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The Role of Movement Restrictions in Limiting the Economic Impact of Livestock Infections

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29 **Abstract**

30 **Movements are essential for the economic success of the livestock industry. These**
31 **movements however bring the risk of long-range spread of infection, potentially bringing**
32 **infection to previously disease-free areas where subsequent localised transmission can**
33 **be devastating. Mechanistic predictive models usually consider controls that minimize**
34 **the number of livestock affected without considering other costs of an ongoing**
35 **epidemic. However, it is more appropriate to consider the economic burden, as**
36 **movement restrictions have major consequences for the economic revenue of farms.**
37 **Using mechanistic models of foot-and-mouth disease (FMD), bluetongue virus (BTV) and**
38 **bovine tuberculosis (bTB) in the UK, we contrast the economically optimal control**
39 **strategies for these diseases. We show that for FMD, the optimal strategy is to ban**
40 **movements in a small radius around infected farms; the balance between disease control**
41 **and maintaining 'business as usual' varies between regions. For BTV and bTB, we find**
42 **that the cost of any movement ban is more than the epidemiological benefits due to the**
43 **low within-farm prevalence and slow rate of disease spread. This work suggests that**
44 **movement controls need to be carefully matched to the epidemiological and economic**
45 **consequences of the disease, and optimal movement bans are often far shorter than**
46 **existing policy.**

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56 Recent outbreaks have shown the sensitivity of farming industries to invasion by novel
57 pathogens, with examples including: the 2001 outbreak of foot and mouth disease (FMD) in the
58 UK and the Netherlands [1-3]; the 2006-7 outbreaks of bluetongue virus (BTV) to Northern
59 Europe [4]; the 2014 invasion of Lumpy Skin disease to Greece and the Balkans [5-6]; and the
60 pan-European spread of Schmallenberg virus since 2011 [7-8]. These recent experiences have
61 increased fears about novel infections that may threaten livestock industries in disease free
62 countries in the future, such as avian influenza, african swine fever, Newcastle disease, Rift
63 Valley fever or brucellosis, in addition to those above. Once established, there are considerable
64 difficulties in controlling endemic diseases in the livestock industry, as exemplified by infections
65 in the UK such as Footrot [9], Scrapie [10] and bovine tuberculosis (bTB) [11-12]. Many of these
66 novel and endemic diseases spread easily between the animals on a farm, which are kept at
67 relatively high densities, and can spread between farms through a mixture of air-borne infection,
68 fomites, vector-transmission and animal movements [13]. Of these transmission routes, animal
69 movements have the potential to lead to very long-distance dispersal of infection, and yet can
70 be readily prevented through emergency legislation [14]. For this reason, local, regional or
71 national scale movement restrictions (often banning the non-essential movement of all farm
72 livestock) are often one of the first control policies to be adopted when an outbreak occurs [15].
73 Such bans have the advantage (in comparison to say vaccination or other treatments) that they
74 are independent of disease etiology and therefore can be enacted before the causative agent
75 has been fully identified.

76

77 The revenue of livestock farms is largely based on the movement of animals, either through
78 selling animals to other farms or by moving animals to slaughter. Therefore, adopting any form
79 of movement restrictions may have substantive economic consequences for the livestock
80 industry. In the UK, a nationwide ban on animal movements and the “closing of the countryside”

81 during the 2001 FMD outbreak had huge economic implications for the tourist industry and the
82 wider rural economy [16]. Given these extreme financial implications, and that money provides a
83 unified measure for comparing multiple consequences, here we optimise infection control in
84 terms of minimising the economic consequences of any intervention measure. We adopt an
85 aggregate, national economic perspective and consider the total costs of an epidemic and the
86 associated movement controls to both the livestock industry and beyond. In particular we focus
87 on outbreaks of FMD and BTV, and endemic bTB, which offer contrasting behaviour. FMD is
88 characterized by extremely rapid within-farm transmission and localized airborne or fomite
89 spread [2-3]. BTV is a more cryptic infection, often only infecting only a proportion of the animals
90 on a farm and can spread over large distances by infected midge vectors [17]. bTB is a much
91 slower infection, generally infecting just one or two animals on a farm; problems with control are
92 exacerbated by poor test sensitivity [12] and potential reservoirs of infection in wildlife
93 populations [18-19].

94
95 Quantifying the economic impact of an animal disease and its management is complex. The
96 economic costs of an outbreak fall into three broad categories: costs due to loss of production,
97 control costs and wider economic costs [20]. The large-scale 2001 UK FMD outbreak provided
98 some of the most comprehensive data available; it is estimated that this outbreak cost the UK
99 livestock sector £3.1 billion with similar additional costs to the wider economy. However, it is
100 acknowledged that these wider costs were more challenging to calculate as losses in one area
101 (e.g. tourism) may have led to gains in other areas of the economy [16]. In addition, economic
102 impacts may depend in a highly non-linear manner on the scale of an outbreak; a short duration
103 outbreak may have a limited impact on farming, whereas a protracted outbreak can leave the
104 industry unable to recover [21].

105 In the event of livestock disease outbreaks or the management of endemic disease, there are
106 economic trade offs that need to be taken into account when considering a set of control options

107 [22] and the policy that is deemed to be optimal may be dependent upon specific demographic
108 characteristics and the state of the outbreak as it evolves in time [23-25]. Recently, complex
109 economic models have been developed which capture the multitude of economic interactions
110 that are perturbed by an infectious disease outbreak and the subsequent control measures.
111 These have been used to calculate the economic impact of outbreaks such as FMD in the UK
112 [26] and South America [27], avian influenza in the Netherlands [28] and Rift Valley Fever in
113 Kenya [29]. Here we use a simpler approach in which the cost calculation is comprised of the
114 economic impact on up to five different sectors, linearly dependent on different attributed of
115 each disease. This approach is designed to enable comparisons between different policies and
116 indicate those that are optimal in reducing outbreak costs; we recognise that this is a
117 simplification of the true economic cost of an outbreak, especially if different controls can
118 generate extremes of epidemic size and duration.

119

120 In this paper, we use state of the art mathematical models [2,12, 30-31] to investigate the cost-
121 effectiveness of local and regional movement control upon outbreaks of FMD and BTV and the
122 endemic dynamics of bTB in the UK. Such policies, if implemented effectively, could balance the
123 need of containing and controlling the spread of infection with the economic incentive of
124 maximising business continuity for a large number of unaffected farms.

125 For all three diseases we used sophisticated stochastic spatial simulations, which are matched
126 to historical epidemiological data; these are used to address how costs (including culling,
127 testing, loss of exports and tourism) vary with the scale and nature of movement restrictions. All
128 simulations reflect disease-specific transmission routes and control measures. As such,
129 localized high-risk (dangerous contact) culling is implemented for FMD, a range of movement
130 zones (protection and surveillance zones) are enforced for BTV, while for bTB a targeted test-
131 and-slaughter policy is enacted. Greater information on the formulation of the models is included
132 in the Supplementary Material. These three infections reflect different contributions of

133 movements to the spread of infection; in the absence of movement controls, the movement of
134 cattle accounts for 28% (26%-31%), 4% (2%-15%) and 13% (7%-22%) for FMD, BTV and bTB
135 respectively (95% confidence intervals are given in brackets).

136

137 For a given set of movement controls, we consider five factors that may contribute to the overall
138 national cost of the outbreak: (i) the number (and type) of animals infected, and their eventual
139 fate; (ii) the number (and type) of animals culled as part of the control; (iii) the duration of the
140 outbreak; (iv) the number of movements prevented by the restrictions and (v) the amount of
141 testing that was undertaken (for bTB only). These epidemic descriptors are used to calculate the
142 economic losses to different sectors:

- 143 ● **Direct costs to farms** are a weighted sum of the number of animals infected or culled.
- 144 ● Costs due to **Welfare culls** are proportional to the number of farm days (farms × days)
145 where movements are completely banned.
- 146 ● Costs to the wider **Agricultural Sector** are proportional to the number of animal
147 movements that are prevented by movement restrictions.
- 148 ● **Loss of Exports** is proportional to the duration of the epidemic plus a delay to achieve
149 disease-free status.
- 150 ● **Impact on Tourism** is proportional to the number of farm days where movements are
151 completely banned, assumed to give a measure of the regions of the countryside that
152 are closed (FMD only).
- 153 ● **Testing Costs** (bTB only) are proportional to the number of animals tested, and include
154 both costs to the farmer and those met by government.

155 The precise formula used to calculate these costs are given in more detail in Table 1 (the
156 implications of changes to each economic value upon the optimal policies can be assessed
157 using the Shiny app: https://livestockmovements.shinyapps.io/movement_control/). We now consider

158 how movement restrictions of different types can minimise the overall expected economic cost
159 of the disease, as well as which controls minimise economic extremes (as captured by the
160 upper 95th percentiles). In this paper we take a national perspective, minimising the total losses
161 to the country including government, farmers, wider rural economy and tourism where
162 appropriate.

163
164 The costs associated with FMD outbreaks differ considerably according to the scale of the
165 movement ban and the origin of the outbreak (figures 1A and B correspond to outbreaks starting
166 in Cumbria and Devon respectively; other regions are shown in the Supplementary Material,
167 Supplementary Figure 1). We consider the outbreak costs from multiple simulations with
168 interventions including culling of livestock on infected premises and on farms considered high-
169 risk (dangerous contacts; [32]), together with a localized movement ban surrounding infected
170 premises. We show by bars the mean total cost (together with 95% confidence intervals) broken
171 down into five key losses; it is clear that direct costs to the farm (dark blue) and impact on
172 tourism (orange) dominate but show opposite trends with the radius of movement control. We
173 also consider extreme ‘worse-case’ costs (red dots) which are defined as the upper 95%
174 prediction interval of all simulations.

175 For Devon (figure 1B), direct farm costs predominate and the economic optimum occurs at
176 relatively small radius movement bans (12-38 km – horizontal black bar); for radii below this
177 optimum, the scale of potentially extreme ‘worst-case’ costs (red dots) increases and hence
178 small-scale bans are far less effective. Even if the effects of tourism are ignored and we focus
179 only on costs to the whole agricultural sector, there is still an optimal radius although this is
180 increased (42-48 km – horizontal blue bar). Finally, if the main concern is mitigating ‘worst-case’
181 costs, the optimal radius is larger than when considering the mean (22-48 km – horizontal red
182 bar).

183 For Cumbria the patterns look subtly different. Due to higher densities of livestock, outbreak
184 sizes and hence direct costs remain relatively high even when movement restrictions are
185 enacted nationally. An implication of this is that the total costs associated with national control
186 are higher than those when there are no movement restrictions: it may be more cost effective to
187 allow all movements rather than ban all movements. For Cumbria the optimal radius for
188 movement bans is more tightly defined compared with Devon where there is more stochastic
189 variability: the optimal ban radius for mean total costs is around 20 km, when tourism costs are
190 excluded this increases to 52-63 km, whilst when mitigating 'worst-case' costs the optimal
191 radius reduces to just 7.5-13 km.

192

193 For BTV the potential control options are very different; culling has very little impact and
194 therefore was not used as a practical control measure. In addition, while the 2001 (and 2007)
195 FMD epidemics led to national movement bans, the 2007 BTV outbreak was controlled by the
196 establishment of localised zones around infected areas, where movements from higher risk to
197 lower risk zones were banned. Mirroring this strategy we focus on the optimal generation of
198 three zones: an inner zone with a complete movement ban, a high-risk protection zone (PZ) and
199 an outer lower-risk surveillance zone (SZ). All farms within the inner zone are completely
200 banned from moving livestock either off-farm or on-farm. Livestock movements are not
201 completely restricted for farms within either the PZ or SZ, however livestock could not be moved
202 from a farm in a higher risk zone to a farm in a lower risk zone.

203 Our results focus on outbreaks initiating in Devon (although results are qualitatively generic; see
204 Supplementary Figure 2 for outbreaks in Suffolk, where the 2007 outbreak started), which are
205 generally larger due to a combination of warmer summers and higher host density necessary for
206 sustained transmission. Figure 1C compares five different radii for the complete movement ban
207 (different colours) and four combinations of protection and surveillance zones (PZ and SZ
208 respectively, x-axis). We consistently find that not having any complete ban (purple)

209 outperforms all other strategies from an economic perspective, irrespective of the size of the PZ
210 and SZ. In part this is due to rapidly increasing losses due to tourism, to the wider agricultural
211 sector and due to welfare as the number of farms experiencing a complete ban increases; even
212 ignoring tourism these results still hold. When no complete bans take place around infected
213 farms, Figure 1D focuses on the optimal radii for the protection and surveillance zone --
214 assuming that the SZ radius is twice that of the PZ. For BTV (and assuming no complete bans)
215 it is only the direct costs to farms (blue) and agricultural sector losses (green) that impact on the
216 economic costs. We note that agricultural sector losses increase with the radii of the two zones,
217 but the epidemic size (and hence direct costs to farms) is largely independent of movement
218 bans, leading to the situation where it is optimal to allow free movement of livestock. Our model
219 prediction of ineffectiveness of movement bans in controlling BTV broadly agrees with another
220 UK BTV transmission modelling study [33], where movement bans were found to have a limited
221 impact on controlling farm-to-farm spread even without the ancillary consideration of economic
222 impact.

223

224 Finally, for endemic bTB, we consider the impact of a combined movement ban and testing
225 protocol, such that, in addition to the standard (test and cull) policy, once a farm tests positive all
226 surrounding farms within a given radius are also placed under a cattle-only movement ban until
227 they clear a subsequent test within 60 days. As such, waves of testing and cattle movement
228 bans can propagate through highly infected regions. A scenario is also considered where no
229 movement controls are imposed even when infected animals are detected (and culled). We
230 consistently find that this no-movement-ban policy has the lowest economic costs (figure 1E) as
231 it eliminates the costs to the agricultural sector that arise from movement restrictions, and that
232 larger radii bans are increasingly costly. (An alternative policy that only bans movements from
233 infected farms but still generates tests within a given radius, has a local minimum cost at a
234 radius of around 2km; Supplementary Figure 3). The economically optimal policy, however,

235 leads to a long-term increase in the number of infected cattle (figure 1F), whereas large-radii
236 ban-and-test strategies are predicted to lead to far lower incidence. Importantly we note that
237 there is relatively little difference in incidence between the no-ban strategy and the current
238 policy of only banning movements from infected farms (0km).

239

240 The results for both BTV and bTB contrast with the findings for FMD; this may be explained by
241 the different within-farm dynamics of the infections. Given that FMD is directly transmitted and
242 highly infectious, any movement of an infected animal into a naive farm leads to rapid infection
243 of all livestock on the farm, hence movements are extremely detrimental. In contrast, BTV is
244 vector transmitted such that infection can readily escape the farm environment by the
245 movement of vectors. In addition the weakly transmissible nature of both bTB and BTV means
246 that there is only limited saturation (density dependent effects) of infection on farms; this means
247 that the movement of an infected animal simply transfers the risk of infection to animals on the
248 new farm rather than on the farm of origin.

249

250 The economic parameters used in this work (Table 1) have been based on government agency
251 assessments of national costs associated with each disease. However, such parameters are
252 open to different interpretations and will be influenced by both the scale of the outbreak and the
253 current economic climate. In addition different organisations may wish to alternative
254 perspectives, by focusing on losses to particular sectors, such as the farming industry or
255 government. This entire range of sensitivity can be explored through the online Shiny app
256 (https://livestockmovements.shinyapps.io/Movement_Control/), which allows the individual
257 economic parameters to be varied (although sensitivity to individual economic values is
258 considered in the Supplementary Material – see Supplementary Figure 4). In general we find
259 that the optimal movement ban radius for FMD is most sensitive to the costs of livestock and

260 tourism losses, while for BTV and bTB the optimal radius only changes at extremes of economic
261 costs.

262
263 For a policy of movement bans to be effective, it must be enforceable. There is an argument
264 that a nationwide ban, where all livestock movements are prevented, could be more enforceable
265 as it is more obvious when the ban is being broken. In addition, a regional ban may meet
266 opposition from farmers just within the radius of the movement ban who view themselves
267 penalised relative to farms just outside the radius. However, localised movement bans (of the
268 form instigated during the 2006 bluetongue epidemic) allow resources to be concentrated into a
269 smaller regions, and hence it may be easier to enforce compliance. This may be particularly the
270 case in lower and middle income countries, when typically interventions are initiated at the local
271 level in response to livestock disease outbreaks [33]. Incorporating such factors into
272 mathematical models requires the ability to predict farmer behaviour which is likely to be
273 complex and heterogeneous, and beyond the scope of this work.

274
275 This suite of model predictions demonstrate that movement restrictions have a dramatic impact
276 on the national cost of livestock diseases, such that large-scale movement bans are generally
277 prohibitively expensive. By considering these three very different infections, we draw the
278 general conclusion that movement bans are most needed for diseases like FMD, where there is
279 considerable within farm transmission and where movements form a dominant source of long-
280 range transmission. For slower spreading infections, exemplified by bTB and BTV, it may be
281 economically preferable to allow movements to continue unrestricted. Optimisation of movement
282 restrictions, informed by bespoke predictive models, has the potential to dramatically reduce the
283 cost of an outbreak: balancing the need for control and containment with the desire to maintain
284 the economic viability of the livestock industry.

285

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377

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385 **Author Contributions**

386 MJT, SB, EBP and MW carried out simulations using the three livestock disease models. NB
387 developed the Shiny app for visualisation of sensitivity analysis. MJK and MJT analysed the
388 outputs of the simulation models. MJK led the sensitivity analysis of the modelling results and
389 provided intellectual expertise on all three livestock disease models. All authors contributed to
390 the writing of this manuscript.

391 **Data Availability Statement**

392 The raw simulation data used to create figure 1 in the main text and all figures in the
393 supplementary material can be made available upon acceptance of this manuscript. The
394 authors do not have permission to share the farm level data for the United Kingdom. However,
395 the demographic data that includes farm locations, farm sizes and species composition, as well
396 as the data on livestock movements between farms can be via the RADAR system by
397 emailing RADAR@apha.gsi.gov.uk.

398 **Code Availability Statement**

399 The code used to create analyse the raw data and produce the figures presented in this
400 manuscript will be made available upon acceptance of this manuscript. The code for the
401 simulation models can be accessed by contacting the relevant contributing author: (i) for the
402 foot-and-mouth disease model, Mike Tildesley; (ii) for the Blue tongue virus model, Sam Brand
403 and (iii) for the bovine Tuberculosis model Ellen Brooks Pollock.

404 **Competing Interests Statement**

405 The authors declare that they have no competing interests as defined by Nature Research, or
406 other interests that might be perceived to influence the interpretation of the article.

407 **Figure Legends**

408 **FIGURE 1. Impact of movement bans on the cost of livestock infectious diseases.** Panels A and B
409 show results for FMD epidemics seeded in 5 infected farms in Cumbria and Devon, respectively. Stacked
410 (coloured) bars represent the different costs: direct farm losses, welfare loses, loses to the general
411 agricultural sector, lost revenue due to export bans and the losses to the tourist industry (as quantified in

412 Table 1). Red points (with confidence intervals from bootstrapping) represent the upper 95% prediction
 413 interval on the costs. Horizontal bars show the optimal movement ban radius to minimise different
 414 economic measures: black bar average total costs; blue bar average cost without tourism losses; red bar
 415 the upper 95% prediction interval. Panels **C** and **D** focus on bluetongue outbreaks initiated in Devon. In **C**
 416 we consider the mean outbreak cost, and vary both the inner radius where movements are completely
 417 banned (colours) and the Protection / Surveillance zones where only outward movements are banned
 418 (grouped on the x-axis). In **D** we focus solely on the Protection / Surveillance zones, using the same
 419 format as graphs A and B. Panels **E** and **F** present results for bovine tuberculosis, simulations are run for
 420 14 years with alternative movement controls and testing implemented for the last 6 years, and the costs
 421 averaged across all years of alternative control. As in other panels, in **E** we show means, extremes and
 422 the associated confidence intervals. In **F**, we demonstrate the epidemiological consequences of
 423 alternative control policies, showing the incidence of new infections that we note can be very different
 424 from the number of detected infections owing to both test sensitivity and spatial patterns of testing.

425 **Table**

Type of Cost	Calculated as:	Reference
Direct Farm Costs (FMD)	$\text{£}1962 \times \text{Culled Cattle} + \text{£}523 \times \text{Culled Sheep}$	[16, 35]
Direct Farm Costs (BTV)	$\text{£}145 \times \text{Infected Cattle} + \text{£}29 \times \text{Infected Sheep} + \text{£}203 \times \text{Sheep Deaths}$	[36]
Direct Farm Costs (bTB)	$\text{£}1557 \times \text{Infected Cattle} + \text{£}531 \times \text{Breakdowns}$	[37]
Welfare Costs	$\text{£}8.00 \times \text{Farm Days Restricted}$	[16, 35]
Agricultural Sector losses	$\text{£}227 \times \text{Animal Movements Prevented}$	[16, 35]
Export Losses (FMD only)	$\text{£}655,000 \times (\text{Duration of Export Ban})$	[16, 35]
Tourism (FMD & BTV)	$\text{£}271 \times \text{Farm Days Restricted}$	[16, 35]
Testing (bTB only)	$\text{£}10 \times \text{Cattle tested}$ (approx $\text{£}2.50$ to farmer and $\text{£}7.50$ for performing the test)	[37]

426

427 **TABLE 1.** Costs related to movement bans for the three livestock diseases: Foot-and-Mouth Disease
 428 (FMD), Bluetongue Virus (BTV) and bovine Tuberculosis (bTB). All costs have been inflated from the date
 429 the assessments were made to generate prices relevant for 2019. Here Farm Days Restricted refers to
 430 the number of farms each day that are placed under movement restrictions summed across the epidemic.

431

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433

434 **Methods**

435 **The FMD Model**

436 The mathematical model utilised in this paper is a modified version of the FMD model used both
 437 during and after the 2001 outbreak by Keeling and co-workers to predict the spread of disease
 438 and the impact of control [2, 26]. Infection between farms can occur via two mechanisms –
 439 movements of infected livestock and local, distance-dependent transmission. The local
 440 transmission component of the model encapsulates the risks associated with aerosol spread,
 441 direct contact of infectious and susceptible animals or fomites (i.e. contaminated vehicles or
 442 farm equipment). The rate at which an infectious farm j transmits infection to a susceptible farm i
 443 via local spread is given by:

$$R_{i,j} = \sum_k \sigma_k N_{k,i}^{p_k} \times \sum_l \tau_l N_{l,j}^{q_k} \times K(d_{ij})$$

444 σ_k represents the susceptibility of species k on susceptible farm i , τ_l is the transmissibility of
 445 species l on farm j , $N_{k,i}$ is the number of animals of species k on farm i and p_k and q_k are power-
 446 law parameters accounting for a non-linear increase in susceptibility and transmissibility as
 447 animal numbers on a farm increase. Previous work has found that this power-law model
 448 provides a closer fit to the 2001 data than one in which the powers are set to unity [38-41]. $K(d_{ij})$
 449 is a distance dependent transmission kernel that is estimated from contact tracing data from the
 450 2001 outbreak [2]. In line with previous work [39], all model parameters are estimated for five

451 distinct regions: Cumbria, Devon, the rest of England (excluding Cumbria and Devon), Wales
452 and Scotland. This allows the model to account for regional variation in FMD epidemiology and
453 animal husbandry.

454 In order to assess the daily risk of between farm infection occurring via movement of live
455 animals, a movement network (A) is integrated into the model, mimicking the impact of animal
456 movements from infected farms. The probability of a susceptible farm i being infected by an
457 exposed or infectious farm (E_j or I_j) through a live animal movement, is given by:

$$\lambda_i = \sum_j A_{ji}(E_j + I_j)$$

458 Here A_{ji} is the daily risk of movement occurring from farm j to farm i , calculated by averaging
459 recorded cattle movements across a year; these livestock movement data were obtained from
460 DEFRA and the Scottish Government and have been analysed in a number of studies (e.g. [14,
461 42-44]). Given our assumptions that infection acts at the level of the entire farm, we are only
462 concerned with batches of livestock movements, not the number of animals in these batches. E_j
463 and I_j are indicator variables (0 or 1) which inform about the current status of farm j in the
464 simulation.

465 Simulations in this paper are seeded by infecting 5 (randomly chosen) farms in a 5 km cluster
466 (in a randomly chosen location) within a given county to approximate the initial conditions of a
467 localised outbreak; detection of the first case and the implementation of controls then follows. In
468 line with previous work, we assume that all livestock on IPs are culled within 24 hours of being
469 reported and all associated dangerous contacts (DCs) are culled within 48 hours [30].
470 Contiguous premises (CP) culling is not performed.

471 In order to determine the effectiveness of a livestock movement ban, we utilise data from the
472 2001 FMD epidemic that detail the costs associated with the outbreak. The economic costs of
473 the 2001 outbreak fell into 5 distinct categories: direct costs, indirect costs, costs associated
474 with welfare culls, losses to the agricultural sector and losses to tourism [35]. We will utilise this

475 economic framework to translate our simulation results into a national epidemic cost, although
476 alternative scenarios could be considered, such as minimising the cost to the farming industry or
477 to the UK tax-payer. In 2001 (and 2007) national scale movement bans were imposed such that
478 animals could only be moved under specific veterinary licence. Here we relax this control
479 measure and consider a range of movement bans that act upon all farms within a given radius
480 of infected premises. We impose this radius based on the straight-line distance between the
481 recorded point location (which generally identifies the farmhouse) of each pair of farms; in
482 practise regional control teams would presumably account for the location of livestock, although
483 this distinction is likely to be negligible for large radii. The parameters used in the FMD
484 simulations are taken from matching regional prevalence from simulations to the results of the
485 2001 FMD outbreak (see Supplementary Table 1).

486

487 **The BTV model**

488 Our model for BTV operates at the level of individual animals, replicating the known pattern of
489 animal movements and captures the transmission of infection through spatially dispersing midge
490 vectors that are affected by climatic conditions in a similar fashion to other spatial models of
491 BTV transmission [33, 45-47].

492 The model describes each farm as a stochastic metapopulation of sheep and cattle [33, 45], the
493 two main ruminant hosts of BTV amongst European commercial livestock. The livestock
494 population at each farm i is subdivided by their species k and BTV infection status: susceptible
495 ($S_{k,i}$), infected and infectious ($I_{k,i}$) and recovered and immune ($R_{k,i}$). The total population at
496 each farm is assumed to remain static except for movement of infected animals and disease
497 induced mortality. The infectious duration for BTV in a given animal is modelled as a multi-stage
498 Erlang process according to commonly used estimates of BTV viraemia amongst cattle and
499 sheep [48]. *Culicoides* biting midge spatial population dynamics are described using a spatial
500 grid overlaying the UK at a 5 x 5km resolution, therefore each grid might contain 0, 1, 2 or more

501 farms. The grid cell locations and daily mean temperature for each cell was drawn from the
 502 UKCP09 [49] retrospective data for 2007, the year of the first UK BTV outbreak. The midge
 503 population in the spatial grid at coordinate location x is described by a Poisson distribution for
 504 the number of latently infected midges ($E_{M,x}$) and actively infectious midges ($I_{M,x}$). The mean of
 505 these two distributions is determined by biting on infected livestock within the grid, and by
 506 dispersal of infected midges from nearby grids (see below). The latency duration (or extrinsic
 507 incubation period) of infected midges is modelled as a 10 stage temperature dependent Erlang
 508 process [31, 50].

509 The daily number of bites emanating from the infectious midges in the grid square at location x
 510 is Poisson distributed with mean $\alpha(t, x)I_{M,x}$, where $\alpha(t, x)$ is the biting rate for midges using the
 511 mean daily temperature on day t at the grid square x [31, 48]. The expected proportion of all
 512 daily infectious bites distributed to a single animal of species k in farm i within the spatial grid
 513 box at x is:

$$\phi_{k,i} = \frac{\pi_k (\sum_l \pi_l N_{l,i})^{p-1}}{\sum_{j \in x} (\sum_m \pi_m N_{m,j})^p}$$

514 where π_k is the relative preference of midges for species k and p is a parameter tuning the
 515 seeking preference of midges for larger farms within the grid cell. The sum in the denominator is
 516 over all the farms in the grid box at x . Therefore, the risk of the animal being infected on each
 517 day t is:

$$1 - \exp(-P_H \phi_{k,i} \alpha(t, x) I_{M,x}).$$

519 where P_H is the probability of BTV transmission per bite from an infectious midge.

520 We assume that the expected number of susceptible midges arriving to bite each animal each
 521 day is proportional to the expected prediction of a seasonal and temperature dependent
 522 generalised linear mixed-effect model (GLMM) inferred from wide-scale midge trapping
 523 experiments in the UK and specialised to the activity of *C. Obsoletus* females [31, 51].
 524 Underlying GLMM random effects were drawn either once per simulation for each farm (for farm

525 level random effects) or daily for each farm (overdispersion and autocorrelation random effects).
 526 We denote the unscaled mean biting rate prediction from the GLMM, conditional on local
 527 temperature and random effects for each farm on each day t , $B(t, x)$. Therefore, the expected
 528 number of newly infected midges in the grid cell at x on day t is:

$$529 \quad qP_V B(t, x) \sum_{j \in x} \sum_k \pi_k I_{k,j}.$$

530 Where P_V is the midge BTV infection probability per bite on an infected host, and q is a
 531 parameter that scales the difference between the biting rate and the trap capture rate.

532 In line with the known biting behaviour of *Culicoides* midges [52-53] we assume that all biting
 533 occurs over short dusk/dawn periods and that otherwise midges are in oogenesis, seeking
 534 oviposition sites or seeking new hosts. We model the movement of midges between daily biting
 535 as an inhomogeneous diffusion process with the local diffusion rate at each grid square x as:

$$536 \quad D(x) = \frac{D_0}{1 + \xi \sum_{j \in x} (\sum_m \pi_m N_{m,j})^p}.$$

537 where D_0 is the reference diffusivity of midges in a grid square devoid of commercial livestock
 538 hosts and ξ is a tunable scalar. The diffusion rate for the grid box x depends on the denominator
 539 for the proportion of bites per animal; this quantity acts as an effective population size for the
 540 grid box. That is, we model diffusion as decreasing with more animals per grid square and
 541 higher values of the seeking behaviour parameter.

542 The daily number of BTV-infected animals introduced into a farm i due to livestock movement
 543 from farm j was calculated in three steps for each day: 1) for each farm pair a movement was
 544 generated with probability A_{ji} (see above), 2) if a movement occurred in step 1 it was chosen
 545 randomly to be a batch of sheep or cattle according the relative population density in the farm
 546 sending the batch, 3) a batch size was randomly generated according to species type and
 547 infected animals of the chosen species were sampled uniformly without replacement from the
 548 total population of the chosen species at the sending farm. Only infected animals were moved

549 within the simulation, in order to better minimise population flux and in line with other simulation
550 studies of BTV in the UK [33].

551 The morbidity and mortality rates associated with BTV serotype 8 infection were low during the
552 2006 outbreak [17]. Therefore, we assume that the introduction of BTV into the UK is initially
553 cryptic (occurring on 1st June) and the virus spreads without movement bans until it is detected
554 by either a) the death of an animal due to disease induced mortality, or b) clinical signs of BTV
555 are detected amongst infected animals. The probability of clinical detection per farm per species
556 per day is:

$$557 \quad Q_{k,i} = 1 - (1 - p_{D,k})^{I_{k,i}}.$$

558 where $p_{D,k}$ is the daily chance of an infected animal of species k showing clinical signs of BTV.

559 After detection of a BTV outbreak we assume that DEFRA recommendations are followed and
560 all farms within 15km of the initial IP have all their animals investigated for BTV [54]. The initial
561 zones (CZ, PZ and SZ) are constructed around all the detected IPs, and are extended as new
562 IPs are detected during the ongoing outbreak. Parameters used in the BTV model are provided
563 in Supplementary Tables 2 and 3.

564

565 **bTB Model**

566 In this paper we make use of a national-scale stochastic metapopulation model of bTB
567 transmission and detection [12]. In essence the model operates at the scale of individual farms,
568 but (unlike the FMD model) captures the stochastic cattle-level infection dynamics within a farm;
569 this is necessary as an infected farm is likely to contain only a few infected cattle. Each farm is
570 defined by its location and the number of susceptible, latently infected and infectious cattle
571 present on a given day; sheep, pigs and other livestock species are assumed to have no role in
572 bTB transmission.

573 The transmission and disease progression processes within the model are stochastic, and occur
 574 in discrete time as follows: for farm i the number of Susceptible, Exposed and Infectious cattle
 575 are given by:

$$\begin{aligned}
 S_i(t+1) &= S_i(t) - A_{i,t} & A_{i,t} &= \text{Bin}(S_i(t), 1 - \exp(-\lambda_{i,t})) \\
 E_i(t+1) &= E_i(t) + A_{i,t} - A_{i,t} & A_{i,t} &= \text{Bin}(E_i(t), \alpha) \\
 I_i(t+1) &= I_i(t) + A_{i,t}
 \end{aligned}$$

576 where λ is the force of infection acting on cattle within the farm (see below), and α is the rate at
 577 which latent animals become infectious.

578 In addition there are three deterministic demographic processes acting on the farm – births,
 579 deaths and movements – which follow the recorded pattern from the UK's Cattle Tracing
 580 System (CTS), which is run by the British Cattle Movement Service (part of the Department for
 581 Environment, Food and Rural Affairs, DEFRA). All three of these processes can be considered
 582 as a movement; births are movements onto a farm without an origin and deaths are movement
 583 from a farm without a destination. For all of these movements, an individual animal is chosen
 584 randomly independent of its infection status or its history of movements. The recorded
 585 movement of ~30,000 cattle per day is one of the primary mechanisms of long-range
 586 transmission of infection from the movement of infected animals.

587 Transmission to cattle on a given farm comes from three different sources: cattle-to-cattle
 588 transmission, transmission from infection within the farm environment and transmission from
 589 infection within the wider environment. Hence the force of infection, λ , to cattle on farm i is given
 590 by:

$$\lambda_{i,t} = \beta \frac{I_i(t)}{N_i(t)} + f v_i(t) + F V_i(t)$$

591 where $N_i (= S_i + E_i + I_i)$ is the number of cattle on farm i , v is the level of infection in the farm
 592 environment, and V is the level of infection in the wider environment which is considered to be
 593 the local parish [12]. The level of infection in the environment is increased by the proportion of
 594 infectious cattle, but wanes over time as the bacteria become non-viable.

$$\frac{dv_i}{dt} = \frac{I_i}{N_i} - \epsilon v_i$$

$$\frac{dV_i}{dt} = \frac{\sum_{j \in Parish} I_j}{\sum_{j \in Parish} N_j} - \epsilon V_i$$

595

596

597 These two local reservoirs of infection could both represent the persistence of infectious matter
598 on pasture or persistence in a local wildlife reservoir.

599 In addition, we simulate routine testing for surveillance, which follows the DEFRA rules
600 appropriate for the time and varies between annual and 4-yearly testing depending on location.

601 This test is not perfect [55] and we therefore use a test sensitivity of ρ for infectious cattle and
602 $\rho_E \times \rho$ for exposed / latent animals. Once infected cattle are detected within a farm, the animals
603 are culled and the farm placed under movement restrictions until all its cattle clear a further two
604 tests at 60-day intervals; in addition these farms are also subjected to further testing after 6 and
605 12 months.

606 The model parameter are inferred by matching simulations to the number of reactors (positive
607 cattle) and number of failed herd tests recorded per county per year between 1997 and 2007
608 using Sequential Monte Carlo Approximate Bayesian Computation [12]; the main parameters
609 are given below.

610 The model was adapted to allow us to investigate the addition of radial movement restrictions.
611 Given that bTB is an endemic disease (unlike FMD and BTV), movement restrictions must be
612 temporary with some means in which they are lifted from given farms in the future. In our
613 adapted model, when a herd is first identified as being infected (that is an animal tests positive
614 on a farm that is not under restrictions), we assume that movements from the infected farm and
615 those within a radius of the infected farm are banned. (although we also simulate the extreme
616 case where there are no movement bans, even on the infected farms). The infected farm is
617 subject to the usual measures, with the positive animal(s) culled and movement restrictions in

618 place until two follow-up tests (at 60-day intervals) are all clear; additional tests at both 6 and 12
619 months are scheduled. For those farms within the radius (which may be considered at risk due
620 to their proximity) movements are banned until a follow-up test after 30 days can be performed
621 – following the results of this test either movements are resumed or the farm is identified as
622 infected and the entire process is repeated. In this way, waves of testing spread through high
623 prevalence areas. Results from such control policies are shown in the main paper.

624 A modification to this control policy is explored further below. Farms with cattle testing positive
625 are handled as described above; farms within the surrounding radius are only subject to follow-
626 up tests but do not have their cattle movements restricted. This policy is extended to have
627 slightly higher incidence (due to movement of cattle to new regions) but significantly lower
628 economic costs due to the reduction in movement restrictions.

629 Simulations begin in 1998 and utilise the pattern of recorded movements and random herd-level
630 test; changes to the control policy (additional radial controls and testing) is assumed to begin at
631 the start of 2005, and its impact over 6 years on the progress of the endemic recorded.

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