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.

Keywords (max of 6)

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

41 in the uptake of vaccine or the decision to vaccinate children (Cellini et al., 2022; Dolby et
42 al., 2022), and this concept translates to farmers with the decision to protect their livestock.
43 The heterogeneity in farmer behaviour for disease control is in part due to psychosocial and
44 behaviour factors. Trust is a key component underlying cooperation (Kuipers, 2022) and
45 trust in other farmers improves willingness to join disease control schemes (Heffernan et al.,
46 2016; Shortall et al., 2016). However, trust in other farmers is also associated with farmers
47 not controlling specific diseases such as bovine viral diarrhoea (Prosser et al., 2022).
48 Increased trust means that farmers are more likely to believe that purchased animals will be
49 disease-free. Trust also has implications for sources of advice, with farmers preferring to
50 trust veterinary rather than Government advice (Bard et al., 2019; Brennan and Christley,
51 2013; Fisher, 2013). Related to trust is psychological proximity (closeness) to others.
52 Psychological proximity includes close feelings and behaviours, and connection,
53 interdependence and similarities with the other person (Aron et al., 1992). Psychological
54 proximity has implications for human health behaviour (Shamloo et al., 2023; Thiessen et al.,
55 2021; Tu et al., 2021) but to date has received little investigation in farmer behaviour for
56 controlling livestock disease. Farmers with high psychological proximity to their veterinarian
57 are more likely to control bovine viral diarrhoea in their herd (Prosser et al., 2022). Behaviour
58 is also influenced by capability, opportunity and motivation which are theorised in the COM-B
59 behaviour change framework (Michie et al., 2011). Capability is the physical ability (physical
60 capability) and the knowledge and understanding (psychological capability) required to
61 perform a behaviour. Opportunity is the time and money (physical opportunity) and the
62 support from others (social opportunity) that enable a behaviour. Finally, motivation is
63 decision-making and goals (reflective motivation) and habits and emotions (automatic
64 motivation). Factors that make up this framework are often investigated in isolation in the
65 context of disease control and use of the entire COM-B framework in livestock disease is
66 rare. One study that used the COM-B framework found that farmers with high automatic and
67 reflective motivation, high psychological capability and high physical opportunity were more
68 likely to control disease in their herds (Prosser et al., 2022).
69
70 There has been a growing interest in the incorporation of psychosocial factors and
71 behavioural heterogeneity into disease transmission models (Bedson et al., 2021), which will
72 allow improved model predictions for successful disease control. A fundamental component
73 of delivering these methodological advances is having appropriate, well-informed
74 behavioural data available to parameterise models and enhance the robustness of model
75 outputs. One previous example of such data collection activities includes Merrill *et al*. (2019),
76 who conducted an experimental simulation game to quantitatively explore the effect of
77 interventions that would increase information sharing among stakeholders. Nevertheless, a
78 known challenge of fusing livestock infectious disease models and dynamic human
79 behavioural change is a dearth of quantitative behavioural data (and behavioural data
80 collection methodologies) that can capture relationships between psychosocial factors and
81 the heterogeneity in behavioural response for a given context (Hidano et al., 2018).
82
83 Through an interdisciplinary approach, we strive to form a methodological pipeline that can
84 generate novel quantitative data on farmer beliefs and hone epidemiological-behavioural
85 models so the gathered data is amenable for direct usage (and equally, a pipeline where
86 model outputs can inform what attributes may require particular focus in future data
87 collection). To make initial advancements in this emerging research space - establishing a
88 proof-of-concept - requires a well-defined scenario to make elicitation feasible. In this study,

89   we investigated farmer behaviour in a fast, spatially spreading disease outbreak scenario by
90   creating a graphical user interface (GUI) to dynamically show farmers the progress of the
91   epidemic and elicit when they would each use a vaccine that was available to them. This is
92   an important scenario to consider as a pathogen spreading rapidly between farms has the
93   potential to cause substantial negative impacts, albeit a rare occurrence in Great Britain, and
94   would likely need a concerted effort by farmers to control. We chose vaccination as an
95   intervention response because the types of heterogeneity observed in vaccination behaviour
96   and attitudes has been well documented (Böhm et al., 2016; Dudley et al., 2020; Weiss et
97   al., 2016).
98
99   Using multiple validated measures, we studied how trust, psychological proximity and COM-
100   B factors were associated with farmer vaccination behaviour in the face of the disease
101   outbreak. We then used the attained behavioural groups within an infectious disease model
102   to explore, through computational simulation, the impact on anticipated epidemiological
103   outcomes (outbreak size, outbreak duration) and economic metrics (associated with cost-
104   effectiveness) when making specific assumptions regarding heterogeneity in behaviour
105   towards disease management. It is revealed how omitting heterogeneity in farmers' disease
106   management of livestock infections can result in ill-judged assessments of the likely
107   projected distributions and threshold statistics associated with outbreak size, outbreak
108   duration and health economic measures.

109   Methods

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

117   GUI

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

128   Elicitation exercise (farmer interviews)

129   For the second phase of our study, we conducted interactive online interviews with cattle
130   farmers in Great Britain. The interactive online interviews consisted of three parts: (i)

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

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

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

168 Analysis of elicitation data

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

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

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

187 The covariates selected by a higher proportion of the models were more likely to be truly
188 associated with when farmers vaccinated (Green et al., 2021; Lima et al., 2021, Hyde et al.,
189 2022). We calculated the stability of each covariate (the proportion of multinomial logistic
190 regression models fit to the 500 bootstrapped datasets that selected the covariate) to
191 mitigate overfitting in this wide dataset (Lima et al., 2021). We calculated stability thresholds
192 for different probabilities of a variable being a true positive using the methods by Green *et al.*
193 (2021) and Hyde et al. (2022). Selected covariates had a stability higher than a threshold
194 where covariates had a 15% probability of not being associated with when farmers
195 vaccinated. We calculated odds ratios of the stable covariates by refitting the model to the
196 bootstrapped datasets with the candidate covariates limited to those above the stability
197 threshold and taking the mean of the coefficients. Finally, model fit was assessed by fitting
198 the multinomial logistic regression model to the full dataset and comparing the observed and
199 expected data using a Hosmer-Lemeshow goodness-of-fit test and decile plots (Fagerland
200 and Hosmer, 2012), and by comparing predicted vaccination class from the full and 10 x 10-
201 fold cross validated models.

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

210 Mathematical transmission model of infectious livestock disease

211 For the final portion of our investigation, we sought to ascertain the impact of differing
212 population compositions with regards to behavioural stances on intervention usage on an
213 emergent outbreak of a fast-spreading pathogen. To inform this problem, we used a
214 mathematical transmission model to simulate a livestock disease epidemic process in Great
215 Britain amongst holdings with cattle. Within this subsection we overview: (i) the data sources
216 used to inform cattle demography, (ii) the epidemiological model framework that was
217 conceptually based on a swift, locally spreading pathogen with no long-range movement of

218 animals, (iii) our implementation of vaccination, (iv) expanded details on the eight
219 behavioural configurations and (v) the simulation protocol used to compare scenarios with
220 and without inclusion of behavioural heterogeneity.

221 **Livestock data description**

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

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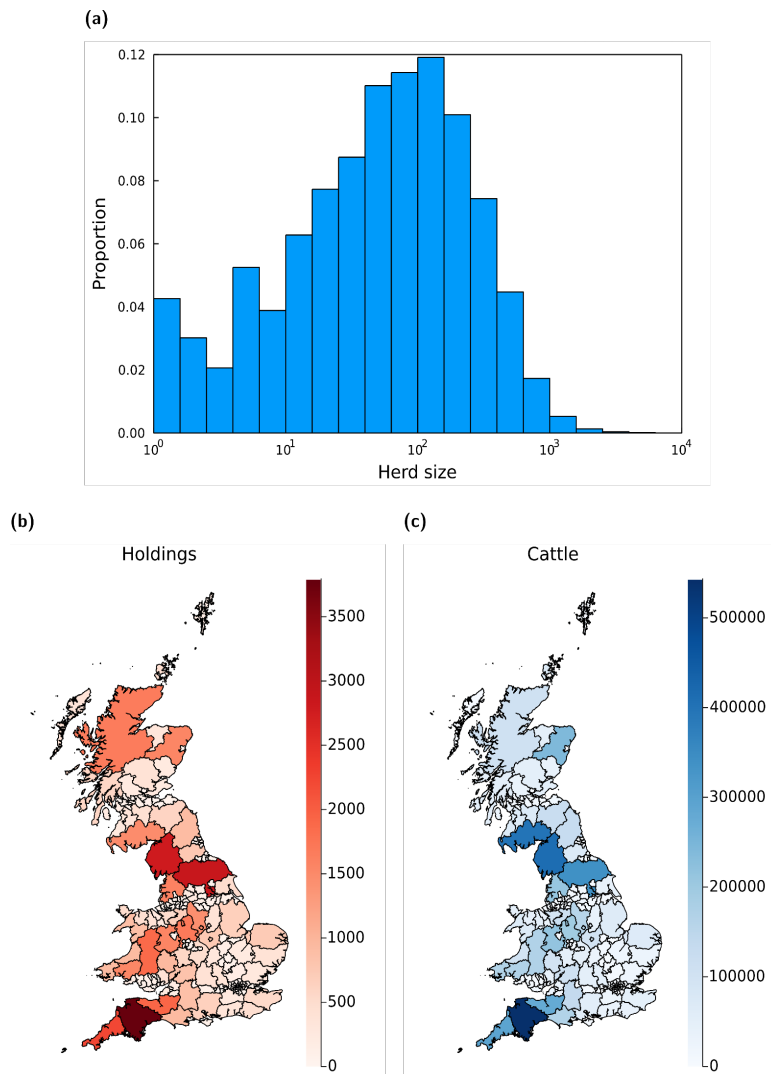231 (Fig. 1).

(a)

(b) Holdings

(c) Cattle

232

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

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:

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

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

In detail, the force of infection between two herds, λ_{ij}, was a nonlinear function of the transmissibility of cattle (ξ), the number of cattle on the infectious holding (term N_i^ψ) and the number of cattle on the susceptible holding (term N_j^ϕ). For the herd size exponents, ψ and ϕ, 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 50km:

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

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

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

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

283 **Table 1. Summary of the livestock disease model epidemiological and intervention parameter**
284 **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

285 **Implementation of vaccination**

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

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

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

296 **Intervention behaviour configurations**

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

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

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

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

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

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

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

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

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

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

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

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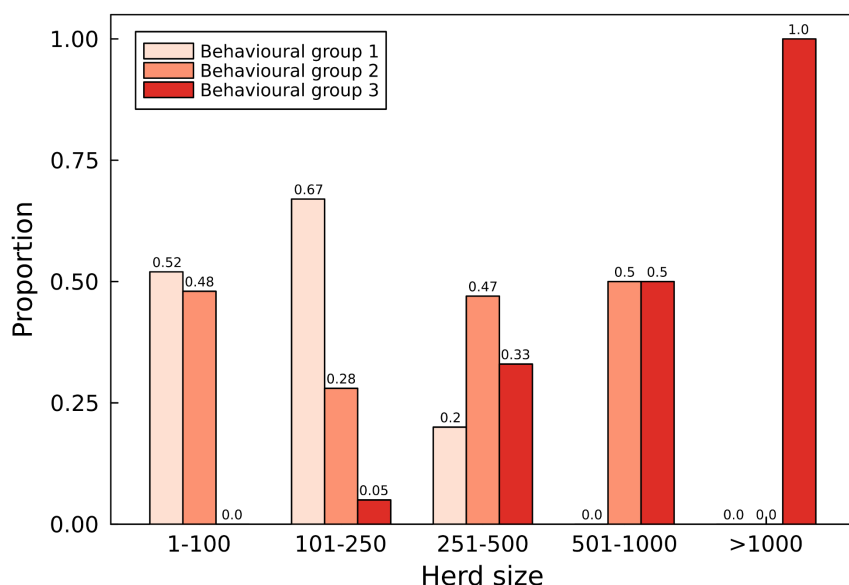
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Fig. 2: For the "Herd size dependent" behavioural configuration, the probability of a holding being assigned to each of the three behavioural groups with respect to the herd size. The bars depict the probability of a holding being assigned to each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

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

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

Results

Elicitation findings

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

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

410 **Table 2:** The number of infected herds, the distance of the nearest infected herd from the
411 interviewee's herd and the number of farmers that vaccinated for each week during the
412 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

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

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

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

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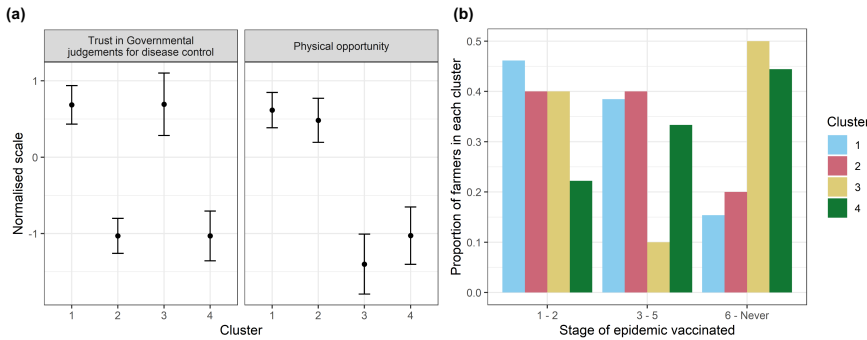

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450 **Fig. 3: The farmer groups from k-means clustering conducted on the two most stable**
451 **covariates** (Trust in Governmental judgements about disease control and Physical
452 opportunity). **(a)** The mean (point) and 95% confidence interval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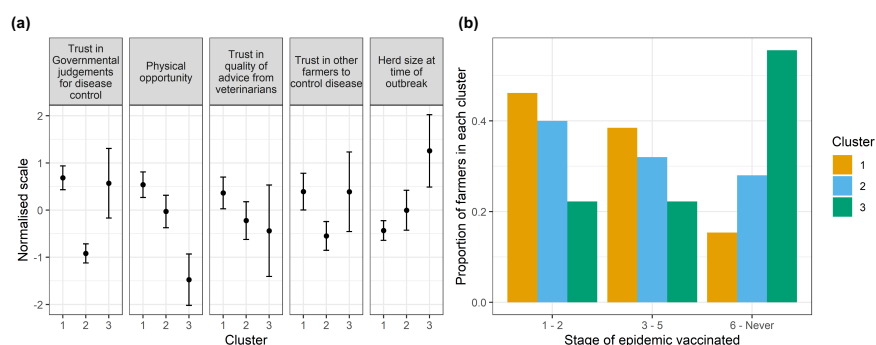456 1 and Supplementary Table 2.

457

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

487 holdings were infected, returning a median outbreak size of 99.5% of all holdings (Fig. 5(a)).
488 We therefore observed very few instances of small-scale outbreaks. The percentage of
489 simulations that had greater than 1%, 10% and 20% of all holdings infected was 98.4% for
490 all three threshold values (Fig. 5(b)). This contrasted with everyone having *strong parasitism*
491 (the next slowest to vaccinate). Although the majority of these simulations did still result in
492 large outbreaks, with 96.2% of simulations having more than 20% of holdings infected, there
493 was a greater prospect that outbreak size could be curtailed without the majority of holdings
494 applying interventions. Explicitly, whilst for everyone being *uncooperative* meant less than
495 1% of holdings became infected in 1.6% of simulations, under the *strong parasitism*
496 configuration the chance of fewer than 1% of holdings being infected more than doubled
497 (approximately 3.8% of simulations). Having all farmers being more precautionary,
498 resembling our *weak parasitism* configuration, many outbreaks were small-scale. The
499 median outbreak size was just 1.6% of holdings infected and no simulations resulted in more
500 than 10% of holdings being infected. The *mutual cooperation* set up resulted in no
501 outbreaks, as intended by its construction.

502 Analysing outbreak duration (which may be a major consideration for some outbreaks), our
503 reference *uncooperative* behavioural configuration gave outbreaks with a duration typically in
504 the region of 200 - 300 days, with a median of 252 days (Fig. 5(c)). The majority of simulated
505 outbreaks (93.3%) lasted more than 180 days (Fig. 5(d)). For *strong parasitism*, the outbreak
506 duration was reduced compared with the *uncooperative* scenario (median of 152 days),
507 although it remained likely that outbreaks would last in excess of 100 days (96.2% of
508 simulations). Under *weak parasitism* there was little variation in outbreak duration, with no
509 realisations exceeding an outbreak duration of 30 days.

510 Pivoting to economic considerations and analysis of the threshold cost per intervention unit
511 (Figs. 5(e,f)), where we recall that for our application the threshold intervention unit cost was
512 the maximum cost per vaccine dose (measured as a relative cost of vaccination compared to
513 the cost of infection and removal of a single cow) where the costs saved from averted
514 infections equals the total cost of vaccination. For our *strong parasitism* realisations there
515 were examples where outbreaks resulted in few onward infections beyond the initial three
516 infected holdings (seeded with infection at the beginning of the simulation). In such
517 instances, one would be willing to spend a higher amount per intervention unit whilst keeping
518 the strategy cost-effective compared with the baseline strategy (reflected by 2.3% of
519 simulations returning a threshold unit intervention cost above 2). Meanwhile, the threshold
520 unit intervention cost exhibited more variability for *weak parasitism* than in most other
521 scenarios, spanning 0 to 11.5. It was very likely to be in the range of 0.5 to 1, with a small
522 chance of it being larger than 2 (achieved in 10.2% of simulations). Finally, though outbreaks
523 were prevented under *mutual cooperation*, for the pre-emptive use of vaccination by all to be
524 cost effective, the intervention unit cost would have to be less than the cost of infection of a
525 single cow.

526 **Non-data informed, heterogenous behavioural configuration outcomes**

527 We next examine our epidemiological metrics for our simple implementations of
528 heterogeneity in behaviour amongst the population, with a uniform split of specified
529 behavioural groups across holdings (*Coop-Parasitism-FR* and *Coop-Parasitism*). We found
530 similar lower bounds across the configurations. As anticipated, the *Coop-Parasitism-FR*

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539 configuration - having a quarter of the population in the non-vaccination group - resulted in a
540 greater median and upper uncertainty bounds for holdings infected and outbreak duration.
541 There was a striking difference in the number of simulations that resulted in more than 20%
542 of holdings infected, 96.1% vs 2.3% (Fig. 5(b)), and in an outbreak duration of more than
543 180 days, 59.7% vs 14.1% (Fig. 5(d)). We found quantitatively similar intervention unit
544 threshold costs (Figs. 5(e,f)), with a median relative cost versus infection of 0.74 (for *Coop-*
545 *Parasitism-FR)* and 0.77 (for *Coop-Parasitism).*

Data informed, heterogenous behavioural configuration outcomes

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

Role of seed infection region

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

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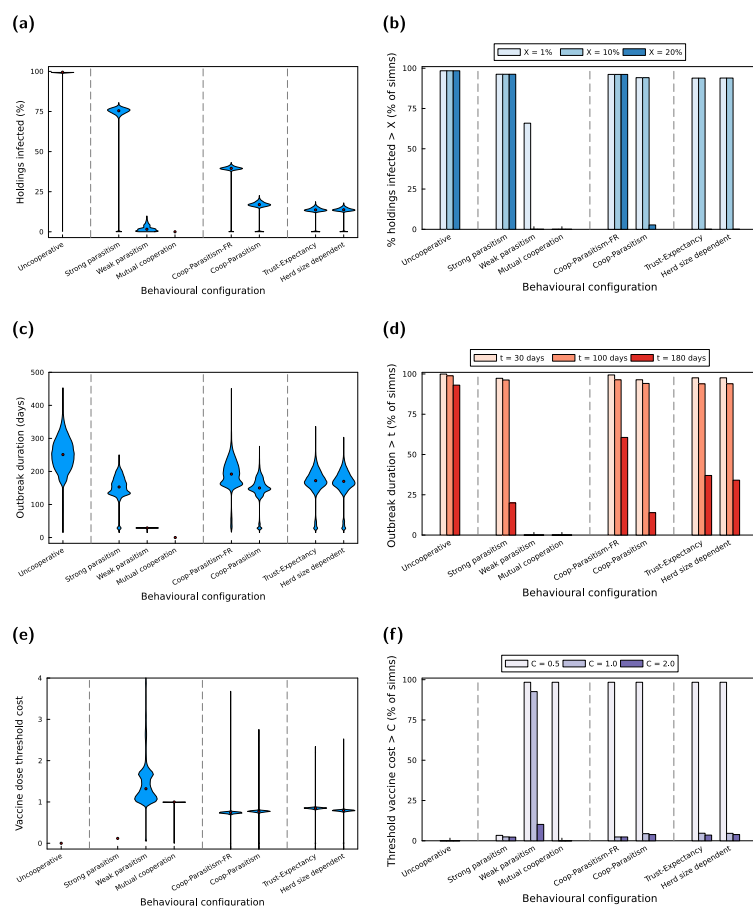
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Fig. 5: Epidemiological summary statistics for Great Britain when aggregating outbreaks over all 89 infection seed regions. We computed the summary statistics for each behavioural configuration using 44,500 replicates (500 replicates for each of the 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

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

635 Farmers with high trust in advice from the veterinary profession and high trust in other
636 farmers to control disease were most likely to vaccinate mid-epidemic. This behaviour is
637 consistent with the behavioural label of parasitism (Bshary and Bergmüller, 2008), waiting to
638 see what happens to others first and expecting to be protected by other farmers vaccinating
639 their herds, only vaccinating if it becomes necessary. Other research has identified that high
640 trust in farmers to control disease can reduce the disease prevention behaviours farmers
641 use in their own herd because they perceive their risk of disease from other farms to be low
642 (Oliveira et al., 2018; Prosser et al., 2022), therefore this can be a barrier in disease control.
643 Veterinary advice is generally trusted by farmers (Bard et al., 2019; Brennan and Christley,
644 2013) and this could be a route to promoting interventions to achieve prompt uptake and
645 better epidemic control.

646 Our infectious disease model assessment, considering how different modelling assumptions
647 with respect to farmer disease control behaviour impacted epidemiological outcomes for a
648 fast-spreading disease outbreak scenario, revealed a disconnect in outcomes between the
649 configurations that assumed homogeneity in farmer behaviour (*Strong parasitism, Weak*
650 *parasitism, Mutual cooperation*) and those that used the empirical estimates for psychosocial
651 profile clusters from the interview data (*Trust-Expectancy* and *Herd size dependent*). In
652 contrast, our simplistic assumption for a heterogeneous behavioural profile composition
653 amongst the farmer population (*Coop-Parasitism*) resulted in a closer correspondence
654 across outbreak size, outbreak duration and threshold intervention cost metrics to results
655 obtained for our *Trust-Expectancy* and *Herd size dependent* scenarios. In the absence of
656 behavioural response data, these observations imply that a simplified implementation of
657 heterogeneity in farmer intervention response (e.g. our *Coop-Parasitism* configuration) may
658 deliver commensurate modelling findings compared to circumstances where the behavioural
659 profile of the population of farmers was known. Though not explored here, another route of
660 investigation would concern the requirements of behavioural-targeted interventions (altering
661 the behavioural profile of farmers towards disease management) to return an overall most
662 cost-efficient solution. Such an investigation we expect would be highly computationally
663 intensive and meriting its own study.

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

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

677 disease prevention behaviour. It has been argued that behavioural science has a key role to
678 play in helping manage responses to pandemics (Van Bavel et al., 2020), encouraging
679 vaccination behaviour (Brewer et al., 2017) and health based philanthropy (Ferguson et al.,
680 2019; Ferguson, 2021). However, the focus on heterogeneity in behaviour that is central to a
681 behavioural science approach needs to be incorporated within large-scale policy-based
682 approaches. In this study, we have shown how this can be achieved in the context of farmer
683 vaccination decisions to an approaching infectious livestock disease. Modelling at the
684 population level would not only say which population strategies may be more effective, but
685 how they could be tailored. The same principles can be applied to any disease outbreak or
686 behaviour that rests on human cooperative and shared action.

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

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

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

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

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

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

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

Funding statement

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.

Code availability

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

References

Agriculture & Horticulture Development Board, 2019. The UK Cattle Yearbook 2019. Agriculture and Horticulture Development Board, Stoneleigh, UK.

Agriculture & Horticulture Development Board, 2018. Understanding how to influence farmers' decision-making behaviour: a social science literature review. AHDB, Stoneleigh, UK.

Andreoni, J., 1990. Impure altruism and donations to public-goods - A theory of warm-glow giving. Econ. J. 100, 464–477. https://doi.org/10.2307/2234133

Armstrong, D., Gow, L., 2021. Is the end in sight for bovine viral diarrhoea virus, or is it just a mirage? Livestock 26, 220–226. https://doi.org/10.12968/live.2021.26.5.220

Aron, A., Aron, E.N., Smollan, D., 1992. Inclusion of other in the self scale and the structure of interpersonal closeness. J. Pers. Soc. Psychol. 63, 596–612. https://doi.org/10.1037/0022-3514.63.4.596

Bard, A.M., Main, D., Roe, E., Haase, A., Whay, H.R., Reyher, K.K., 2019. To change or not to change? Veterinarian and farmer perceptions of relational factors influencing the enactment of veterinary advice on dairy farms in the United Kingdom. J. Dairy Sci. 102, 10379–10394. https://doi.org/10.3168/jds.2019-16364

807 Bedson, J., Skrip, L.A., Pedi, D., Abramowitz, S., Carter, S., Jalloh, M.F., Funk, S., Gobat,
808   N., Giles-Vernick, T., Chowell, G., de Almeida, J.R., Elessawi, R., Scarpino, S.V.,
809   Hammond, R.A., Briand, S., Epstein, J.M., Hébert-Dufresne, L., Althouse, B.M.,
810   2021. A review and agenda for integrated disease models including social and
811   behavioural factors. Nat. Hum. Behav. 5, 834–846. https://doi.org/10.1038/s41562-
812   021-01136-2
813 Bennett, R., Cooke, R., 2005. Control of bovine TB: preferences of farmers who have
814   suffered a TB breakdown. Vet. Rec. 156, 143–145.
815   https://doi.org/10.1136/vr.156.5.143
816 Bhatia, S., Mullett, T.L., 2018. Similarity and decision time in preferential choice. Q. J. Exp.
817   Psychol. 71, 1276–1280. https://doi.org/10.1177/1747021818763054
818 Böhm, R., Betsch, C., Korn, L., 2016. Selfish-rational non-vaccination: Experimental
819   evidence from an interactive vaccination game. J. Econ. Behav. Organ.,
820   Experimental and Behavioral Economics of Healthcare 131, 183–195.
821   https://doi.org/10.1016/j.jebo.2015.11.008
822 Bradley, A., Lawrence, C., Ferguson, E., 2018. Does observability affect prosociality? Proc.
823   R. Soc. B-Biol. Sci. 285, 20180116. https://doi.org/10.1098/rspb.2018.0116
824 Brennan, M.L., Christley, R.M., 2013. Cattle producers' perceptions of biosecurity. BMC Vet.
825   Res. 9, 71. https://doi.org/10.1186/1746-6148-9-71
826 Brewer, N.T., Chapman, G.B., Rothman, A.J., Leask, J., Kempe, A., 2017. Increasing
827   vaccination: Putting psychological science into action. Psychol. Sci. Public Interest
828   18, 149–207. https://doi.org/10.1177/1529100618760521
829 British Cattle Movement Service, 2021. Report and record cattle movements [WWW
830   Document]. URL https://www.gov.uk/guidance/report-and-record-cattle-movements
831   (accessed 29 Aug 2023).
832 Bshary, R., Bergmüller, R., 2008. Distinguishing four fundamental approaches to the
833   evolution of helping. J. Evol. Biol. 21, 405–420. https://doi.org/10.1111/j.1420-
834   9101.2007.01482.x
835 BVDFree England, 2019. BVDFree England Scheme [WWW Document]. URL
836   https://bvdfree.org.uk/ (accessed 29 Aug 2023).
837 Cellini, M., Pecoraro, F., Rigby, M., Luzi, D., 2022. Comparative analysis of pre-Covid19
838   child immunization rates across 30 European countries and identification of
839   underlying positive societal and system influences. PLoS One 17, e0271290.
840   https://doi.org/10.1371/journal.pone.0271290
841 Chater, N., Loewenstein, G., in press. The i-frame and the s-frame: How focusing on
842   individual-level solutions has led behavioral public policy astray. Behav. Brain Sci.
843   https://doi.org/10.1017/S0140525X22002023
844 Dolby, T., Finning, K., Baker, A., Fowler-Dowd, L., Khunti, K., Razieh, C., Yates, T., Nafilyan,
845   V., 2022. Monitoring sociodemographic inequality in COVID-19 vaccination uptake in
846   England: a national linked data study. J. Epidemiol. Community Health 76, 646–652.
847   https://doi.org/10.1136/jech-2021-218415
848 Dudley, M.Z., Limaye, R.J., Omer, S.B., O'Leary, S.T., Ellingson, M.K., Spina, C.I.,
849   Chamberlain, A.T., Brewer, S.E., Bednarczyk, R.A., Malik, F., Frew, P.M., Salmon,
850   D.A., 2020. Latent class analysis of maternal vaccine attitudes and beliefs. Health
851   Educ. Behav. 47, 765–781. https://doi.org/10.1177/1090198120939491
852 Ent, M.R., Sjåstad, H., von Hippel, W., Baumeister, R.F., 2020. Helping behavior is non-
853   zero-sum: Helper and recipient autobiographical accounts of help. Evol. Hum. Behav.
854   41, 210–217. https://doi.org/10.1016/j.evolhumbehav.2020.02.004
855 Enticott, G., Little, R., 2022. Playing games with "good farming": exploring the potential
856   impact of disease control policies on farmers' cattle purchasing practices. J. Rural
857   Stud. 92, 371–382. https://doi.org/10.1016/j.jrurstud.2022.04.008
858 Fagerland, M.W., Hosmer, D.W., 2012. A generalized Hosmer-Lemeshow goodness-of-fit
859   test for multinomial logistic regression models. Stata J. 12, 447–453.
860   https://doi.org/10.1177/1536867x1201200307
861 Ferguson, E., 2021. What blood and organ donation can tell us about cooperation? Curr.

862   Opin. Psychol. 44, 202–207. https://doi.org/10.1016/j.copsyc.2021.09.005.
863 Ferguson, E., Dawe-Lane, E., Khan, Z., Reynolds, C., Davison, K., Edge, D., Brailsford,
864   S.R., 2022. Trust and distrust: Identifying recruitment targets for ethnic minority blood
865   donors. Transfus. Med. 32, 276–287. https://doi.org/10.1111/tme.12867
866 Ferguson, E., Murray, C., O'Carroll, R.E., 2019. Blood and organ donation: health impact,
867   prevalence, correlates, and interventions. Psychol. Health 34, 1073–1104.
868   https://doi.org/10.1080/08870446.2019.1603385
869 Fisher, R., 2013. "A gentleman's handshake": The role of social capital and trust in
870   transforming information into usable knowledge. J. Rural Stud. 31, 13–22.
871   https://doi.org/10.1016/j.jrurstud.2013.02.006
872 Green, M., Lima, E., Hyde, R., 2021. Selection stability in high dimensional statistical
873   modelling: Defining a threshold for robust model inference.
874   https://doi.org/10.21203/rs.3.rs-738092/v1
875 Hartigan, J.A., Wong, M.A., 1979. Algorithm AS 136: A K-means clustering algorithm. Appl.
876   Stat. 28, 100–108. https://doi.org/10.2307/2346830
877 Heffernan, C., Azbel-Jackson, L., Brownlie, J., Gunn, G., 2016. Farmer attitudes and
878   livestock disease: exploring citizenship behaviour and peer monitoring across two
879   BVD control schemes in the UK. PLoS One 11, e0152295.
880   https://doi.org/10.1371/journal.pone.0152295
881 Hernández-Jover, M., Higgins, V., Bryant, M., Rast, L., McShane, C., 2016. Biosecurity and
882   the management of emergency animal disease among commercial beef producers in
883   New South Wales and Queensland (Australia). Prev. Vet. Med. 134, 92–102.
884   https://doi.org/10.1016/j.prevetmed.2016.10.005
885 Hidano, A., Enticott, G., Christley, R.M., Gates, M.C., 2018. Modeling dynamic human
886   behavioral changes in animal disease models: Challenges and opportunities for
887   addressing bias. Front. Vet. Sci. 5, 137. https://doi.org/10.3389/fvets.2018.00137
888 Hill, E.M., Prosser, N.S., Ferguson, E., Kaler, J., Green, M.J., Keeling, M.J., Tildesley, M.J.,
889   2022. Modelling livestock infectious disease control policy under differing social
890   perspectives on vaccination behaviour. PLOS Comput. Biol. 18, e1010235.
891   https://doi.org/10.1371/journal.pcbi.1010235
892 Hyde, R.B., O'Grady, L., Green, M., 2022. Stability selection for mixed effect models with
893   large numbers of predictor variables: A simulation study. Prev. Vet. Med. 206,
894   105714. https://doi.org/10.1016/j.prevetmed.2022.105714
895 Jones, P.J., Marier, E.A., Tranter, R.B., Wu, G., Watson, E., Teale, C.J., 2015. Factors
896   affecting dairy farmers' attitudes towards antimicrobial medicine usage in cattle in
897   England and Wales. Prev. Vet. Med. 121, 30–40.
898   https://doi.org/10.1016/j.prevetmed.2015.05.010
899 Keeling, M.J., Woolhouse, M.E., Shaw, D.J., Matthews, L., Chase-Topping, M., Haydon,
900   D.T., Cornell, S.J., Kappey, J., Wilesmith, J., Grenfell, B.T., 2001. Dynamics of the
901   2001 UK foot and mouth epidemic: stochastic dispersal in a heterogeneous
902   landscape. Science 294, 813–817. https://doi.org/10.1126/science.1065973
903 Kuipers, B., 2022. Trust and cooperation. Front. Robot. AI 9, 676767.
904   https://doi.org/10.3389/frobt.2022.676767
905 Lima, E., Hyde, R., Green, M., 2021. Model selection for inferential models with high
906   dimensional data: synthesis and graphical representation of multiple techniques. Sci.
907   Rep. 11, 412. https://doi.org/10.1038/s41598-020-79317-8
908 Mashek, D., Cannaday, L.W., Tangney, J.P., 2007. Inclusion of community in self scale: A
909   single-item pictorial measure of community connectedness. J. Community Psychol.
910   35, 257–275. https://doi.org/10.1002/jcop.20146
911 Maye, D., Enticott, G., Naylor, R., 2017. Using scenario-based influence mapping to
912   examine farmers' biosecurity behaviour. Land Use Policy 66, 265–277.
913   https://doi.org/10.1016/j.landusepol.2017.04.026
914 Merrill, S.C., Koliba, C.J., Moegenburg, S.M., Zia, A., Parker, J., Sellnow, T., Wiltshire, S.,
915   Bucini, G., Danehy, C., Smith, J.M., 2019. Decision-making in livestock biosecurity
916   practices amidst environmental and social uncertainty: Evidence from an

917   experimental game. PLOS ONE 14, e0214500.
918   https://doi.org/10.1371/journal.pone.0214500
919 Michie, S., Atkins, L., West, R., 2014. Understand the behaviour, in: The Behaviour Change
920   Wheel: A Guide to Designing Interventions. Silverback Publishing, Great Britain, pp.
921   31–106.
922 Michie, S., van Stralen, M.M., West, R., 2011. The behaviour change wheel: A new method
923   for characterising and designing behaviour change interventions. Implement. Sci. 6,
924   42. https://doi.org/10.1186/1748-5908-6-42
925 Milinski, M., 2016. Reputation, a universal currency for human social interactions. Philos.
926   Trans. R. Soc. B-Biol. Sci. 371, 20150100. https://doi.org/10.1098/rstb.2015.0100
927 Mingolla, C., van Mol, W., Hudders, L., Cauberghe, V., Claerebout, E., 2021. Unravelling
928   Belgian Blue cattle farmers' adoption intention towards diagnostic tools: Integrating
929   insights from behavioural economics and socio-cognitive theories. Prev. Vet. Med.
930   188, 105238. https://doi.org/10.1016/j.prevetmed.2020.105238
931 Nowak, M.A., 2006. Five rules for the evolution of cooperation. Science 314, 1560–1563.
932   https://doi.org/10.1126/science.1133755
933 Nowak, M.A., Sigmund, K., 2005. Evolution of indirect reciprocity. Nature 437, 1291–1298.
934   https://doi.org/10.1038/nature04131
935 Oliveira, V.H.S., Anneberg, I., Voss, H., Sorensen, J.T., Thomsen, P.T., 2018. Attitudes of
936   Danish dairy farmers towards biosecurity. Livest. Sci. 214, 153–160.
937   https://doi.org/10.1016/j.livsci.2018.06.004
938 Orsel, K., de Jong, M.C.M., Bouma, A., Stegeman, J.A., Dekker, A., 2007. The effect of
939   vaccination on foot and mouth disease virus transmission among dairy cows.
940   Vaccine 25, 327–335. https://doi.org/10.1016/j.vaccine.2006.07.030
941 Prosser, N.S., Green, M.J., Ferguson, E., Tildesley, M.J., Hill, E.M., Keeling, M.J., Kaler, J.,
942   2022. Cattle farmer psychosocial profiles and their association with control strategies
943   for bovine viral diarrhea. J. Dairy Sci. 105, 3559–3573.
944   https://doi.org/10.3168/jds.2021-21386
945 R Core Team, 2022. R: A language and environment for statistical computing.
946 Rand, D.G., Nowak, M.A., 2013. Human cooperation. Trends Cogn. Sci. 17, 413–425.
947   https://doi.org/10.1016/j.tics.2013.06.003
948 Ruminant Health & Welfare, 2021. Bold plans to eradicate BVD and sheep scab by 2031
949   [WWW Document]. URL https://ruminanthw.org.uk/2021/07/12/bold-plans-to-
950   eradicate-bvd-and-sheep-scab-by-2031/ (accessed 29 Aug 2023).
951 Sellman, S., Tsao, K., Tildesley, M.J., Brommesson, P., Webb, C.T., Wennergren, U.,
952   Keeling, M.J., Lindström, T., 2018. Need for speed: An optimized gridding approach
953   for spatially explicit disease simulations. PLOS Comput. Biol. 14, e1006086.
954   https://doi.org/10.1371/journal.pcbi.1006086
955 Shamloo, S.E., Cocco, V.M., Visintin, E.P., Trifiletti, E., Vezzali, L., 2023. I love you too
956   much to keep social distance: Closeness in relationships and (dis)engagement in
957   preventive behaviors during the COVID-19 pandemic. J. Appl. Soc. Psychol. 53, 62–
958   68. https://doi.org/10.1111/jasp.12926
959 Shortall, O., Ruston, A., Green, M., Brennan, M., Wapenaar, W., Kaler, J., 2016. Broken
960   biosecurity? Veterinarians' framing of biosecurity on dairy farms in England. Prev.
961   Vet. Med. 132, 20–31. https://doi.org/10.1016/j.prevetmed.2016.06.001
962 Silk, M.J., Hodgson, D.J., Rozins, C., Croft, D.P., Delahay, R.J., Boots, M., McDonald, R.A.,
963   2019. Integrating social behaviour, demography and disease dynamics in network
964   models: applications to disease management in declining wildlife populations. Philos.
965   Trans. R. Soc. B Biol. Sci. 374, 20180211. https://doi.org/10.1098/rstb.2018.0211
966 Sok, J., Hogeveen, H., Elbers, A.R.W., Lansink, A., 2015. Farmers' beliefs and voluntary
967   vaccination schemes: Bluetongue in Dutch dairy cattle. Food Policy 57, 40–49.
968   https://doi.org/10.1016/j.foodpol.2015.09.006
969 Sok, J., van der Lans, I.A., Hogeveen, H., Elbers, A.R.W., Lansink, A., 2018. Farmers'
970   preferences for bluetongue vaccination scheme attributes: An integrated choice and
971   latent variable approach. J. Agric. Econ. 69, 537–560.

972   TBhub, 2019. TB hub - Bovine TB Advice & Tuberculosis Information for Cattle Farmers
973   [WWW Document]. URL https://tbhub.co.uk/ (accessed 29 Aug 2023).
974   Thiessen, C., Gannon, J., Li, S., Skrip, L., Dobosz, D., Gan, G.L., Deng, Y.H., Kennedy, K.,
975   Gray, D., Mussell, A., Reese, P.P., Gordon, E.J., Kulkarni, S., 2021. Quantifying risk
976   tolerance among potential living kidney donors with the donor-specific risk
977   questionnaire. Am. J. Kidney Dis. 78, 246–258.
978   https://doi.org/10.1053/j.ajkd.2020.11.028
979   Tildesley, M.J., Deardon, R., Savill, N.J., Bessell, P.R., Brooks, S.P., Woolhouse, M.E.J.,
980   Grenfell, B.T., Keeling, M.J., 2008. Accuracy of models for the 2001 foot-and-mouth
981   epidemic. Proc. R. Soc. B Biol. Sci. 275, 1459–1468.
982   https://doi.org/10.1098/rspb.2008.0006
983   Tildesley, M.J., Vassall, A., Riley, S., Jit, M., Sandmann, F., Hill, E.M., Thompson, R.N.,
984   Atkins, B.D., Edmunds, J., Dyson, L., Keeling, M.J., 2022. Optimal health and
985   economic impact of non-pharmaceutical intervention measures prior and post
986   vaccination in England: a mathematical modelling study. R. Soc. Open Sci. 9,
987   211746.
988   Tu, K., Chen, S., Mesler, R.M., 2021. Trait self-construal, inclusion of others in the self and
989   self-control predict stay-at-home adherence during COVID-19. Personal. Individ.
990   Differ. 175, 110687. https://doi.org/10.1016/j.paid.2021.110687
991   Utomo, D.S., Onggo, B.S.S., Eldridge, S., Daud, A.R., Tejaningsih, S., 2022. Eliciting agents'
992   behaviour and model validation using role playing game in agent-based dairy supply
993   chain model. J. Oper. Res. Soc. 73, 2670–2693.
994   https://doi.org/10.1080/01605682.2021.2013137
995   Van Bavel, J.J., Baicker, K., Boggio, P.S., Capraro, V., Cichocka, A., Cikara, M., Crockett,
996   M.J., Crum, A.J., Douglas, K.M., Druckman, J.N., Drury, J., Dube, O., Ellemers, N.,
997   Finkel, E.J., Fowler, J.H., Gelfand, M., Han, S.H., Haslam, S.A., Jetten, J., Kitayama,
998   S., Mobbs, D., Napper, L.E., Packer, D.J., Pennycook, G., Peters, E., Petty, R.E.,
999   Rand, D.G., Reicher, S.D., Schnall, S., Shariff, A., Skitka, L.J., Smith, S.S., Sunstein,
1000   C.R., Tabri, N., Tucker, J.A., van der Linden, S., van Lange, P., Weeden, K.A., Wohl,
1001   M.J.A., Zaki, J., Zion, S.R., Willer, R., 2020. Using social and behavioural science to
1002   support COVID-19 pandemic response. Nat. Hum. Behav. 4, 460–471.
1003   https://doi.org/10.1038/s41562-020-0884-z
1004   Van de Calseyde, P.P.F.M., Keren, G., Zeelenberg, M., 2014. Decision time as information
1005   in judgment and choice. Organ. Behav. Hum. Decis. Process. 125, 113–122.
1006   Vial, F., Miguel, E., T. Johnston, W., Mitchell, A., Donnelly, C.A., 2015. Bovine tuberculosis
1007   risk factors for British herds before and after the 2001 foot-and-mouth epidemic:
1008   What have we learned from the TB99 and CCS2005 studies? Transbound. Emerg.
1009   Dis. 62, 505–515. https://doi.org/10.1111/tbed.12184
1010   Weiss, C., Schröpfer, D., Merten, S., 2016. Parental attitudes towards measles vaccination
1011   in the canton of Aargau, Switzerland: a latent class analysis. BMC Infect. Dis. 16,
1012   400. https://doi.org/10.1186/s12879-016-1747-0