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

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.

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

38 omit the observed variation in disease management behaviours. Multiple methodological
39 developments are consequently required to overcome these deficiencies.

40 People are well known to show different behaviours with respect to disease control; for
41 example people can be mutually cooperative (acting for the benefit of both the self and other
42 people), or show parasitism (gain benefit from other people taking action) (Bshary and
43 Bergmüller, 2008). This is seen for human infections where there is considerable variability
44 in the uptake of vaccine or the decision to vaccinate children (Cellini et al., 2022; Dolby et
45 al., 2022), and this concept translates to farmers with the decision to protect their livestock.
46 The heterogeneity in farmer behaviour for disease control is in part due to psychosocial and
47 behaviour factors. Trust is a key component underlying cooperation (Kuipers, 2022) and
48 trust in other farmers improves willingness to join disease control schemes (Heffernan et al.,
49 2016; Shortall et al., 2016). However, trust in other farmers is also associated with farmers
50 not controlling specific diseases such as bovine viral diarrhoea (Prosser et al., 2022).
51 Increased trust means that farmers are more likely to believe that purchased animals will be
52 disease-free. Trust also has implications for sources of advice, with farmers preferring to
53 trust veterinary rather than Government advice (Bard et al., 2019; Brennan and Christley,
54 2013; Fisher, 2013). Related to trust is psychological proximity (closeness) to others.
55 Psychological proximity includes close feelings and behaviours, and connection,
56 interdependence and similarities with the other person (Aron et al., 1992). Psychological
57 proximity has implications for human health behaviour (Shamloo et al., 2023; Thiessen et al.,
58 2021; Tu et al., 2021) but to date has received little investigation in farmer behaviour for
59 controlling livestock disease. Farmers with high psychological proximity to their veterinarian
60 are more likely to control bovine viral diarrhoea in their herd (Prosser et al., 2022). Behaviour
61 is also influenced by capability, opportunity and motivation which are theorised in the COM-B
62 behaviour change framework (Michie et al., 2011). Capability is the physical ability (physical
63 capability) and the knowledge and understanding (psychological capability) required to
64 perform a behaviour. Opportunity is the time and money (physical opportunity) and the
65 support from others (social opportunity) that enable a behaviour. Finally, motivation is
66 decision-making and goals (reflective motivation) and habits and emotions (automatic
67 motivation). Factors that make up this framework are often investigated in isolation in the
68 context of disease control and use of the entire COM-B framework in livestock disease is
69 rare. One study that used the COM-B framework found that farmers with high automatic and
70 reflective motivation, high psychological capability and high physical opportunity were more
71 likely to control disease in their herds (Prosser et al., 2022).

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

85
86 Through an interdisciplinary approach, we strive to form a methodological pipeline that can
87 generate novel quantitative data on farmer beliefs and hone epidemiological-behavioural
88 models so the gathered data is amenable for direct usage (and equally, a pipeline where
89 model outputs can inform what attributes may require particular focus in future data
90 collection). To make initial advancements in this emerging research space - establishing a
91 proof-of-concept - requires a well-defined scenario to make elicitation feasible. In this study,
92 we investigated farmer behaviour in a fast, spatially spreading disease outbreak scenario by
93 creating a graphical user interface (GUI) to dynamically show farmers the progress of the
94 epidemic and elicit when they would each use a vaccine that was available to them. This is
95 an important scenario to consider as a pathogen spreading rapidly between farms has the
96 potential to cause substantial negative impacts, albeit a rare occurrence in Great Britain, and
97 would likely need a concerted effort by farmers to control. We chose vaccination as an
98 intervention response because the types of heterogeneity observed in vaccination behaviour
99 and attitudes has been well documented (Böhm et al., 2016; Dudley et al., 2020; Weiss et
100 al., 2016).
101
102 Using multiple validated measures, we studied how trust, psychological proximity and COM-
103 B factors were associated with farmer vaccination behaviour in the face of the disease
104 outbreak. We then used the attained behavioural groups within an infectious disease model
105 to explore, through computational simulation, the impact on anticipated epidemiological
106 outcomes (outbreak size, outbreak duration) and economic metrics (associated with cost-
107 effectiveness) when making specific assumptions regarding heterogeneity in behaviour
108 towards disease management. It is revealed how omitting heterogeneity in farmers' disease
109 management of livestock infections can result in ill-judged assessments of the likely
110 projected distributions and threshold statistics associated with outbreak size, outbreak
111 duration and health economic measures.

Methods

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

GUI

121 We created a graphical user interface (GUI) to dynamically illustrate the spread of an
122 epidemic disease of cattle and used the GUI to investigate farmer behaviour during a
123 simulated disease epidemic. The GUI showed a series of maps, with infected herds plotted,
124 week by week. The outbreak started in southern-central France (epidemic stage 1), was
125 introduced to Great Britain (epidemic stage 2), then spread throughout Great Britain
126 (epidemic stages 3 – 8). The GUI presented a common outbreak experience at each stage
127 of the epidemic, in terms of distance to the nearest infected farm, for each participating
128 farmer regardless of the location of their farm. An example screenshot from the GUI can be

129   seen in Supplementary Fig. 1 and the GUI can be accessed online
130   (https://feed.warwick.ac.uk/map.html).

131   Elicitation exercise (farmer interviews)

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

144   The farmers then proceeded with the scenario using the GUI and were asked at weekly
145   intervals whether they would vaccinate or do any other preventative measures. Farmers
146   answered the questions in the online questionnaire directly after the disease scenario, which
147   used validated measures to investigate trust in others, psychological proximity to others and
148   the COM-B behaviour change framework. Trust in others was measured using five-point
149   Likert-scale statements (from strongly disagree to strongly agree) which investigated both
150   general trust and trust in the context of infectious disease control in other farmers,
151   veterinarians and government (Ferguson et al., 2022; Prosser et al., 2022). The responses
152   to each Likert scale were converted to a numerical response (1 = strongly disagree, 2 =
153   disagree, 3 = neither agree nor disagree, 4 = agree, 5 = strongly agree). Psychological
154   proximity to their cows, other farmers, veterinarians and government was measured using
155   the Inclusion of Other in the Self (IOS) scale on a 1 - 7 score, with higher scores
156   representing feeling closer to the specific 'other' (Aron et al., 1992; Mashek et al., 2007). The
157   COM-B factors were investigated using Likert-scale statements (using the same scale used
158   to investigate trust) that investigated aspects of each COM-B factor in the context of
159   infectious disease control (Michie et al., 2011; Michie et al., 2014). The mean of the scores
160   for a farmer for the Likert statements within a COM-B factor were taken as that factor score.
161   The questions used to investigate trust, psychological proximity and the COM-B factors are
162   in Supplementary Text 2. The survey web page generated an individual code for each
163   respondent, which was used to anonymously link the responses with the interview
164   responses once all interviews were completed.

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

171 Analysis of elicitation data

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

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

186 To mitigate overfitting, we fit the model to 500 bootstrapped datasets and assessed the
187 stability of the model covariates. Bootstrapping was implemented by randomly selecting
188 farmers from the dataset 60 times with replacement. This was repeated 500 times to result in
189 500 slightly different datasets, though all with data obtained from the 60 interviewed farmers.

190 The covariates selected by a higher proportion of the models were more likely to be truly
191 associated with when farmers vaccinated (Green et al., 2021; Lima et al., 2021, Hyde et al.,
192 2022). We calculated the stability of each covariate (the proportion of multinomial logistic
193 regression models fit to the 500 bootstrapped datasets that selected the covariate) to
194 mitigate overfitting in this wide dataset (Lima et al., 2021). We calculated stability thresholds
195 for different probabilities of a variable being a true positive using the methods by Green *et al.*
196 (2021) and Hyde et al. (2022). Selected covariates had a stability higher than a threshold
197 where covariates had a 15% probability of not being associated with when farmers
198 vaccinated. We calculated odds ratios of the stable covariates by refitting the model to the
199 bootstrapped datasets with the candidate covariates limited to those above the stability
200 threshold and taking the mean of the coefficients. Finally, model fit was assessed by fitting
201 the multinomial logistic regression model to the full dataset and comparing the observed and
202 expected data using a Hosmer-Lemeshow goodness-of-fit test and decile plots (Fagerland
203 and Hosmer, 2012), and by comparing predicted vaccination class from the full and 10 x 10-
204 fold cross validated models.

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

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

Livestock data description

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

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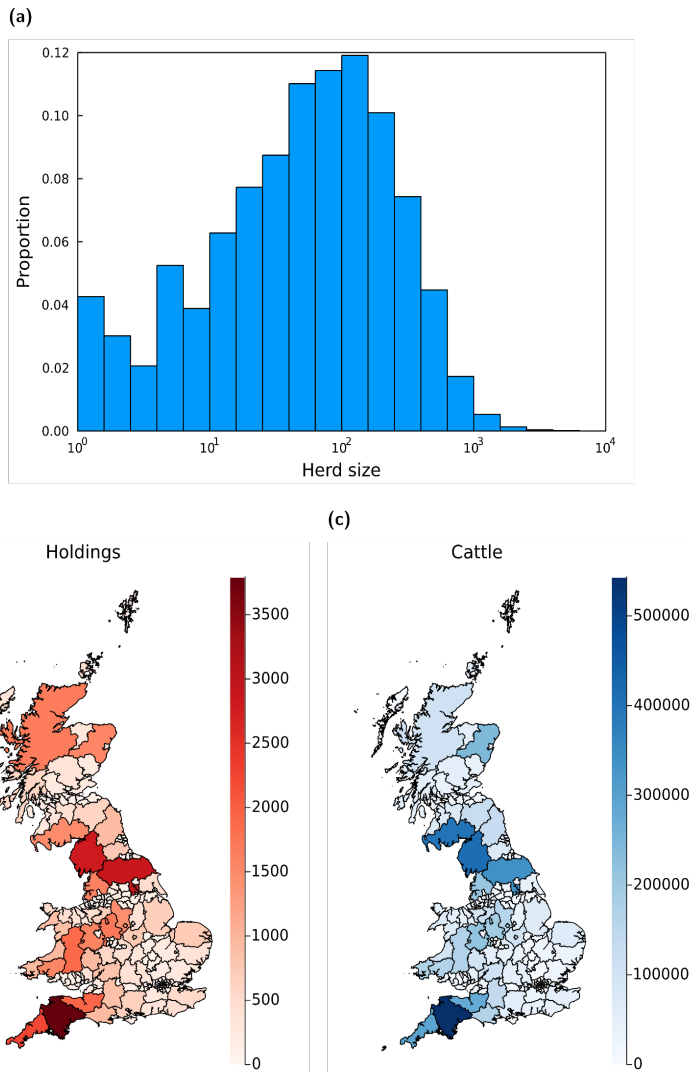234   (Fig. 1).

235

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.

Epidemiological model

246

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

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

254
$$p_{ij} = 1 - exp(\lambda_{ij})$$

255
$$\text{where, } \lambda_{ij} = \xi N_i^{\psi} N_j^{\phi} K(d_{ij})$$

256 In detail, the force of infection between two herds, λ_{ij}, was a nonlinear function of the
257 transmissibility of cattle (ξ), the number of cattle on the infectious holding (term N_i^{ψ}) and the
258 number of cattle on the susceptible holding (term N_j^{ϕ}). For the herd size exponents, ψ and
259 ϕ, we used cattle epidemiological parameter estimates inferred from the 2001 UK foot-and-
260 mouth disease (FMD) epidemic for Cumbria (Tildesley et al., 2008).

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

264
$$K(d_{ij}) = \frac{k_1}{1 + (\frac{d}{k_2})^{k_3}}, \text{ for } 0 \le d_{ij} \le 50000; \text{ Otherwise, } K(d_{ij}) = 0.$$

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

276 Upon a holding becoming infected, we assumed a latent period of five days (based on
277 epidemiological and veterinary records from the 2001 UK FMD outbreak (Keeling et al.,
278 2001)). Thereafter, the entire livestock population at that holding was considered infectious
279 for a period of eight days (days 6 - 13 after infection). We assumed all infected holdings
280 provided notification of infection nine days after the initial infection event, meaning there was
281 no under-reporting of infection, but there was a four-day delay between the holding
282 becoming infectious and subsequent notification of infection. At the end of the infectious

283 period (13 days after infection) the cattle herd and holding were considered removed from
284 the population.

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

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

Notation	Description	Value
Epidemiological parameters		
λ_{ij}	Infectious pressure on susceptible holding j from infectious holding i.	Variable
N_i	Number of cattle on premises i	Variable
ξ	Transmissibility of cattle.	10^6
ψ	Exponent on the cattle population on an infectious holding, for calculating the infectious pressure.	0.42
ϕ	Exponent on the cattle population on a susceptible holding, for calculating the infectious pressure.	0.41
k_1	Transmission kernel normalisation constant (to 2 s.f.)	1.2x10^-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

288 **Implementation of vaccination**

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

291 We present the idealised situation of having a vaccine available with 100% effectiveness in
292 blocking infection. As per the description of the vaccine product in the interview script, we
293 included a lag for the vaccine inducing an immune response (fixed at 5 days, based on

294 measures of FMD virus titres in milk from inoculated cows in the days post-inoculation (Orsel
295 et al., 2007)). As the vaccine could be administered to an infected population during its latent
296 phase (thus prior to onset of symptoms and subsequent notification of infection), in these
297 circumstances it was feasible for a cattle herd at a holding to be vaccinated but to still
298 become infected.

299 **Intervention behaviour configurations**

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

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

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

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

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

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

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

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

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

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

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

354   *Herd size dependent*: Partitioning of holdings into three behavioural groups, using the
355   empirical estimates for psychosocial profile clusters from the model comprising the
356   covariates selected by stability thresholds for a 15% probability of not being associated with
357   when farmers vaccinated. For details on the attributes associated with each of the three
358   behavioural groups, see Fig. 4 and the "Elicitation findings" subsection of the Results.
359   Specific to the *Herd size dependent* configuration, herd size determined the probability of the
360   holding being assigned to each of the three behavioural groups (Fig. 2).
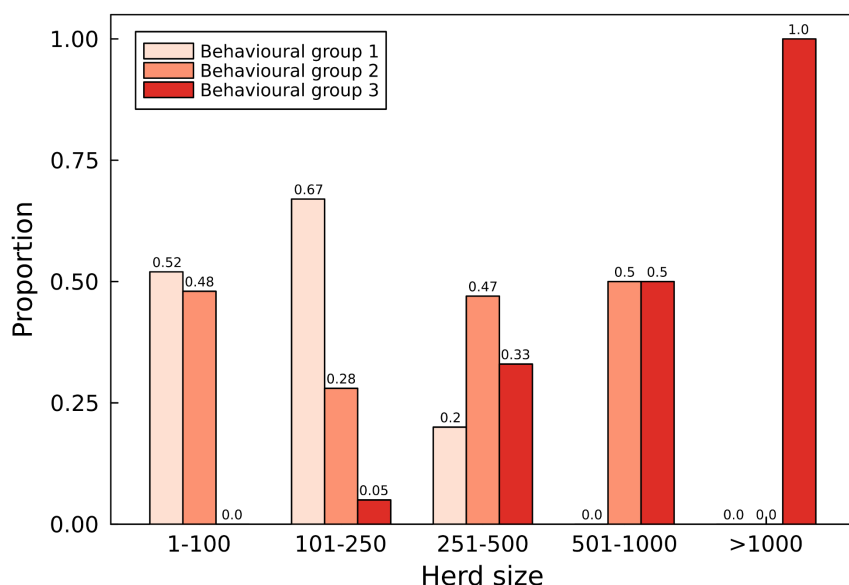
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Fig. 2: For the "Herd size dependent" behavioural configuration, the probability of a
holding being assigned to each of the three behavioural groups with respect to the
herd size. The bars depict the probability of a holding being assigned to each 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 the "Elicitation findings" subsection of the Results.

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.

387 In general terms, the threshold intervention unit cost is the maximum cost per intervention
388 unit where the costs saved from averted infections (i.e., the cost of removing cattle at those
389 additional holdings that would have been infected had the intervention not been used)
390 equals the total intervention cost. For our application, an intervention unit was a vaccine
391 dose, with the intervention cost being a relative cost of vaccination compared to the cost of
392 infection and removal of a single cow (i.e., an intervention cost of 1 meant the cost of a
393 vaccine dose equalled the cost of the loss of a single cow due to infection and removal).

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

Results

Elicitation findings

401 Sixty farmers (39 beef and 21 dairy) completed the elicitation interview and interviews took
402 place between April and June 2022. Forty-four (73%) were from England, nine (15%) from
403 Scotland and seven (12%) from Wales. The median number of cows in the herd was 155
404 cows for dairy herds (range = 30 – 330, one herd only reared heifers) and 35 for beef herds
405 (range = 5 – 200, one herd only fattened cattle). The herd sizes were slightly larger than the
406 national averages and English farmers were slightly over-represented (Agriculture &
407 Horticulture Development Board, 2019).

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

413 **Table 2:** The number of infected herds, the distance of the nearest infected herd from the
414 interviewee's herd and the number of farmers that vaccinated for each week during the
415 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

416 **Table 3:** The stability and mean odds ratio (OR) and the central 95% range of the odds
417 ratios from the model fit to the bootstrapped datasets (95% CI) of the covariates associated
418 with when farmers vaccinated their cattle in a hypothetical disease epidemic, above the
419 stability threshold for a 15% probability of a covariate reaching the threshold without being
420 truly associated with when farmers vaccinated their cattle (stability threshold value: 0.20).
421 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)

422 We fit multinomial logistic regression models testing for associations between the
423 psychosocial and behaviour change factors and when farmers vaccinated to bootstrap
424 repeats of the dataset. Two covariates were above a stability threshold when there was only
425 a 10% probability of not being associated with when farmers vaccinated (stability threshold

426 value: 0.24). These covariates were: trust in governmental judgements about how to control
427 infectious diseases in cattle; and physical opportunity (Table 3). Three additional covariates
428 were selected when the stability threshold was relaxed to a 15% probability of not being
429 associated with when farmers vaccinated (stability threshold value: 0.20), which were: trust
430 in the quality of advice from the veterinary profession; trust in other farmers nationally to
431 control infectious diseases; and herd size at time of disease outbreak. There was no
432 evidence of poor model fit in a Hosmer-Lemeshow goodness-of-fit test (p = 0.814), by visual
433 inspection of a decile plot of the observed and expected vaccination classes (Supplementary
434 Fig. 2), or when comparing the proportion of farmers for which the model predicted the
435 correct vaccination class between the full model (proportion of farmers with class correctly
436 predicted = 0.62) and the 10 x 10-fold cross-validated models (mean proportion of farmers
437 with class correctly predicted = 0.58).

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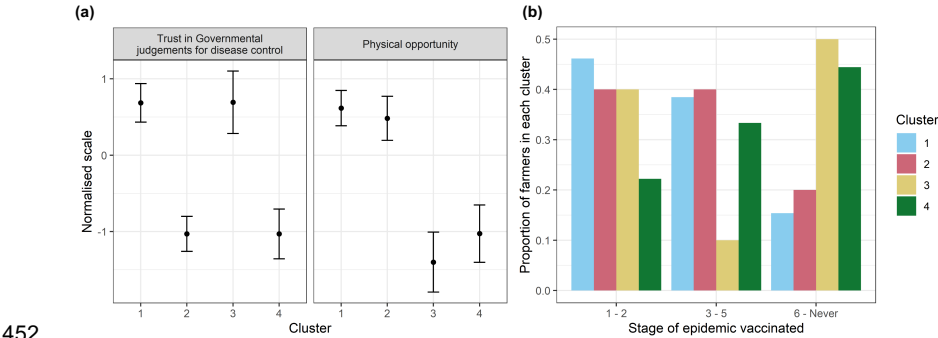

452

453 **Fig. 3: The farmer groups from k-means clustering conducted on the two most stable**
454 **covariates** (Trust in Governmental judgements about disease control and Physical
455 opportunity). **(a)** The mean (point) and 95% confidence interval (error bars) scores of the
456 covariates for each group. **(b)** The proportion of farmers in each group that vaccinated at
457 different stages of the epidemic (Epidemic stages 1 - 2, Epidemic stages 3 - 5 and Epidemic
458 stage 6 - 8 or never uses vaccination). Associated values are given in Supplementary Table
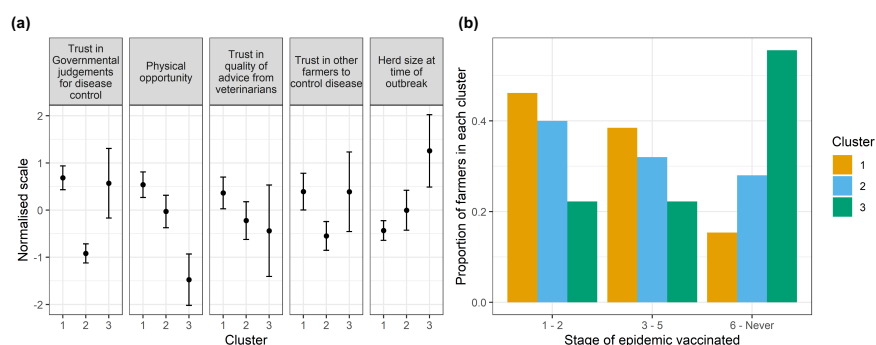459 1 and Supplementary Table 2.

460

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.

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.

Intervention behaviour configurations

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).

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%, 5% and 10% 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 93.5% of simulations having more than 10% 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 was roughly four times greater (approximately 6.4% of simulations). Having all farmers being more precautionary, resembling our *weak parasitism* configuration, many outbreaks were small-scale. The median outbreak size was just 0.6% of holdings infected and no simulations resulted in more than 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 257 days (Fig. 5(c)). The majority of simulated outbreaks (94.8%) lasted more than 180 days (Fig. 5(d)). For *strong parasitism*, the outbreak duration was reduced compared with the *uncooperative* scenario (median of 160 days), although it remained likely that outbreaks would last in excess of 100 days (93.5% 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 (Figs. 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 4.9% of simulations returning a threshold unit intervention cost above 2). Meanwhile, for *weak parasitism* the threshold unit intervention cost was predominately in the range of 0.5 to 1, with a small chance of it being larger than 2 (achieved in 11.4% of simulations). Finally, though outbreaks were prevented under *mutual cooperation*, for the pre-emptive use of vaccination by all to be cost effective, the intervention unit cost would have to be less than the cost of infection of a single cow.

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

558 greater median and upper uncertainty bounds for holdings infected and outbreak duration.
559 There was a striking difference in the number of simulations that resulted in more than 10%
560 of holdings infected, 95.6% vs 0.0% (Fig. 5(b)), and in an outbreak duration of more than
561 180 days, 86.7% vs 23.8% (Fig. 5(d)). We found quantitatively similar 95% prediction
562 intervals for the intervention unit threshold costs (Figs. 5(e,f)), of 0.86-3.15 for *Coop-*
563 *Parasitism-FR* and 0.98-2.49 for *Coop-Parasitism*, respectively.

564 **Data informed, heterogenous behavioural configuration outcomes**

565 We conclude our modelling analysis by viewing the configurations informed by the interview
566 data (*Trust-Expectancy* and *Herd size dependent*). Comparing these two behavioural
567 configurations, we observed both quantitatively similar distributions and threshold summary
568 statistics. That being said, a marked result was the distributions and threshold outcomes
569 being distinct from the other assessed behavioural configurations (Fig. 5). Epidemiological
570 outcomes most closely resembled the *Coop-Parasitism* configuration, with an increased risk
571 of larger outbreaks and an increase in the likelihood of outbreaks being elongated. For the
572 economic metric, rather than asserting homogeneity in behaviour or simple uniform splits
573 between groups, when we grounded the behavioural configurations with empirical data the
574 intervention unit threshold cost was close to 1 on average (medians of 0.96 for *Trust-*
575 *Expectancy* and 0.94 for *Herd size dependent*). Additionally, the threshold unit intervention
576 cost was very likely to be in the range of 0.5 to 1.

577 **Role of seed infection region**

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

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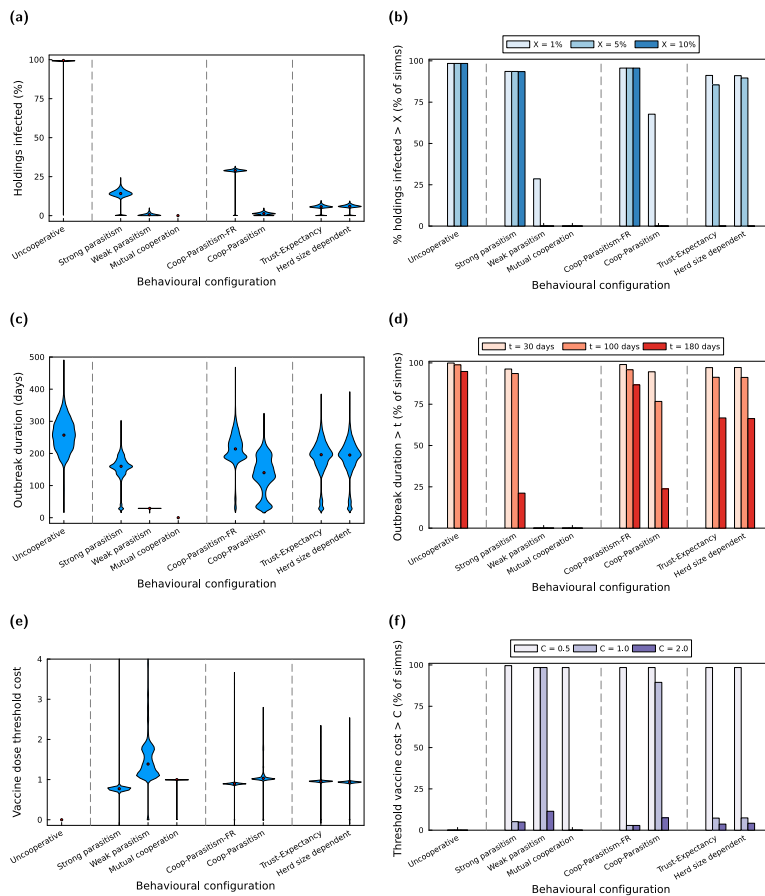Deleted: , mimicking outcomes under the *Coop-Parasitism* scenario…

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.
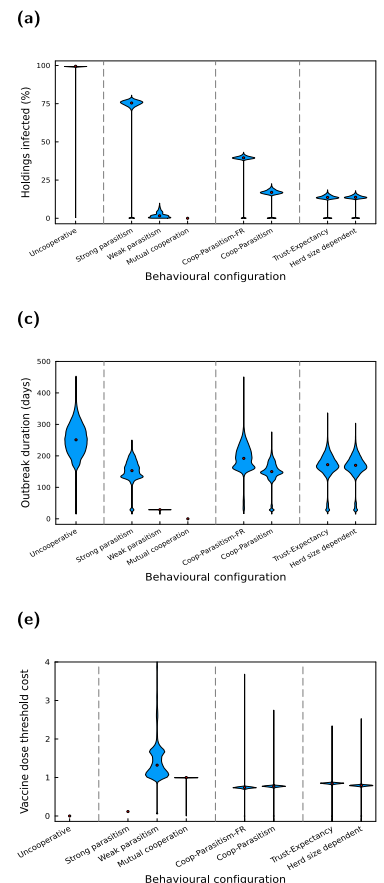
Discussion

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, in press), 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 & 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

666 impractical (Bennett and Cooke, 2005), and a large level of subsidisation was required to
667 increase the preference for bluetongue vaccination in the Netherlands (Sok et al., 2015).

668 Farmers with high trust in advice from the veterinary profession and high trust in other
669 farmers to control disease were most likely to vaccinate mid-epidemic. This behaviour is
670 consistent with the behavioural label of parasitism (Bshary and Bergmüller, 2008), waiting to
671 see what happens to others first and expecting to be protected by other farmers vaccinating
672 their herds, only vaccinating if it becomes necessary. Other research has identified that high
673 trust in farmers to control disease can reduce the disease prevention behaviours farmers
674 use in their own herd because they perceive their risk of disease from other farms to be low
675 (Oliveira et al., 2018; Prosser et al., 2022), therefore this can be a barrier in disease control.
676 Veterinary advice is generally trusted by farmers (Bard et al., 2019; Brennan and Christley,
677 2013) and this could be a route to promoting interventions to achieve prompt uptake and
678 better epidemic control.

679 Our infectious disease model assessment, considering how different modelling assumptions
680 with respect to farmer disease control behaviour impacted epidemiological outcomes for a
681 fast-spreading disease outbreak scenario, revealed a disconnect in outcomes between the
682 configurations that assumed homogeneity in farmer behaviour (*Strong parasitism, Weak*
683 *parasitism, Mutual cooperation*) and those that used the empirical estimates for psychosocial
684 profile clusters from the interview data (*Trust-Expectancy* and *Herd size dependent*). In
685 contrast, our simplistic assumption for a heterogeneous behavioural profile composition
686 amongst the farmer population (*Coop-Parasitism*) resulted in a closer correspondence
687 across outbreak size, outbreak duration and threshold intervention cost metrics to results
688 obtained for our *Trust-Expectancy* and *Herd size dependent* scenarios. In the absence of
689 behavioural response data, these observations imply that a simplified implementation of
690 heterogeneity in farmer intervention response (e.g. our *Coop-Parasitism* configuration) may
691 deliver commensurate modelling findings compared to circumstances where the behavioural
692 profile of the population of farmers was known. Though not explored here, another route of
693 investigation would concern the requirements of behavioural-targeted interventions (altering
694 the behavioural profile of farmers towards disease management) to return an overall most
695 cost-efficient solution. Such an investigation we expect would be highly computationally
696 intensive and meriting its own study.

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

705 Our methodological approach has explored how, through behavioural elicitation,
706 heterogeneity in behavioural approach influences vaccination decisions to an approaching
707 epidemic and how this information can be incorporated into a mathematical model of a
708 livestock disease outbreak. Though our approach has only been applied to a farming
709 population in this study, the principles and findings have immediate applicability to wider

710 disease prevention behaviour. It has been argued that behavioural science has a key role to
711 play in helping manage responses to pandemics (Van Bavel et al., 2020), encouraging
712 vaccination behaviour (Brewer et al., 2017) and health based philanthropy (Ferguson et al.,
713 2019; Ferguson, 2021). However, the focus on heterogeneity in behaviour that is central to a
714 behavioural science approach needs to be incorporated within large-scale policy-based
715 approaches. In this study, we have shown how this can be achieved in the context of farmer
716 vaccination decisions to an approaching infectious livestock disease. Modelling at the
717 population level would not only say which population strategies may be more effective, but
718 how they could be tailored. The same principles can be applied to any disease outbreak or
719 behaviour that rests on human cooperative and shared action.

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

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

742 As with any model, the disease transmission model we devised here is not capable of
743 perfectly replicating the biological real-world system and multiple simplifying assumptions
744 have been made. Relaxing these constraints presents opportunities for further investigation,
745 though was beyond the scope of this study. A primary example is that in the model we
746 focused on a limited set of interventions. Expansions in the intervention space can be
747 conceived, such as considering a vaccine with imperfect efficacy and/or requiring multiple
748 doses, evaluating other intervention methods such as pre-emptive culling or enhanced
749 biosecurity, and making assessments for scenarios where a package of multiple
750 interventions may be used collectively. Furthermore, for optimising the cost of the
751 intervention we took one perspective. In prior work we have shown how there can be a
752 divergence in the optimal scale of reactive voluntary vaccination response to a fast-
753 spreading livestock pathogen between a 'population' perspective - seeking an outcome that
754 brings the greatest total benefit across all farmers (stakeholder responsible for supporting

755 the livestock industry) - versus an 'individual' perspective that maximises the benefit from the
756 viewpoint of sole livestock owners (Hill et al., 2022). We also recognise that we have
757 considered only one particular set of epidemiological parameters, representing a highly
758 contagious, fast-spreading pathogen amongst cattle. Our choice was partially motivated by
759 the grave impacts of historic foot and mouth disease outbreaks in the UK, driving our interest
760 in the implications of farmers' behaviour towards disease management in a fast-spreading
761 epidemic with a costly but very effective intervention. Pragmatic decisions were also taken to
762 make the results generalisable, notably the intervention being 100% effective (if applied
763 early enough) to reduce the variability that the farmers had to consider. For epidemics with
764 less transmission potential, though there may be a general reduction in the effect of
765 behavioural heterogeneity on study outcomes, with the non-linearities present in the system
766 dynamics we conjecture that there may be emergent non-trivial interactions between the
767 epidemiological and behavioural components of the system dynamics. Therefore, both the
768 qualitative and quantitative implications on the epidemiological outcomes and economic
769 metrics of different behavioural assumptions (given a different reference scenario) requires
770 further study.

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

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

788 In conclusion, our bespoke GUI successfully allowed us to identify heterogeneity in farmer
789 behaviour in a realistic disease epidemic scenario. We have been able to identify new
790 psychosocial and demographic factors that are associated with the timing of farmers
791 vaccinating their herd in response to an outbreak of a fast-spreading livestock pathogen.
792 With these data, we have subsequently demonstrated how ignoring behavioural differences
793 in disease management of livestock infections can increase the prospect of misinformed
794 judgments being drawn from models of infectious disease dynamics. We therefore contend
795 that the integration of behavioural heterogeneity into veterinary health decision making
796 merits continued study.

804 Data availability

805 The authors were supplied holding-level records from the Cattle Tracing System by the
806 Rapid Analysis and Detection of Animal-related Risks (RADAR) team at the Animal and
807 Plant Health Agency (APHA). These data contain confidential information, with public data
808 deposition non-permissible for socioeconomic reasons. For data access, the RADAR team
809 at APHA can be contacted on RADAR@apha.gov.uk.
810
811 Spatial maps display digital vector boundaries for countries, counties and unitary authorities
812 in Great Britain that are owned and made available by ONSGeography_data. Source: Office
813 for National Statistics licensed under the Open Government Licence v.3.0. Contains OS data
814 © Crown copyright and database right 2022. Terms and conditions of supply for the digital
815 boundaries and reference maps are provided at
816 https://www.ons.gov.uk/methodology/geography/licences.
817
818 All other data utilised in this study are publicly available, with relevant references and data
819 repositories stated within the main manuscript.

820 Code availability

821 The code repository for the study is available at
822 https://github.com/EdMHill/FEED_farmer_disease_management_heterogeneity.

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