used the Cattle Tracing System database to procure average cattle herd sizes throughout 2020 for each holding. The Cattle Tracing System contains virtually complete records of the births, deaths, and movements of individual cattle in Great Britain since 2001 (British Cattle Movement Service, 2021).

These data contained 59,774 holdings. Cattle herd sizes ranged from 1 to 7634, with a median of 58, interquartile range of 16–155, and 97.5th percentile of 622. There was regional variation in the number of holdings and total number of cattle. Most populous regions included the south-west of England (particularly Devon), south-west Wales, north-west England (most notably Cumbria) and Dumfries and Galloway in south-west Scotland (Fig. 1).

#### 2.4.2. Epidemiological model

We formulated the infectious disease dynamics as a stochastic, spatially explicit, holding level Susceptible-Exposed-Infectious-Removed (SEIR) model. With the epidemiological unit being a holding (rather than at the individual animal level), we inherently assumed that once infection had entered the cattle herd on the holding the within-premises disease spread occurred rapidly, leaving the whole cattle herd infected.

Time was discretised into daily time steps. The daily probability of a susceptible holding $j$ becoming infected by an infectious holding $i$ obeyed:

$$p_{ij} = 1 - \exp(\lambda_{ij})$$

where, $\lambda_{ij} = \xi N_i^{\psi} N_j^{\phi} K(d_{ij})$.

In detail, the force of infection between two herds, $\lambda_{ij}$, was a

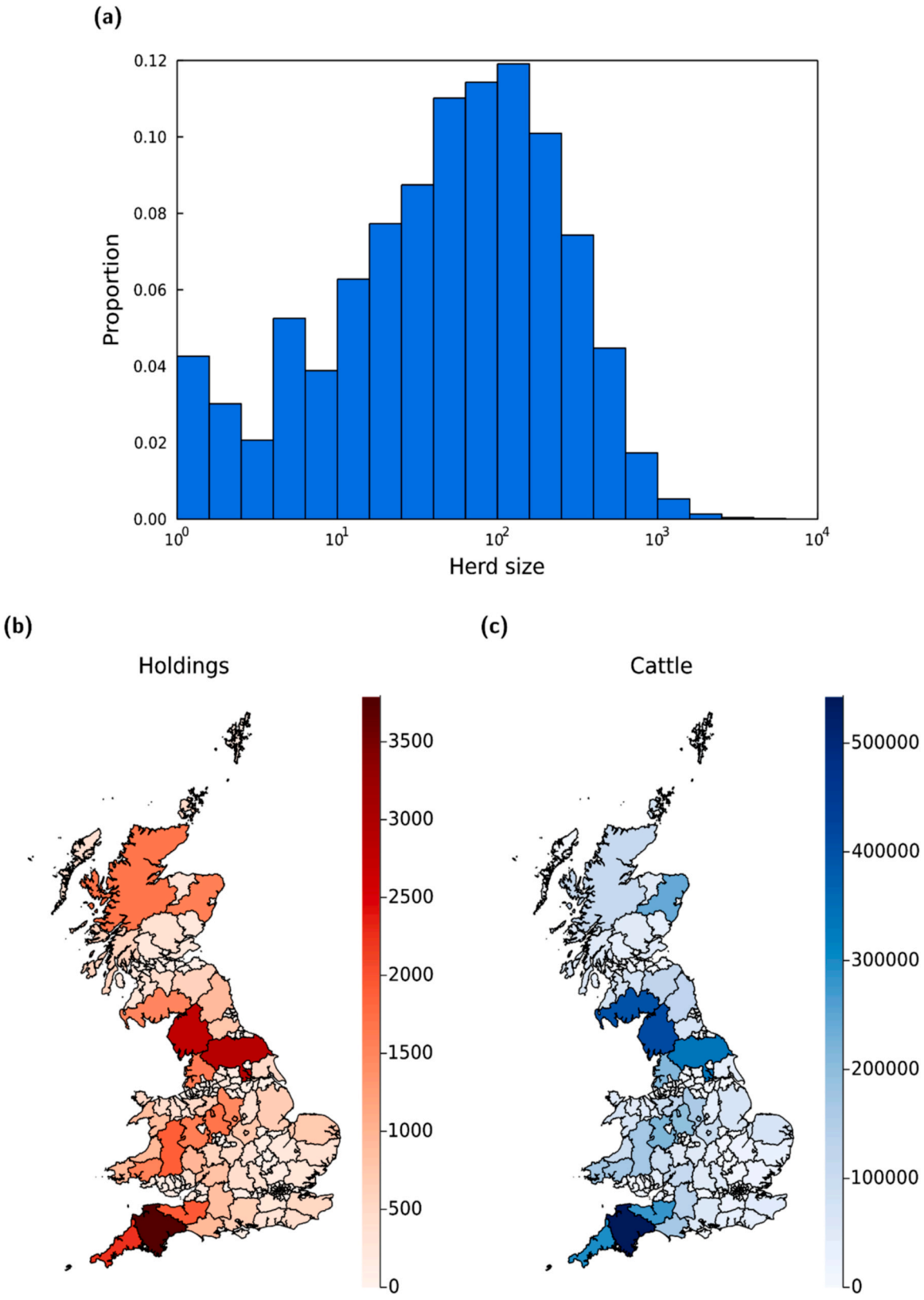


**Fig. 1.** Size and spatial distribution of cattle herds in Great Britain. We used the Cattle Tracing System database with data from 2020 to estimate an average cattle herd size for each holding. These data contained 59,774 holdings. (a) Distribution of cattle herd sizes. Note the x-axis is presented on a log scale. Cattle herd sizes ranged from 1 to 7634, with a median of 58, interquartile range of 16–155, and 97.5th percentile of 622. (b) Number of holdings with cattle present per region. Darker shading corresponds to higher counts. (c) Number of cattle present per region. Darker shading corresponds to higher counts. There was regional variation in the number of holdings and total number of cattle. Most populous regions included Devon in the south-west of England, Cumbria in north-west England, and Dumfries and Galloway in south-west Scotland.

nonlinear function of the transmissibility of cattle ($\xi$), the number of cattle on the infectious holding (term $N_i^{\psi}$) and the number of cattle on the susceptible holding (term $N_j^{\phi}$). For the herd size exponents, $\psi$ and $\phi$, we used cattle epidemiological parameter estimates inferred from the 2001 UK foot-and-mouth disease (FMD) epidemic for Cumbria (Tildesley et al., 2008).

The fourth contributor to the force of infection was the transmission kernel $K$, which was a function of the Euclidean distance between holdings $i$ and $j$ ($d_{ij}$, measured in metres). We applied a power-law transmission kernel, with a maximum range of 50 km:

$$K(d_{ij}) = \frac{k_1}{1 + \left(\frac{d}{k_2}\right)^{k_3}}, \text{for } 0 \leq d_{ij} \leq 50000;\ Otherwise, K(d_{ij}) = 0.$$

We obtained plausible orders of magnitude for the transmission kernel distance length scaling ($k_2$) and exponential parameter on the distance component ($k_3$) from prior modelling studies (Tildesley et al., 2008). We then calibrated these parameter values so that, in the absence of additional controls beyond infected holdings, the simulated outbreaks were extensive irrespective of the seed infection location. These baseline outcomes gave us the conditions to then test the impact on outbreak metrics of heterogeneity in farmer behaviour towards a livestock disease intervention. We recognise that our parameterisation of the force of infection is an amalgamation of values that were inferred for an FMD-like pathogen in different contexts. Yet, for demonstrating the utility of the model framework, in particular how one may use behavioural-associated data gathered from an elicitation study, our chosen parameterisation suited the investigative purposes of our study.

Upon a holding becoming infected, we assumed a latent period of five days (based on epidemiological and veterinary records from the 2001 UK FMD outbreak (Keeling et al., 2001)). Thereafter, the entire livestock population at that holding was considered infectious for a period of eight days (days 6–13 after infection). We assumed all infected holdings provided notification of infection nine days after the initial infection event, meaning there was no under-reporting of infection, but there was a four-day delay between the holding becoming infectious and subsequent notification of infection. At the end of the infectious period (13 days after infection) the cattle herd and holding were considered removed from the population.

See Table 1 for an overview of the epidemiological model values.

**Table 1**
Summary of the livestock disease model epidemiological and intervention parameter notation, descriptions and values.

| Notation | Description | Value |
|---|---|---|
| Epidemiological parameters | | |
| $\lambda_{ij}$ | Infectious pressure on susceptible holding $j$ from infectious holding $i$. | Variable |
| $N_i$ | Number of cattle on premises $i$ | Variable |
| $\xi$ | Transmissibility of cattle. | 10^6 |
| $\psi$ | Exponent on the cattle population on an infectious holding, for calculating the infectious pressure. | 0.42 |
| $\phi$ | Exponent on the cattle population on a susceptible holding, for calculating the infectious pressure. | 0.41 |
| $k_1$ | Transmission kernel normalisation constant (to 2 sf.) | 1.2 × 10^− 8 |
| $k_2$ | Transmission kernel distance length scaling | 2000 |
| $k_3$ | Transmission kernel exponential parameter on the distance component | 2 |
| $t_{incub}$ | Time elapsed until end of latent period (relative to the day of infection) | 5 days |
| $t_{notif}$ | Time elapsed until notification (relative to the day of infection) | 9 days |
| $t_{removal}$ | Time elapsed until removal (relative to the day of infection) | 13 days |
| Intervention parameters | | |
| $v_{eff}$ | Vaccine efficacy | 100 % |
| $v_{delay}$ | Delay in vaccine effectiveness | 5 days |

#### 2.4.3. Implementation of vaccination

To correspond with the intervention descriptions in the interview study, we modelled the administration of vaccine to livestock (relevant parameter values are contained in Table 1).

We present the idealised situation of having a vaccine available with 100 % effectiveness in blocking infection. As per the description of the vaccine product in the interview script, we included a lag for the vaccine inducing an immune response (fixed at 5 days, based on measures of FMD virus titres in milk from inoculated cows in the days post-inoculation (Orsel et al., 2007)). As the vaccine could be administered to an infected population during its latent phase (thus prior to onset of symptoms and subsequent notification of infection), in these circumstances it was feasible for a cattle herd at a holding to be vaccinated but to still become infected.

#### 2.4.4. Intervention behaviour configurations

We tested eight different behavioural group population compositions, referred to as configurations, each governing the proportion of the population that would implement interventions at a given time (with respect to the outbreak situation). Note that in all configurations controls are applied at holdings with confirmed infection. As the basis for naming the different groupings, we used the conceptual framework to categorise cooperation suggested by Bshary and Bergmüller (2008), with the vaccination behaviour with respect to epidemic stage being labelled as mutually cooperative (vaccinates during epidemic stages 1–2), weak parasitism (vaccinates during epidemic stages 3–5), strong parasitism (vaccinates during epidemic stages 6–8) or uncooperative (never vaccinates).

In four behavioural configurations we imposed a homogeneous assumption to farmer vaccination behaviour, assuming all farmers had the same disease management behaviour.

*Uncooperative.* Controls only applied at holdings with confirmed infection (cattle removed). No holdings applied vaccination, irrespective of the epidemiological situation.

*Strong parasitism.* All holdings administered vaccines in their herds upon infection being confirmed within 50 km (approximately 30 miles) of their holding. This configuration resembles a situation where all individuals wait to see what is happening, how the infection spreads and as such they are exploiting others or benefit from what happens to others.

*Weak parasitism.* All holdings administered vaccines in their herd upon infection being confirmed within 320 km (approximately 200 miles) of their holding. Similar to the strong parasitism scenario, where all individuals observe the epidemiological situation and as such they are exploiting others or benefit off what happens to others, although in this instance all individuals are more precautionary.

*Mutual cooperation.* All holdings vaccinated their herds prior to pathogen emergence (no outbreak occurs). Represents a scenario where all individuals cooperate to produce the maximum epidemiological benefit to all.

In two behavioural configurations we sought to represent a situation where there was an absence of behavioural response data, but there was a desire to include heterogeneity in farmer intervention response through subjectively chosen distributions. To enable us to examine the implications of including or omitting *uncooperative* farmers in such an assumption, we explored two parsimonious, uniform stratifications of the population across intervention stance groups. The first included *uncooperative* farmers, named *Cooperation-Parasitism-Free riders* (*Coop-Parasitism-FR*), whilst the second omitted *uncooperative* farmers, named *Cooperation-Parasitism* (*Coop-Parasitism*).

*Cooperation-Parasitism-Free riders (Coop-Parasitism-FR).* Uniform partitioning of the population across four intervention stance groups. A quarter of holdings never vaccinated, irrespective of the epidemiological situation (free-riders); a quarter of holdings vaccinated their herd upon infection being confirmed within 50 km of their holding (strong parasitism); a quarter of holdings vaccinated their herd upon infection being confirmed within 320 km of their holding (weak parasitism); a quarter of holdings vaccinated their herds prior to pathogen emergence (cooperators).

*Cooperation-Parasitism (Coop-Parasitism).* Uniform partitioning of the population across the three intervention timing groups. A third of holdings vaccinated their herd upon infection being confirmed within 50 km (strong parasitism) of their holding; a third of holdings vaccinated their herd upon infection being confirmed within 320 km (weak parasitism) of their holding; a third of holdings vaccinated their herds prior to pathogen emergence (cooperators).

In our final two configurations, we used the elicitation findings to parameterise: (i) the split of holdings between behavioural groups; (ii) within each behavioural group, the partitioning of the holdings between the different intervention timings.

*Trust-Expectancy.* Partitioning of holdings into four behavioural groups, using the empirical estimates for psychosocial profile clusters from the model comprising the covariates selected by stability thresholds for a 10 % probability of not being associated with when farmers vaccinated. The four groups covered combinations of two trust groups (high, low) and two "expectancy" groups, their ability to physically intervene (high, low).

*Herd size dependent.* Partitioning of holdings into three behavioural groups, using the empirical estimates for psychosocial profile clusters from the model comprising the covariates selected by stability thresholds for a 15 % probability of not being associated with when farmers vaccinated. For details on the attributes associated with each of the three behavioural groups, see Section 3.1. Specific to the *Herd size dependent* configuration, herd size determined the probability of the holding being assigned to each of the three behavioural groups (Fig. 2).

### 2.4.5. Simulation outline

We considered the fast-spreading pathogen first emerging in a spatially localised area of Great Britain from a low case level. Therefore, in each simulation replicate we seeded infection in a randomly selected cluster of three premises (we selected one premises at random and found the two premises that were closest in terms of Euclidean distance). A replicate terminated upon there being no premises in an infected state.

For each behaviour configuration, to explore the sensitivity of epidemiological and economic outcomes to the geographical location of initial infected premises we assessed 89 different seed region scenarios. We ran 500 replicates for each scenario, comprising a behaviour configuration and seed infection region.

To assess the implications of differing psychosocial and geographical attributes on epidemiological outcomes, we tracked the percentage of holdings infected and outbreak duration. To evaluate the economic implications of behavioural attributes on intervention usage, relative to the *uncooperative* scenario, we computed threshold intervention unit costs. In general terms, the threshold intervention unit cost is the maximum cost per intervention unit where the costs saved from averted infections (i.e., the cost of removing cattle at those additional holdings that would have been infected had the intervention not been used) equals the total intervention cost. For our application, an intervention unit was a vaccine dose, with the intervention cost being a relative cost of vaccination compared to the cost of infection and removal of a single cow (i.e., an intervention cost of 1 meant the cost of a vaccine dose equalled the cost of the loss of a single cow due to infection and removal).

Given our use of a large-scale spatially explicit model, for our simulation procedure we employed an optimised gridding approach (the conditional subsample algorithm) as described in Sellman et al. (2018). We performed all model simulations and produced plots in Julia v1.8. The code repository for the study is available at https://github.com/EdMHill/FEED_farmer_disease_management_heterogeneity.

## 3. Results

### 3.1. Elicitation findings

Sixty farmers (39 beef and 21 dairy) completed the elicitation interview and interviews took place between April and June 2022. Forty-four (73 %) were from England, nine (15 %) from Scotland and seven (12 %) from Wales. The median number of cows in the herd was 155 cows for dairy herds (range = 30–330, one herd only reared heifers) and 35 for beef herds (range = 5–200, one herd only fattened cattle). The herd sizes were slightly larger than the national averages and

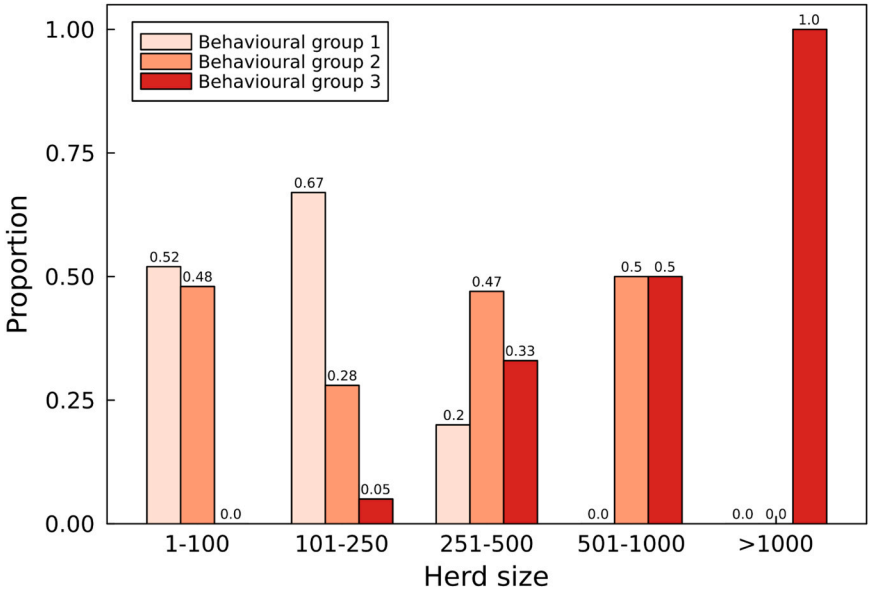


**Fig. 2.** For the "Herd size dependent" behavioural configuration, the probability of a holding being assigned to each of the three behavioural groups with respect to the herd size. The bars depict the probability of a holding being assigned to each of the behavioural groups with respect to the stated herd size stratification. Above each bar, we state the associated probability to a precision of at most 2 decimal places. The three behavioural groups correspond to psychosocial profile clusters from the model comprising the covariates selected by stability thresholds for a 15 % probability of not being associated with when farmers vaccinated. For details on the attributes associated with each of the three behavioural groups, see Fig. 4 and Section 3.1.

English farmers were slightly over-represented (Agriculture and Horticulture Development Board, 2019).

The farmers differed in when they used preventive vaccination, with 58 (96.7 %) using vaccination at some point during the scenario: eight (13.3 %) vaccinated at the first opportunity (a localised outbreak restricted to southern France), 16 (26.7 %) vaccinated when cases were first detected in Great Britain and 34 (56.7 %) vaccinated at a later stage of the Great Britain epidemic (Table 2).

We fit multinomial logistic regression models testing for associations between the psychosocial and behaviour change factors and when farmers vaccinated to bootstrap repeats of the dataset. Two covariates were above a stability threshold when there was only a 10 % probability of not being associated with when farmers vaccinated (stability threshold value: 0.24). These covariates were: trust in governmental judgements about how to control infectious diseases in cattle; and physical opportunity (Table 3). Three additional covariates were selected when the stability threshold was relaxed to a 15 % probability of not being associated with when farmers vaccinated (stability threshold value: 0.20), which were: trust in the quality of advice from the veterinary profession; trust in other farmers nationally to control infectious diseases; and herd size at time of disease outbreak. There was no evidence of poor model fit in a Hosmer-Lemeshow goodness-of-fit test ($p = 0.814$), by visual inspection of a decile plot of the observed and expected vaccination classes (Supplementary Fig. 2), or when comparing the proportion of farmers for which the model predicted the correct vaccination class between the full model (proportion of farmers with class correctly predicted = 0.62) and the 10 × 10-fold cross-validated models (mean proportion of farmers with class correctly predicted = 0.58).

Using k-means clustering (Hartigan and Wong, 1979), we clustered farmers by their scores for the psychosocial and behaviour change covariates that were selected by the above regression models. A model consisting of four groups of farmers gave the best fit when using the two most stable covariates. Three groups gave the best fit using the five most stable covariates (Supplementary Fig. 3). In brief, for the clustering on the two most stable covariates, the four clusters were: (1) high trust in Governmental judgements for disease control and high physical opportunity; (2) low trust in Governmental judgements for disease control and high physical opportunity; (3) high trust in Governmental judgements for disease control and low physical opportunity; (4) low trust in Governmental judgements for disease control and low physical opportunity (Fig. 3). For the clustering on the five most stable covariates, the three clusters were: (1) high general trust, high physical opportunity and small herd size; (2) low trust in Governmental judgements for disease control and in other farmers to control disease; (3) high trust in Governmental judgements for disease control and in other farmers to control disease, low physical opportunity and a large herd (Fig. 4).

**Table 2**
The number of infected herds, the distance of the nearest infected herd from the interviewee's herd and the number of farmers that vaccinated for each week during the disease epidemic scenario.

| Stage of epidemic | Time since previous stage (weeks) | Number of infected herds (in Great Britain) | Distance to nearest infected herd (km) | Number of farmers vaccinating (/60) | Cumulative number of farmers vaccinating (/60) |
|---|---|---|---|---|---|
| 1 | 2 | 0 | >500* | 8 | 8 |
| 2 | 2 | 2 | 322 | 16 | 24 |
| 3 | 1 | 10 | 322 | 5 | 29 |
| 4 | 1 | 40 | 161 | 14 | 43 |
| 5 | 1 | 100 | 161 | 1 | 44 |
| 6 | 1 | 150 | 48 | 10 | 54 |
| 7 | 1 | 450 | 16 | 3 | 57 |
| 8 | 1 | 600 | 5 | 1 | 58 |

* Epidemic confined to southern-central France.

**Table 3**
The stability and mean odds ratio (OR) and the central 95 % range of the odds ratios from the model fit to the bootstrapped datasets (95 % CI) of the covariates associated with when farmers vaccinated their cattle in a hypothetical disease epidemic, above the stability threshold for a 15 % probability of a covariate reaching the threshold without being truly associated with when farmers vaccinated their cattle (stability threshold value: 0.20). The reference category for the OR was epidemic stage 1–2.

| Covariate | Stability | Mean OR (95 % CI) when farmers vaccinated | |
|---|---|---|---|
| | | Epidemic stage 3 – 5 | Epidemic stage 6 – never |
| Trust in governmental judgements for infectious disease control | 0.28 | 0.29 (0.10–0.57) | 0.66 (0.28–1.60) |
| Physical opportunity | 0.26 | 0.85 (0.25–3.68) | 0.19 (0.06–0.65) |
| Trust in quality of advice from the veterinary profession | 0.22 | 1.82 (0.34–11.01) | 0.14 (0.02–0.83) |
| Trust in other farmers nationally to control infectious diseases | 0.20 | 6.18 (2.36–25.56) | 1.25 (0.36–3.76) |
| Herd size at time of disease outbreak | 0.20 | 1.01 (1.00–1.01) | 1.01 (1.00–1.02) |

### 3.2. Impact of heterogeneity assumptions for farmer vaccination behaviour on livestock disease modelling assessments

In the final component of our analyses, we constructed a disease transmission model for a fast-spreading pathogen amongst cattle, first emerging in a spatially localised area of Great Britain from a low case level. With this model, we evaluated the ramifications on disease modelling assessments of differing assumptions on the amount of heterogeneity in vaccination behaviour amongst farmers (for a vaccine that had similar properties as that described to the interviewed farmers), including examples that incorporated the empirical findings from the elicitation exercise.

We tested our eight different behavioural group configurations, each governing the proportion of the population that would implement interventions at a given time with respect to the outbreak situation. Note that in all configurations we applied controls at holdings with confirmed infection (i.e., removal of cattle).

#### 3.2.1. Homogeneous behavioural configuration outcomes

We first inspected outbreak size, outbreak duration and threshold cost per intervention unit outcomes for the four homogeneous configurations: where all farmers had uniform disease management behaviour (i.e., all *uncooperative*, all *strong parasitism*, all *weak parasitism*, or all *mutual cooperation*).

By its construction, for the *uncooperative* behavioural configuration (where interventions were only used on holdings with confirmed infection) in all simulation replicates most holdings were infected, returning a median outbreak size of 99.5 % of all holdings (Fig. 5(a)). We therefore observed very few instances of small-scale outbreaks. The percentage of simulations that had greater than 1%, 10 % and 20 % of all holdings infected was 98.4 % for all three threshold values (Fig. 5(b)). This contrasted with everyone having *strong parasitism* (the next slowest to vaccinate). Although the majority of these simulations did still result in large outbreaks, with 96.3 % of simulations having more than 20 % of holdings infected, there was a greater prospect that outbreak size could be curtailed without the majority of holdings applying interventions. Explicitly, whilst for everyone being *uncooperative* meant less than 1 % of holdings became infected in 1.6 % of simulations, under the *strong parasitism* configuration the chance of fewer than 1 % of holdings being infected more than doubled (3.7 % of simulations). Having all farmers being more precautionary, resembling our *weak parasitism* configuration, many outbreaks were small-scale. The median outbreak size was just 1.6 % of holdings infected and no simulations resulted in more than

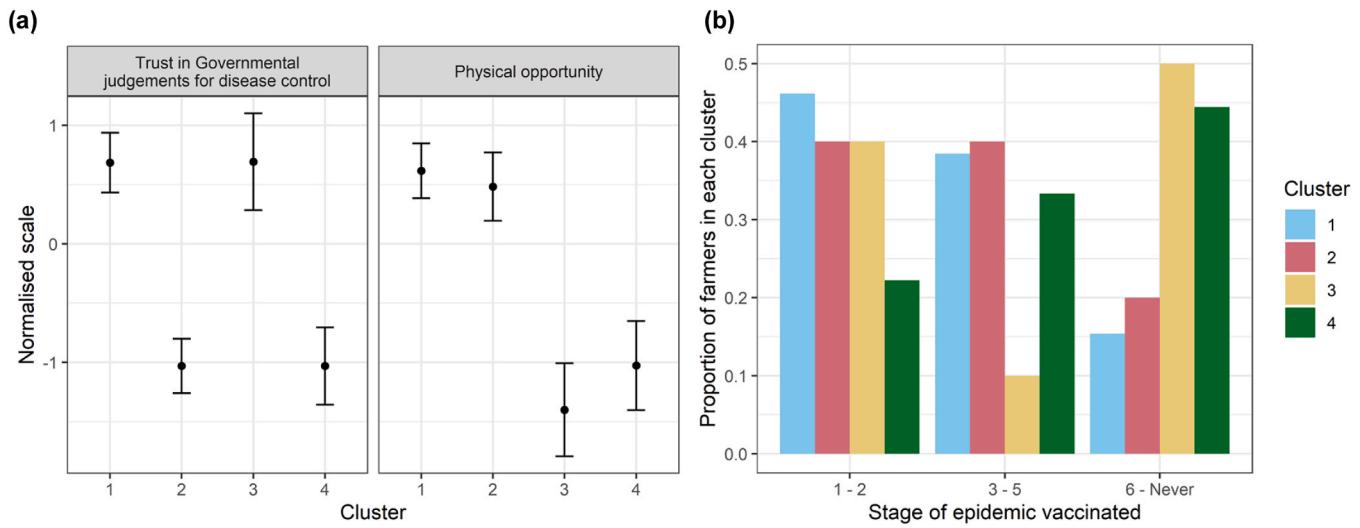


**Fig. 3.** The farmer groups from k-means clustering conducted on the two most stable covariates (Trust in Governmental judgements about disease control and Physical opportunity). (a) The mean (point) and 95 % confidence interval (error bars) scores of the covariates for each group. (b) The proportion of farmers in each group that vaccinated at different stages of the epidemic (Epidemic stages 1–2, Epidemic stages 3–5 and Epidemic stage 6–8 or never uses vaccination). Associated values are given in Supplementary Table 1 and Supplementary Table 2.

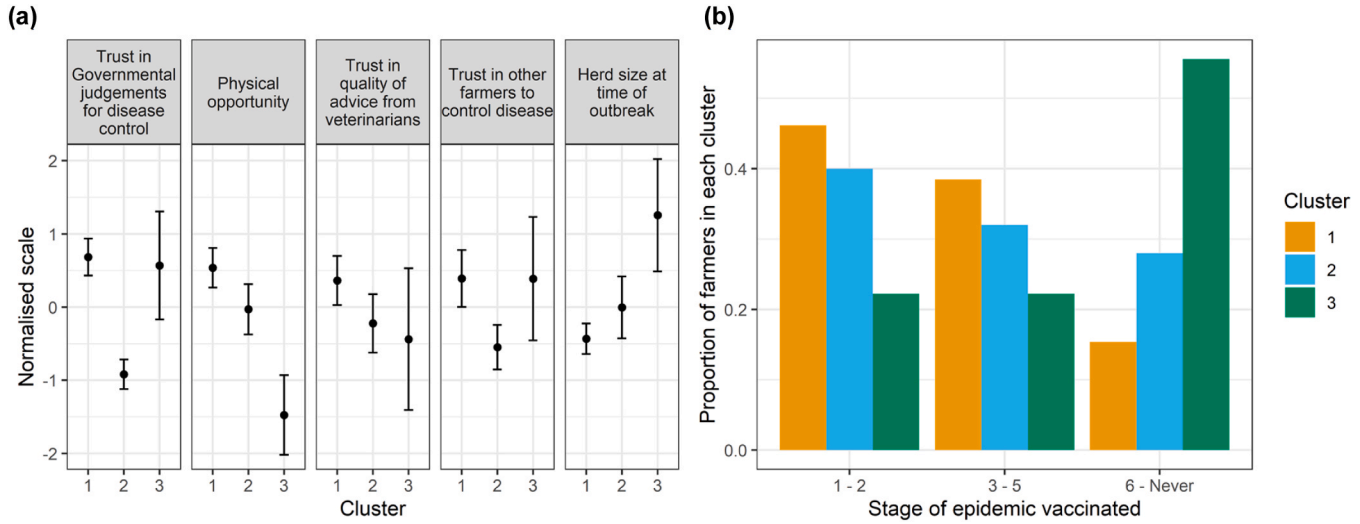


**Fig. 4.** The farmer groups from k-means clustering conducted on the five most stable covariates (Trust in Governmental judgements about disease control, Physical opportunity, Trust in quality of advice from the veterinary profession, Trust in other farmers nationally to control infectious diseases and Herd size at time of outbreak). (a) The mean (point) and 95 % confidence interval (error bars) scores of the covariates for each group. (b) The proportion of farmers in each group that vaccinated at different stages of the epidemic (Epidemic stages 1–2, Epidemic stages 3–5 and Epidemic stage 6–8 or never uses vaccination). Associated values are given in Supplementary Table 1 and Supplementary Table 2.

10 % of holdings being infected. The *mutual cooperation* set up resulted in no outbreaks, as intended by its construction.

Analysing outbreak duration (which may be a major consideration for some outbreaks), our reference *uncooperative* behavioural configuration gave outbreaks with a duration typically in the region of 200–300 days, with a median of 251 days (Fig. 5(c)). The majority of simulated outbreaks (93.1 %) lasted more than 180 days (Fig. 5(d)). For *strong parasitism*, the outbreak duration was reduced compared with the *uncooperative* scenario (median of 153 days), although it remained likely that outbreaks would last in excess of 100 days (96.3 % of simulations). Under *weak parasitism* there was little variation in outbreak duration, with no realisations exceeding an outbreak duration of 30 days.

Pivoting to economic considerations and analysis of the threshold cost per intervention unit (Fig. 5(e,f)), where we recall that for our application the threshold intervention unit cost was the maximum cost per vaccine dose (measured as a relative cost of vaccination compared to the cost of infection and removal of a single cow) where the costs saved from averted infections equals the total cost of vaccination. For our *strong parasitism* realisations there were examples where outbreaks resulted in few onward infections beyond the initial three infected holdings (seeded with infection at the beginning of the simulation). In such instances, one would be willing to spend a higher amount per intervention unit whilst keeping the strategy cost-effective compared with the baseline strategy (reflected by 2.2 % of simulations returning a threshold unit intervention cost above 2). Meanwhile, the threshold unit intervention cost exhibited more variability for *weak parasitism* than in most other scenarios, spanning 0–11.5. It was very likely to be in the range of 0.5–1, with a small chance of it being larger than 2 (achieved in 10.1 % of simulations). Finally, though outbreaks were prevented under *mutual cooperation*, for the pre-emptive use of vaccination by all to be

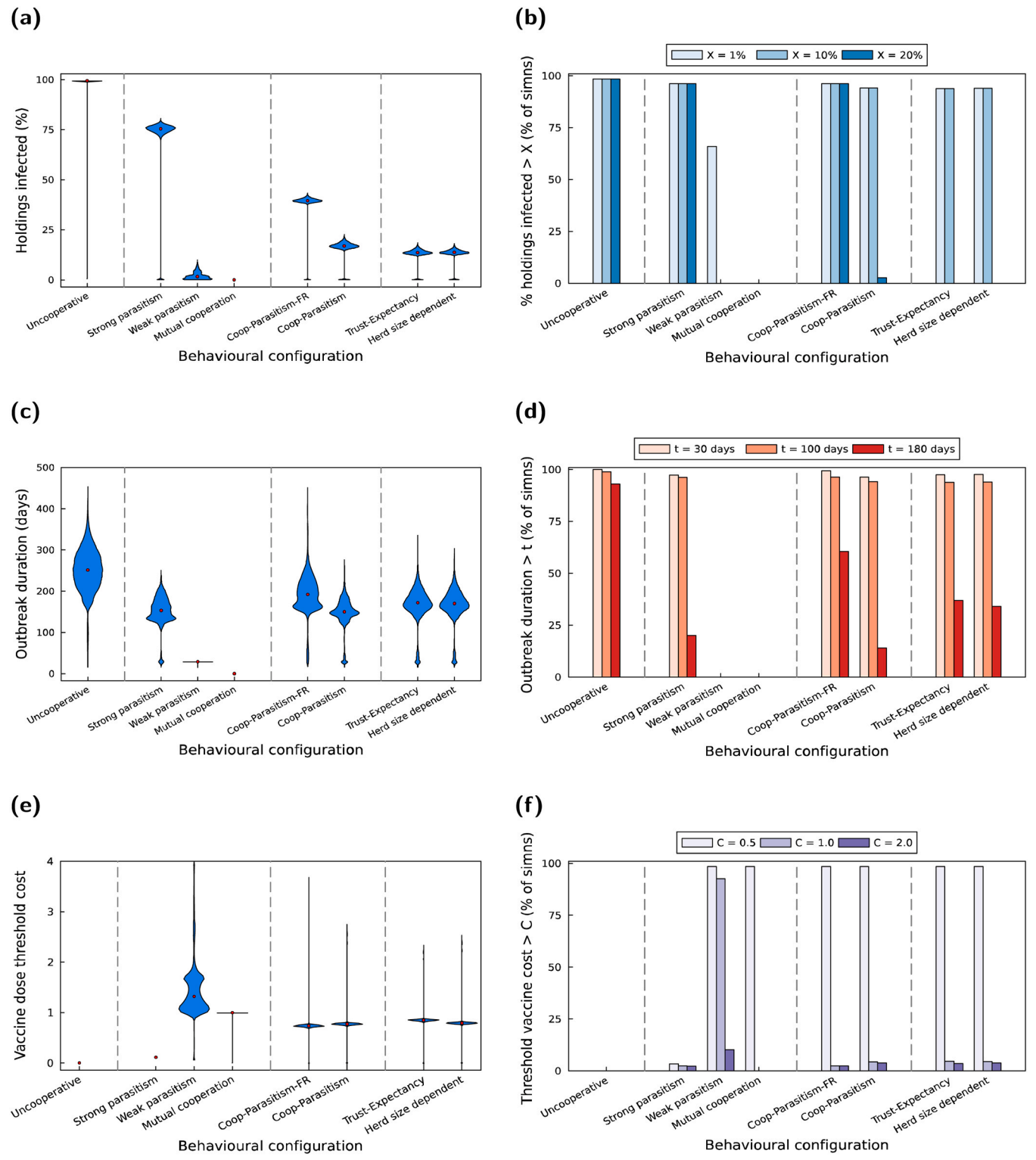


**Fig. 5.** Epidemiological summary statistics for Great Britain when aggregating outbreaks over all 89 infection seed regions. We computed the summary statistics for each behavioural configuration using 44,500 replicates (500 replicates for each of the 89 seed region locations). In (a,c,e), the filled red markers represent the medians and the violin plots depict an estimate of the probability density. In (b,d,f), the bars represent the percentage of simulations where the stated epidemiological outcome was exceeded. Darker shaded bars correspond to a higher valued threshold, with threshold values stated in the figure legends. The summary statistics presented are: (a,b) percentage of holdings infected during the entire outbreak; (c,d) outbreak duration (in days); (e,f) threshold cost per vaccine dose, where the costs saved from averted infections due to use of vaccination equalled the total cost of vaccination (recall the vaccine dose cost was a relative amount compared to the cost of infection and removal for a single cow, i.e. a vaccine dose threshold cost of 1 corresponds to a vaccine dose cost that equals the cost of infection and removal for a single cow). Note that the y-axis limits in panel (e) crops the top of the range for the *weak parasitism* configuration (maximum value of 11.5). Associated values are given in Supplementary Table 3.

cost effective, the intervention unit cost would have to be less than the cost of infection of a single cow.

#### 3.2.2. Non-data informed, heterogenous behavioural configuration outcomes

We next examine our epidemiological metrics for our simple implementations of heterogeneity in behaviour amongst the population, with a uniform split of specified behavioural groups across holdings (*Coop-Parasitism-FR* and *Coop-Parasitism*). We found similar lower bounds across the configurations. As anticipated, the *Coop-Parasitism-FR* configuration - having a quarter of the population in the non-vaccination group - resulted in a greater median and upper uncertainty bounds for holdings infected and outbreak duration. There was a striking difference in the number of simulations that resulted in more than 20 % of holdings infected, 96.2 % vs 0.0 % (Fig. 5(b)), and in an outbreak duration of more than 180 days, 60.6 % vs 13.9 % (Fig. 5(d)). We found quantitatively similar intervention unit threshold costs (Fig. 5(e,f)), with a median relative cost versus infection of 0.74 (for *Coop-Parasitism-FR)* and 0.77 (for *Coop-Parasitism)*.

#### 3.2.3. Data informed, heterogenous behavioural configuration outcomes

We conclude our modelling analysis by viewing the configurations informed by the interview data (*Trust-Expectancy* and *Herd size dependent*). Comparing these two behavioural configurations, we observed both quantitatively similar distributions and threshold summary statistics. That being said, a marked result was the distributions and threshold outcomes being distinct from the other assessed behavioural configurations (Fig. 5). Epidemiological outcomes most closely resembled the *Coop-Parasitism* configuration, with a reduced risk of large outbreaks but an increase in the likelihood of outbreaks being elongated. For the economic metric, rather than asserting homogeneity in behaviour or simple uniform splits between groups, when we grounded the behavioural configurations with empirical data the intervention unit threshold cost was raised (medians of 0.85 for *Trust-Expectancy* and 0.79 for *Herd size dependent*). Additionally, the threshold unit intervention cost was very likely to be in the range of 0.5–1, mimicking outcomes under the *Coop-Parasitism* scenario.

#### 3.2.4. Role of seed infection region

We have primarily focused on the aggregated results from all seed infection realisations, but our spatial simulations allow for inspection of epidemiological and economic metrics dependent upon the region containing the seed infected premises. We provide further details in Supplementary Text 3 and Supplementary Figs. 4 - 9.

## 4. Discussion

By understanding the factors associated with heterogeneity in farmer behaviour towards disease management and intervention response, and their incorporation into mechanistic disease transmission models, we can enhance the likelihood of national disease prevention schemes delivering their desired impact. To that end, we have successfully designed and applied a bespoke GUI for eliciting farmer behaviour in a livestock disease outbreak scenario. The farmers showed diverse behaviour when presented with the disease outbreak and this behaviour was associated with psychosocial factors. For example, prompt uptake of vaccination was associated with high trust in Governmental judgements for disease control and high physical opportunity. We layered these behavioural components into a mathematical transmission model of a fast-spreading pathogen amongst cattle, demonstrating how different modelling assumptions with respect to farmer disease control behaviour can result in vastly disparate simulated epidemiological outcomes. This knowledge could be of substantial value in planning and administering national disease control strategies. Specifically, the effectiveness of policy-level interventions (s-frame), which are generally more successful than targeting interventions on individual behavioural factors (i-frame) (Chater and Loewenstein, 2023), can be enhanced by incorporating individual heterogeneity in behaviour into the s-frame. Thus, the power of s-frames can be consolidated to maximise policy effectiveness. The methods and approach demonstrated here show how this can be easily and effectively implemented.

The GUI was effective in eliciting farmer behaviour and successfully separated farmers out behaviourally. Scenarios and games are occasionally used to elicit farmer behaviour (Enticott and Little, 2022; Maye et al., 2017; Utomo et al., 2022), however their use has focused on routine decision-making and the control of endemic diseases. Sok et al. (2018) used a choice experiment to investigate farmer preferences between possible government strategies for controlling a bluetongue epidemic in the Netherlands, and in a similar way described a hypothetical disease outbreak, however they did not investigate how farmers would behave voluntarily during an epidemic as was done in this study.

The behavioural heterogeneity shown by farmers was associated with psychosocial and behaviour change factors. Farmers with high trust in Governmental judgements for disease control, high physical opportunity and fewer cattle to vaccinate were most likely to vaccinate early, which is consistent behaviour with being mutually cooperative (Bshary and Bergmüller, 2008). This association indicates that increasing the trust that farmers have in Government would improve the efficacy of disease control strategies. Also, farmers are more likely to look to and trust Government advice in uncertain situations (Maye et al., 2017), therefore it is likely that their behaviour would have changed if there was Government advice given during this disease scenario. Physical opportunity and herd size were related in this intervention, with vaccination being more costly and time consuming for farmers with greater numbers of cattle than those with smaller herds. Vaccination was particularly costly in this disease scenario (£50 per animal) and high vaccination costs have been shown to decrease the likelihood of farmers vaccinating in a bluetongue outbreak (Sok et al., 2018). Subsidising an intervention measure is another tool that could change farmer behaviour for earlier intervention use (Agriculture and Horticulture Development Board, 2018), because farmers are more likely to use disease control measures if they are affordable (Jones et al., 2015; Mingolla et al., 2021). However, subsidisation is unlikely to change farmer behaviour if it is impractical (Bennett and Cooke, 2005), and a large level of subsidisation was required to increase the preference for bluetongue vaccination in the Netherlands (Sok et al., 2015).

Farmers with high trust in advice from the veterinary profession and high trust in other farmers to control disease were most likely to vaccinate mid-epidemic. This behaviour is consistent with the behavioural label of parasitism (Bshary and Bergmüller, 2008), waiting to see what happens to others first and expecting to be protected by other farmers vaccinating their herds, only vaccinating if it becomes necessary. Other research has identified that high trust in farmers to control disease can reduce the disease prevention behaviours farmers use in their own herd because they perceive their risk of disease from other farms to be low (Oliveira et al., 2018; Prosser et al., 2022), therefore this can be a barrier in disease control. Veterinary advice is generally trusted by farmers (Bard et al., 2019; Brennan and Christley, 2013) and this could be a route to promoting interventions to achieve prompt uptake and better epidemic control.

Our infectious disease model assessment, considering how different modelling assumptions with respect to farmer disease control behaviour impacted epidemiological outcomes for a fast-spreading disease outbreak scenario, revealed a disconnect in outcomes between the configurations that assumed homogeneity in farmer behaviour (*Strong parasitism, Weak parasitism, Mutual cooperation*) and those that used the empirical estimates for psychosocial profile clusters from the interview data (*Trust-Expectancy* and *Herd size dependent*). In contrast, our simplistic assumption for a heterogeneous behavioural profile composition amongst the farmer population (*Coop-Parasitism*) resulted in a closer correspondence across outbreak size, outbreak duration and threshold intervention cost metrics to results obtained for our *Trust-*

*Expectancy* and *Herd size dependent* scenarios. In the absence of behavioural response data, these observations imply that a simplified implementation of heterogeneity in farmer intervention response (e.g. our *Coop-Parasitism* configuration) may deliver commensurate modelling findings compared to circumstances where the behavioural profile of the population of farmers was known. Though not explored here, another route of investigation would concern the requirements of behavioural-targeted interventions (altering the behavioural profile of farmers towards disease management) to return an overall most cost-efficient solution. Such an investigation we expect would be highly computationally intensive and meriting its own study.

We lastly remark that the inclusion of herd size in assigning farmers to a particular behaviour group in the livestock disease model did not lead to any appreciable difference in modelled outcomes (compared to the *Trust-Expectancy* configuration). Given these two empirically informed configurations gave the most robust fit to the interview data, getting similar outcomes when aggregating across all seed infection regions is not unsurprising. Nevertheless, there was also little difference when inspecting how the results depended upon the seed infection region, despite the spatial variation in the cattle population in Great Britain.

Our methodological approach has explored how, through behavioural elicitation, heterogeneity in behavioural approach influences vaccination decisions to an approaching epidemic and how this information can be incorporated into a mathematical model of a livestock disease outbreak. Though our approach has only been applied to a farming population in this study, the principles and findings have immediate applicability to wider disease prevention behaviour. It has been argued that behavioural science has a key role to play in helping manage responses to pandemics (Van Bavel et al., 2020), encouraging vaccination behaviour (Brewer et al., 2017) and health based philanthropy (Ferguson, 2021; Ferguson et al., 2019). However, the focus on heterogeneity in behaviour that is central to a behavioural science approach needs to be incorporated within large-scale policy-based approaches. In this study, we have shown how this can be achieved in the context of farmer vaccination decisions to an approaching infectious livestock disease. Modelling at the population level would not only say which population strategies may be more effective, but how they could be tailored. The same principles can be applied to any disease outbreak or behaviour that rests on human cooperative and shared action.

The relatively small number of interviews conducted as part of the elicitation exercise is a limitation which precluded the investigation of behavioural cluster compositions at the national or regional level. The consequences of regional correlations between farmer disease management behavioural traits and measurable demographic attributes (such as herd size) on livestock disease outbreak dynamics merits further study. Such advancements would go towards the call for encapsulating social behaviour, demography and disease dynamics within models, meaning the formulation of disease-management strategies fully exploit both behavioural and demographic information (Silk et al., 2019).

There was also no individual covariate that had a stability over a more stringent threshold, where there would only be a 5 % probability of the covariate not being associated with when farmers vaccinated (stability threshold value: 0.30). However, the threshold we used is expected to lead to the selection of fewer false positive covariates than by a model built on the full dataset without bootstrapping (Lima et al., 2021), giving more confidence that the covariates identified are associated with the vaccination behaviour. Also, although the scenario was carefully controlled to investigate vaccination, there are other practices that farmers would have used to lower their risk, which could have different associations with psychosocial factors, and further research will be needed to investigate such combinations of interventions. Furthermore, the farmers differed in the time it took them to make a decision about vaccination at each time point and we could have investigated their certainty in their decision by recording the time taken to make a decision (Bhatia and Mullett, 2018; Van de Calseyde et al., 2014), which would have enhanced our confidence in the behavioural differences shown by the farmers.

As with any model, the disease transmission model we devised here is not capable of perfectly replicating the biological real-world system and multiple simplifying assumptions have been made. Relaxing these constraints presents opportunities for further investigation, though was beyond the scope of this study. A primary example is that in the model we focused on a limited set of interventions. Expansions in the intervention space can be conceived, such as considering a vaccine with imperfect efficacy and/or requiring multiple doses, evaluating other intervention methods such as pre-emptive culling or enhanced biosecurity, and making assessments for scenarios where a package of multiple interventions may be used collectively. Furthermore, for optimising the cost of the intervention we took one perspective. In prior work we have shown how there can be a divergence in the optimal scale of reactive voluntary vaccination response to a fast-spreading livestock pathogen between a 'population' perspective - seeking an outcome that brings the greatest total benefit across all farmers (stakeholder responsible for supporting the livestock industry) - versus an 'individual' perspective that maximises the benefit from the viewpoint of sole livestock owners (Hill et al., 2022). We also recognise that we have considered only one particular set of epidemiological parameters, representing a highly contagious, fast-spreading pathogen amongst cattle. Our choice was partially motivated by the grave impacts of historic foot and mouth disease outbreaks in the UK, driving our interest in the implications of farmers' behaviour towards disease management in a fast-spreading epidemic with a costly but very effective intervention. Pragmatic decisions were also taken to make the results generalisable, notably the intervention being 100 % effective (if applied early enough) to reduce the variability that the farmers had to consider. For epidemics with less transmission potential, though there may be a general reduction in the effect of behavioural heterogeneity on study outcomes, with the non-linearities present in the system dynamics we conjecture that there may be emergent non-trivial interactions between the epidemiological and behavioural components of the system dynamics. Therefore, both the qualitative and quantitative implications on the epidemiological outcomes and economic metrics of different behavioural assumptions (given a different reference scenario) requires further study.

Our study contributes to the need for more quantitative studies into veterinary health associated behaviours that can capture individual, interpersonal and contextual factors. However, the current study design only grants a snapshot assessment of behavioural traits at one point in time. To inform how farmers' attitude, perceptions, beliefs and behaviours on disease management change over time, support is needed to establish longitudinal elicitation studies (Hidano et al., 2018).

Other questions remain open for investigation. Our epidemiological context here was a fast-spreading pathogen, an epizootic scenario. For pathogens that are regularly affecting livestock, an enzootic disease, the appropriate disease management may require bespoke approaches that require elongated usage to tackle a consistent risk of infection flare ups. Two such pathogens of note in Great Britain are bovine tuberculosis (TBhub, 2019) and bovine viral diarrhoea (BVDFree England, 2019). Tailored elicitation exercises (akin to this study) are needed to instruct behavioural group attributes amongst farmers towards control of enzootic diseases, producing data in a format directly usable in mathematical models. In these cases, it would also not necessarily be the case that controls are implemented at the herd level, meaning within-herd transmission dynamics should be considered in such circumstances.

In conclusion, our bespoke GUI successfully allowed us to identify heterogeneity in farmer behaviour in a realistic disease epidemic scenario. We have been able to identify new psychosocial and demographic factors that are associated with the timing of farmers vaccinating their herd in response to an outbreak of a fast-spreading livestock pathogen. With these data, we have subsequently demonstrated how ignoring behavioural differences in disease management of livestock infections can increase the prospect of misinformed judgments being drawn from

models of infectious disease dynamics. We therefore contend that the integration of behavioural heterogeneity into veterinary health decision making merits continued study.

## Declaration of Competing Interest

None.

## Data availability

The authors were supplied holding-level records from the Cattle Tracing System by the Rapid Analysis and Detection of Animal-related Risks (RADAR) team at the Animal and Plant Health Agency (APHA). These data contain confidential information, with public data deposition non-permissible for socioeconomic reasons. For data access, the RADAR team at APHA can be contacted on RADAR@apha.gov.uk. Spatial maps display digital vector boundaries for countries, counties and unitary authorities in Great Britain that are owned and made available by ONSGeography_data. Source: Office for National Statistics licensed under the Open Government Licence v.3.0. Contains OS data © Crown copyright and database right 2022. Terms and conditions of supply for the digital boundaries and reference maps are provided at https://www.ons.gov.uk/methodology/geography/licences. All other data utilised in this study are publicly available, with relevant references and data repositories stated within the main manuscript.

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## Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.prevetmed.2023.106019.

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