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

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Abstract

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

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

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The revenue of livestock farms is largely based on the movement of animals, either through selling animals to other farms or by moving animals to slaughter. Therefore, adopting any form of movement restrictions may have substantive economic consequences for the livestock 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

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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.

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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,

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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.

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287   **<u>References</u>**

288   1. Gibbens, J. C. *et al.* Descriptive epidemiology of the 2001 foot-and-mouth disease epidemic

289   in Great Britain: the first five months. *Veterinary Record* **149**, 729-743 (2001).

290   2. Keeling, M. J. *et al.* Dynamics of the 2001 UK Foot and Mouth Epidemic: Stochastic Dispersal

291   in a Heterogeneous Landscape. *Science* **294**, 813-817 (2001).

292   3. Ferguson, N. M., Donnelly C. A. & Anderson, R. M. The Foot-and-Mouth Epidemic in Great

293   Britain: Pattern of Spread and Impact of Interventions. *Science* **292**, 1155-1160 (2001).

294   4. Saegerman, C., Berkvens, D. & Mellor, P.S. Bluetongue epidemiology in the European Union.

295   Emerging Infectious Diseases. *National Center for Infectious Diseases* **14**(4), 539–544 (2008).

296   5. Mercier, A. *et al.* Spread rate of lumpy skin disease in the Balkans, 2015-16. *Transbound.*

297   *Emerg. Dis*. **65**(1), 240-243 (2018).

298   6. Tasioudi, K.E. *et al.* Emergence of Lumpy Skin Disease in Greece, 2015. *Transbound.*

299   *Emerg. Dis*. **63**(3), 260-265 (2016).

300   7. Docuel, V., *et al.* Epidemiology, molecular virology and diagnostics of Schmallenberg virus,

301   an emerging orthobunyavirus in Europe. *Veterinary Research* **44**, 31 (2013).

302   8. Hoffmann, B. *et al.* Novel Orthobunyavirus in Cattle, Europe, 2011. *Emerging Infectious*

303   *Diseases* **18**(3), 469-472 (2012).

304   9. Green, L. E. & George, T. R. N. Assessment of current knowledge of footrot in sheep with

305   particular reference to *Dichelobacter nodosus* and implications for elimination or control

306   strategies for sheep in Great Britain. *Veterinary Journal* **175**(2), 173-180 (2008).

307   10. Baylis, M. & McIntyre K. M. Scrapie control under new strain. *Nature* **432**, 810-811 (2004).

308   11. Schiller, I. *et al.* Bovine tuberculosis: a review of current and emerging diagnostic techniques

309   in view of their relevance for disease control and eradication. *Transbound. Emerg. Dis*. **57**(4),

310   205-220 (2010).

311   12. Brooks Pollock, E., Roberts, G. O. & Keeling, M. J. A dynamic model of bovine tuberculosis

312   spread and control in Great Britain. *Nature* **511**, 228-231 (2014).

313   13. Garcia-Alvarez, L., Webb, C. R. & Holmes, M. A. A novel field-based approach to validate

314   the use of network models for disease spread between dairy herds. *Epidemiology and Infection*

315   **139**, 1863-1874 (2011).

316   14. Kiss, I. Z., Green, D. M., Kao, R. R. The effect of network mixing patterns on epidemic

317   dynamics and the efficacy of disease contact tracing. *J. Roy. Soc. Interface* **5**(24), 791-799

318   (2008).

319   15. DEFRA *Contingency plan for exotic notifiable diseases of animals in England*.

320   https://www.gov.uk/government/publications/contingency-plan-for-exotic-notifiable-diseases-of-

321   animals-in-england (2017).

322   16. Thompson, D., Muriel, P., Russell, D., Osborne, P. et al. (2002). Economic costs of the foot

323   and mouth disease outbreak in the United Kingdom in 2001. *Rev. Sci. Tech.* **21**(3), 675-687.

324   17. Elbers A. *et al.* Field observations during the bluetongue serotype 8 epidemic in 2006: I.

325   Detection of first outbreaks and clinical signs in sheep and cattle in Belgium, France and the

326   Netherlands. *Preventive Veterinary Medicine* **87**, 21–30 (2008).

327   18. Krebs, J. *et al. Bovine Tuberculosis in Cattle and Badgers*.

328   http://www.bovinetb.info/docs/krebs.pdf (1997).

329   19. Donnelly, C. A. & Nouvellet, P. The contribution of badgers to confirmed tuberculosis in

330   cattle in high-incidence areas in England. *PLoS Curr. Outbreaks*,

331   ecurrents.outbreaks.097a904d3f3619db2fe78d24bc776098 (2013).

332   20. Inamura M., Rushton J. & Antón J. Risk Management of Outbreaks of Livestock Diseases.

333   OECD Food, Agriculture and Fisheries Papers, No. 91, OECD Publishing, Paris (2015).

334   21. Yang, P. C., Chu R. M., Chung W. B., & Sung H. T. Epidemiological characteristics and

335   financial costs of the 1997 foot-and-mouth disease epidemic in Taiwan. *Veterinary Record* **145,**

336   731-734 (1999).

337   22. Bicknell, K.B., Wilen, J.E. & Howitt, R.E. Public policy and private incentives for livestock

338   disease control. *Australian Journal of Agricultural and Resource Economics* **43**(4), 501-521

339   (2002).

340   23. Epanchin-Niell, R.S. & Wilen, J.E. Optimal spatial control of biological invasions. *Journal of*

341   *Environmental Economics and Management* **63**(2), 260-270 (2012).

342   24. Olson, L.J. & Roy, S. Controlling a biological invasion: a non-classical dynamic economic

343   model. *Economic Theory* **36**(3), 453-469 (2008).

344   25. Probert, W.J.M. et al. Real-time decision-making during emergency disease outbreaks.

345   *PLOS Computational Biology* **14**(7), e1006202 (2018).

346   26. Feng, S., Patton, M. & Davis, J. Market Impact of Foot-and-Mouth Disease Control

347   Strategies: A UK Case Study. *Front. Vet. Sci.* **4**:129 (2017).

348   27. Rich, K. M. & Winter-Nelson, A. An Integrated Epidemiological-Economic Analysis of Foot

349   and Mouth Disease: Applications to the Southern Cone of South America, *American Journal of*

350   *Agricultural Economics*, **89**: 682–697 (2007).

351   28. Longworth, N., Mourits, M. C. & Saatkamp H. W. Economic Analysis of HPAI Control in the

352   Netherlands II: Comparison of Control Strategies. *Transbound Emerg Dis*, **61**: 217-232 (2014).

353	29. Rich, K. M. & Wanyoike, F. An assessment of the regional and national socio-economic

354	impacts of the 2007 Rift Valley fever outbreak in Kenya. *Am J Trop Med Hyg*, **83**(2 Suppl):52-7

355	(2017).

356	30. Tildesley, M. J. *et al.* Optimal reactive vaccination strategies for a foot-and-mouth outbreak

357	in the UK. *Nature* **440**, 83-86 (2016).

358	31. Brand, S. P. C. & Keeling, M. J. The impact of temperature changes on vector- borne

359	disease transmission: Culicoides midges and bluetongue virus. *J. R. Soc. Interface* **14**,

360	20160481 (2017).

361	32. Woolhouse, M. *et al.* Epidemiology. Foot-and-mouth disease under control in the UK. *Nature*

362	**411**, 258-259 (2001).

363	33. Sumner, T., Orton, R. J., Green, D. M., Kao, R. R. & Gubbins, S. Quantifying the roles of

364	host movement and vector dispersal in the transmission of vector-borne diseases of livestock.

365	*PLoS Comput Biol.* **13**(4), e1005470–22 (2017).

366	34. Casey-Bryars, M. *et al.* Waves of endemic foot-and-mouth disease in eastern Africa suggest

367	feasibility of proactive vaccination approaches. *Nature Ecology and Evolution*. **2**(9), 1449-1457

368	(2018).

369	35. Anderson, I. *Foot & mouth disease 2001: lessons to be learned inquiry report*. The

370	Stationary Office; London, UK (2002).

371	36. Gunn, G. *et al.* Assessing the economic impact of different bluetongue virus (BTV) incursion

372	scenarios in Scotland. Scottish Agricultural College on behalf of the Centre of Excellence in

373	Epidemiology, Population Health and Disease Control. 2008:1-86 (2008).

374	37. DEFRA *Measures to address bovine TB in badgers*.

375	https://www.gov.uk/government/publications/measures-to-address-bovine-tuberculosis-in-

376	badgers-impact-assessment (2011).

377

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)	£1962×Culled Cattle + £523×Culled Sheep	[16, 35]
Direct Farm Costs (BTV)	£145×Infected Cattle + £29×Infected Sheep + £203×Sheep Deaths	[36]
Direct Farm Costs (bTB)	£1557×Infected Cattle + £531×Breakdowns	[37]
Welfare Costs	£8.00×Farm Days Restricted	[16, 35]
Agricultural Sector losses	£227×Animal Movements Prevented	[16, 35]
Export Losses (FMD only)	£655,000× (Duration of Export Ban)	[16, 35]
Tourism (FMD & BTV)	£271×Farm Days Restricted	[16, 35]
Testing (bTB only)	£10×Cattle tested (approx £2.50 to farmer and £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

432

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 l 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

18

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

19

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:

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

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:

518 $$1 - \exp(-P_H \phi_{k,i} \alpha(t,x) I_{M,x}).$$

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

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

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

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:

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

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.

632 **Methods References**

633 38. Diggle, P. (2006) Spatio-temporal point processes, partial likelihood, foot and mouth

634 disease. *Statistical Methods in Medical Research* **15**(4), 325-336 (2006).

635 39. Tildesley, M. J. *et al.* Accuracy of Models for the 2001 UK Foot-and-Mouth Epidemic. Proc.

636 Roy. Soc. B **275** (1641), 1459-1468 (2008).

637 40. Deardon, R. *et al.* Inference for individual-level models of infectious diseases in large

638 populations. Statistica Sinica **20**(1), 239 (2010).

639 41. Jewell, C. P., Kypraios, T., Neal, P. & Roberts, G. O. Bayesian Analysis for Emerging

640 Infectious Diseases. *Bayesian Analysis* **4**(4), 465-496 (2009).

641 42. Kao, R. R., Danon, L., Green, D. M. & Kiss, I. Z. Demographic structure and pathogen

642 dynamics on the network of livestock movements in Great Britain. *Proc. Roy. Soc. B* **273**, 1999-

643 2007 (2006).

644   43. Green, D. M., Kiss, I. Z. & Kao, R. R. Modelling the initial spread of foot-and-mouth disease

645   through animal movements. *Proc. Roy. Soc. B* **273**, 2729-2735 (2006).

646   44. Dawson, P. M., Werkman, M., Brooks Pollock, E. & Tildesley, M. J. Epidemic predictions in

647   an imperfect world: modelling disease spread with partial data. *Proc. R. Soc. B* **282**, 20150205

648   (2015).

649   45. Szmaragd, C. *et al.* A modeling framework to describe the transmission of bluetongue virus

650   within and between farms in Great Britain. *PLoS ONE*. **4**(11), e7741 (2009).

651   46. Turner J., Bowers R. G. & Baylis M. Modelling bluetongue virus transmission between farms

652   using animal and vector movements. *Sci Rep.*, **2**, 319 (2012).

653   47. Græsbøll, K., Bødker, R., Enøe, C. & Christiansen, L. E. Simulating spread of Bluetongue

654   Virus by flying vectors between hosts on pasture. *Sci Rep*. **2**, 863 (2012).

655   48. Gubbins, S., Carpenter, S., Baylis, M., Wood, J. L. N. & Mellor, P. S. Assessing the risk of

656   bluetongue to UK livestock: uncertainty and sensitivity analyses of a temperature-dependent

657   model for the basic reproduction number. *J. Roy. Soc. Interface*. **5**(20), 363–71 (2008).

658   49. Met Office, United Kingdom Climate Projections (UKCP09). (2009). Available from:

659   https://www.metoffice.gov.uk/climatechange/science/monitoring/ukcp09/

660   50. Carpenter, S. *et al.* Temperature Dependence of the Extrinsic Incubation Period of

661   Orbiviruses in Culicoides Biting Midges. *PLoS One* **6**(11), e27987 (2011).

662   51. Sanders C. J. *et al.* Influence of season and meteorological parameters on flight activity of

663   Culicoides biting midges. *J. Appl. Ecol.* **48**(6), 1355–64 (2011).

664   52. Kettle, D. S. The Bionomics and Control of Culicoides and Leptoconops (Diptera,

665   Ceratopogonidae = Heleidae). *Annu Rev Entomol*. **7**(1), 401–18 (1962).

666   53. Mellor P. S., Boorman J. & Baylis M. Culicoides biting midges: their role as arbovirus

667   vectors. *Annu Rev Entomol*. **45**(1), 307–340 (2000).

668   54. DEFRA UK Bluetongue Control Strategy (2008).

669   https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/fi

670   le/343741/bluetongue-control-strategy081201.pdf

671   55. Karolemeas, K., *et al.* Estimation of the Relative Sensitivity of the Comparative Tuberculin

672   Skin Test in Tuberculous Cattle Herds Subjected to Depopulation. *PLoS ONE* **7**(8), e43217

673   (2012).

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