

1                    A generic framework for spatial quantitative risk  
2 assessments of infectious diseases: lumpy skin disease case  
3                    study

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10                    Running Title: Spatial risk assessment framework for infectious diseases

11                    Keywords: Communicable Diseases, Lumpy Skin Disease, Risk Assessment, Spatial Analysis, Stochastic  
12                    Processes

## 13 **Summary**

14 The increase in availability of spatial data and the technological advances to handle such data allow for  
15 subsequent improvements in our ability to assess risk in a spatial setting. We provide a generic framework  
16 for quantitative risk assessments of disease introduction that capitalises on these new data. It can be  
17 adopted across multiple spatial scales, for any pathogen, method of transmission or location. The  
18 framework incorporates the risk of initial infection in a previously uninfected location due to registered  
19 movement (e.g. trade) and unregistered movement (e.g. daily movements of wild animals). We discuss the  
20 steps of the framework and the data required to compute it. We then outline how this framework is  
21 applied for a single pathway using lumpy skin disease as a case study, a disease which had an outbreak in  
22 the Balkans in 2016. We calculate the risk of initial infection for the rest of Europe in 2016 due to trade. We  
23 perform the risk assessment on 3 spatial scales – countries, regions within countries, and individual farms.  
24 We find that Croatia (assuming no vaccination occurred) has the highest mean probability of infection, with  
25 Italy, Hungary and Spain following. Including import detection of infected trade does reduce risk but this  
26 reduction is proportionally lower for countries with highest risk. The risk assessment results are consistent  
27 across the spatial scales, while in addition, at the finer spatial scales, it highlights specific areas or individual  
28 locations of countries on which to focus surveillance.

## 29 **Introduction**

30 The viability and usefulness of spatial quantitative risk assessment has been increasing with the availability  
31 of larger datasets, more detailed data, and improved computational power. This has been manifest across  
32 human, animal and plant health, following the growth of data on, for example, human movement via air  
33 travel (Grais et al. 2004, Tatem et al. 2006a, Tatem et al. 2006b), tracking and communication of spread of  
34 diseases using social media tools (Schmidt 2012, Bengtsson et al. 2015), improved climate predictions  
35 (Brownstein et al. 2005, Gale et al. 2012) as well as the development of geospatial software (Wardrop et al.  
36 2012) and next generation sequencing of disease strains (Vayssier-Taussat et al. 2013). Assessing risk on a  
37 spatial scale allows for active surveillance to be directed to areas deemed most at risk, spatially-varying  
38 procedures prepared to prevent infections occurring, and different management plans depending on which  
39 spatial locations become infected, should infection occur. Targeting prevention and control spatially, in this  
40 manner, can save time, money and resources.

41 Whilst there are clear outlines and recommendations on how to perform risk assessment for initial  
42 infections and spread of infectious diseases generally, which include quantifying entry, exposure and  
43 consequence assessments (Murray 2004), there is, however, no generic framework for performing  
44 quantitative risk assessments in a spatial setting. A framework allows for standardisation across different

45 countries and organisations to facilitate policy and decision making. In this paper, we outline a proposed  
46 generic framework for completing spatial quantitative risk assessments for risk of infection. The defining  
47 feature of the framework will be its emphasis on disease introductions from one area to another. However,  
48 the aim is for the framework to be generic across the type of pathogen, method of transmission, species of  
49 host(s) and spatial resolutions. To outline what the framework aims to achieve, we formulate the risk  
50 question as: “*What is the risk of infection of a pathogen in Area B given the presence of that pathogen in*  
51 *Area A?*” It thus focuses on initial infection by means of introduction.

52 We introduce the generic framework and undertake the risk assessment for one pathway, namely the risk  
53 of initial infection by means of registered movement of hosts, using a case study. In the case of livestock  
54 this implies a focus on trade but human movement via airplanes or other ticketed travel between countries  
55 is also applicable. Calculation of the risk of infection due to unregistered movement of hosts across  
56 borders, such as vectors, wild birds or illegal trade, is not considered in our case study. Through this case  
57 study we highlight the degrees of detail possible in the risk assessments using our framework when the risk  
58 assessor has access to data at a country level only, country level data with some regional data, and lastly  
59 detailed individual farm level data.

60 Lumpy skin disease (LSD) is used as the case study for assessing the risk of infection by legal trade. LSD  
61 virus, which affects cattle and buffalo, is in the Capripoxvirus genus along with sheeppox and goatpox. It  
62 causes nodules on the skin, mucus membranes and internal organs; reduction in milk production; fever;  
63 oedema; and sometimes death (Davies 1991, Tuppurainen and Oura 2012). Mortality is usually low (<10%  
64 Kumar (2011)), but it can cause significant economic losses and hence the World Organisation for Animal  
65 Health (OIE) classifies LSD as a notifiable disease. Mechanical transmission by vectors is believed to be the  
66 primary method of transmission but direct contact, infected semen, and contaminated feed and water  
67 sources are also considered as rare but possible routes of transmission (Carn and Kitching 1995b, Magori-  
68 Cohen et al. 2012). There are many different species that have been implicated as mechanical vectors, such  
69 as biting flies (e.g. *Stomoxys calcitrans*, Yeruham et al. (1995)), mosquitoes (e.g. *Aedes aegypti*, Chihota et  
70 al. (2001)) and ixodid (hard) ticks with evidence for transstadial and transovarial transmission in these ticks  
71 (e.g. *Rhipicephalus spp*, Tuppurainen et al. (2011)).

72 There has been rapid geographical spread of LSD over the last 30 years with emergence in south-east  
73 Europe for the first time in 2015. Historically, it had been restricted to sub-Saharan Africa and appeared to  
74 be in decline, but a resurgence occurred in the 1980s and subsequently it has been steadily spreading  
75 northwards (Hunter and Wallace 2001). Although there had been infrequent incursions before, since 2006  
76 it has become endemic throughout the Middle East (Tuppurainen and Oura 2012). Similarly, it has been  
77 present in Turkey since 2013 and is now considered endemic. A few cases of LSD occurred in Greece for the  
78 first time during 2015, followed by a widespread outbreak in the Balkan regions in 2016, specifically in

79 Greece, Bulgaria, The Former Yugoslav Republic of Macedonia, Serbia, Kosovo and Albania, as well as in  
80 Russia (Mercier et al. 2017). These cases and those in 2015 predominantly occurred in the summer months,  
81 highlighting the seasonal nature of the disease spread, likely shaped by the environmental requirements of  
82 arthropod vectors and pastoralism (Thevenin 2011). Given the potential for further spread within the EU,  
83 the disease was considered to be a timely case study for the application of our generic framework.  
84 Estimation of the risk of initial infection within each EU country would provide information to aid targeted  
85 surveillance. In addition, as the disease is notifiable, we anticipated that there would be more data than  
86 would be available for non-notifiable diseases.

87 We demonstrate our generic framework for spatial quantitative risk assessment for risk of initial infection,  
88 specifically due to registered movement of animals or people, by considering the potential import of  
89 infected animals in 2016 during the outbreak of LSD in the Balkan region. This is outlined by the following  
90 specific risk question: *“What is the risk of initial infection of lumpy skin disease in Europe (not including the*  
91 *countries which had notified cases) from legal trade in 2016 due to the presence of lumpy skin disease in the*  
92 *rest of the World?”*

## 93 **Methods**

### 94 **The Generic Framework**

95 We define the risk of infection as the probability of one or more initial infections in the native susceptible  
96 population in Area B. The risk pathway outlining the probabilistic steps involved in risk of infection for the  
97 generic risk question is set out in Figure 1. Infection can only occur if there is incursion of infected species,  
98 non-detection of that species, the survival of that species, and subsequent exposure of native susceptible  
99 hosts resulting in transmission, as shown in Figure 1. We use the term “species” but it could be even more  
100 generic than this, such as infected products or feed, provided that they could be in contact with native  
101 susceptible hosts. The term “contemporaneous survival” in Figure 1 indicates that some species are only  
102 active part of the year (e.g. only summer months in Northern EU countries in the case of vector-borne  
103 diseases) and the two species need to coincide for infection to be possible. It also includes the time period  
104 over which the infected species is infectious. Thus, animals that are imported directly for slaughter are  
105 assumed to have a survival length of 0 days. We combine these steps in the pathway together to produce  
106 the probability of one or more infections occurring in Area B for each pathway. Different methods of  
107 transmission, different infected species entering Area B or even different pathogen strains require different  
108 risk pathways that are then combined together to create the total risk of infection for each location within  
109 Area B. Locations at highest overall risk are of most interest to policy makers.

110 **Risk of Infection**

111 We can mathematically describe and combine the 5 steps of the risk pathway (Figure 1) and can therefore  
112 compute a quantitative probability of initial infection at each location thus giving a spatial risk map. This is  
113 adapted from a model that assesses the risk of species jumps in avian influenza (Hill et al. 2015). At first, we  
114 describe a single disease pathway from  $i$  to  $j$ . Inclusion of other pathways resulting in initial infection in  
115 Area B from Area A, in which species  $i$  and  $j$  may be different, is outlined afterwards. As the risk  
116 assessment may be calculated on different spatial scales, we use  $k$  to denote subregions of Area A and  $g$  for  
117 locations in Area B. Both of these will be determined by the spatial data available. Step 1 of the risk of initial  
118 infection is the estimation of the number of infected hosts ( $I_k$ ) entering Area B. Based on the prevalence in  
119 Area  $A_k$  and the total number of hosts exported, the number of infected hosts ( $I_k$ ) entering location  $g$  of  
120 Area B during a set time interval is given by:

121 
$$I_k(g) \sim \text{Bin}(N_k(g), p_k)$$

122 Here  $N_k(g)$  is the number of hosts imported to or entering location  $g$  from Area  $A_k$  in a unit time interval  
123 and  $p_k$  is the prevalence of infected hosts in Area  $A_k$ . We use a stochastic representation in the number of  
124 imported hosts that will be infected to better describe the potential variability. This requires an assumption  
125 of independence and therefore an assumption that infected and non-infected hosts are equally likely to be  
126 exported. The number of infected hosts entering location  $g$  in Area B from Area A is derived by summing  
127 over all sub-regions in Area A, thus

128 
$$I(g) = \sum_k I_k(g)$$

129 However, some infected hosts may not make it through import control due to detection of symptoms or  
130 testing of hosts, Step 2 in Figure 1. The probability of detection and the sensitivity of the tests can also vary  
131 by location  $g$ . We assume, however, that the probability of detection is independent of which country is  
132 the exporter. Therefore, we denote  $p_D(g)$  as the probability of successfully detecting and removing an  
133 infected host. The actual number of infected hosts  $J(g)$  entering location  $g$  in Area B will be given by

134 
$$J(g) \sim \text{Bin}(I(g), 1 - p_D(g))$$

135 We next calculate Steps 3 – 5 (Figure 1), namely the survival rate of the species, the contact rate between  
136 hosts and the probability of transmission leading to initial infection of susceptible hosts in each location  $g$   
137 of Area B. We combine these components using the basic reproductive number  $R_0$ . The basic reproductive  
138 number gives the number of susceptible hosts likely to be infected by the introduction of one infected host  
139 at each location  $g$ .  $R_0$  is a fundamental metric of disease systems, but the equation to represent  $R_0$   
140 depends on how the transmission of the disease is modelled. Therefore, using  $R_0$  facilitates adaptation to

141 different methods of transmission due to different interactions between species  $i$  and  $j$ , e.g. vector-borne  
 142 transmission, direct transmission or sexual transmission, as well as specific aspects that are only applicable  
 143 in some cases, such as environmental factors, in determining survival of species. For example, direct  
 144 transmission would be represented by the equation:

$$145 \quad R_0(g) = \frac{c\beta S(g)}{r}$$

146 In this equation,  $c$  is the contact rate between hosts (Step 4),  $\beta$  is the probability that contact results in  
 147 successful transmission (Step 5),  $S(g)$  is the population size of susceptible hosts of species  $j$  in location  $g$   
 148 and  $r$  is the recovery rate, based on the length of time infected hosts of species  $i$  remain present and  
 149 infectious in location  $g$  (Step 3). Additionally,  $R_0$  can change depending on the location  $g$  to incorporate  
 150 differences in transmission in different regions. And if the data are available  $R_0$  could be a function of  
 151 temperature, changing for each location based on average temperatures. For calculating the risk of initial  
 152 infection occurring within location  $g$  we assume that there is homogeneous mixing between the newly  
 153 introduced species and the native susceptible population, but this could be adapted to other scenarios in  
 154 which homogeneous mixing is not a good assumption by changing the contact rate  $c$ .

155 Based on our definition of risk of infection, we calculate the probability of one or more infections occurring  
 156 in the susceptible population within location  $g$ , per unit time by combining the information from Steps 1 –  
 157 5. The probability of random events, such as infections, happening is described by a Poisson process with  
 158 parameter  $\lambda$  where  $\lambda$  is the expected number of events occurring per unit time. For each observation of  
 159  $J(g)$  we can estimate the expected number of new infections occurring in a unit time in location  $g$  by  
 160  $R_0(g)J(g)$ . Hence, in our framework the number of new infections per unit time follows a Poisson process  
 161 with parameter  $\lambda = R_0(g)J(g)$ . The probability of no events happening in a Poisson process is  $e^{-\lambda}$ . Hence,  
 162 the risk of infection, alternatively the probability of one or more infections occurring in the susceptible  
 163 population, in location  $g$  from introduction of infected hosts from Area A is given by:

$$164 \quad R_I(g) = 1 - e^{-R_0(g)J(g)}$$

165 If there are multiple routes of transmission (which could involve different species  $i$  and  $j$ ) then all  
 166 parameters, including the contact rates, number of susceptible animals and number of imported infected  
 167 hosts, may be different for each route. To incorporate these different routes, we denote the route with an  
 168 additional subscript  $\omega$  and, hence, re-write the above equation as

$$169 \quad R_{I,\omega}(g) = 1 - e^{-R_{0,\omega}(g)J_\omega(g)}$$

170 for each route  $\omega$ . Therefore, the complete risk of infection over all routes of transmission would become:

171

$$R_I(g) = 1 - \prod_{\omega} [1 - R_{I,\omega}(g)]$$

172 This risk of infection calculation is capable of representing different methods of transmission, a wide range  
173 of pathogens with different environmental requirements, any spatial scale and any route of introduction.

## 174 **Data Requirements**

175 The data requirements necessary to calculate the risk of initial infection are presented in Table 1. The data  
176 needs to be on the spatial scale for which the risk assessment is to be performed as well as a suitable time  
177 scale. The major determinant of the time scale will be the movement data which could be on a daily,  
178 monthly or yearly scale. Data on the quantity of susceptible hosts is not likely to be censored as often but  
179 can be assumed to stay relatively constant. Prevalence data can be on any time scale depending on  
180 availability, although if different from the time scale of the movement data then assumptions either have  
181 to be made that the prevalence is constant over the duration of multiple movements, or on how to split the  
182 movement data up to be on the same time scale as the prevalence data.

## 183 **Lumpy Skin Disease case study**

184 We outline the data that we use to compute the risk of infection for our LSD case study (Table 2). Since we  
185 assess the risk due to the potential import of infected animals in 2016, during the outbreak in the Balkan  
186 region, we use 2016 data as much as possible. Our Area B is defined as all countries in Europe excluding  
187 those countries which had notified cases in 2016, namely Greece, Bulgaria, The Former Yugoslav Republic  
188 of Macedonia, Serbia, Kosovo, Albania, Turkey and Russia. Our Area A is the whole world. To highlight the  
189 ability for the framework to cope with different spatial resolutions, we use three different scales of  
190 locations in Area B. We compute risk of infection for countries, for regions within each country, and at  
191 individual farms within Europe. The spatial regions that we use are based on the NUTS classification  
192 (Nomenclature of territorial units of statistics) which is a system for dividing up the European Union (EU)  
193 into hierarchical levels in order to collect and harmonise European regional statistics. These regional  
194 classifications are created and maintained by Eurostat (Eurostat 2017b), the statistical office for the  
195 European Union. There are three NUTS regions below a country level, which decrease in size and socio-  
196 economic status, labelled as NUTS 1, NUTS 2 and NUTS 3. Some small countries have NUTS 1 and even  
197 NUTS 2 defined to be the whole country. Some non-EU European countries also have NUTS regions and  
198 provide some regional data to Eurostat, namely Iceland, Norway and Switzerland. Those non-EU European  
199 countries which do not have NUTS regions assigned and which do not give regional data to Eurostat are  
200 excluded from our regional and postcode risk assessments, specifically, Belarus, Bosnia and Herzegovina,  
201 Moldova and Ukraine.

## 202 **Trade data ( $N_k(g)$ )**

203 We use two different sources of trade data which represent the most common resolutions of data  
204 available. In the first case, we assume the risk assessor has access to individual farm trade data, i.e. the  
205 number of animals each farm in Area B imports from Area A. Obtaining individual farm trade data across  
206 the whole of Area B is likely to be difficult in many cases, unless Area B is a single country. Nevertheless,  
207 using these data we can calculate the risk of infection for individual farms. In the second case, we assume  
208 the much more frequent scenario, that the risk assessor has access to country trade data only. This allows  
209 for computation of risk of infection at a country level only. However, based on the assumption that it is  
210 often possible to access a higher resolution of data for your own country, we outline a method to infer  
211 regional trade data for all countries based on regional trade data for one country and country-level trade  
212 data for all countries. For specific details on this method see Appendix A. Thus, we compute risk of infection  
213 at a regional level based on country trade data for all countries and regional trade data from one country.  
214 For all trade data, we assume that cattle are imported to a farm and are not moved elsewhere during the  
215 time they are infectious.

216 For the risk of initial infection at individual farm level, we use the Trade Control and Expert System (TRACES  
217 2017), a primarily EU-based trade system. On request TRACES kindly provided us with data on all cattle  
218 trade registered through their system in 2016 and included the postcode of the final destination. The  
219 country trade data which we use for the country and regional risk assessments is the freely available  
220 dataset COMEXT, also provided by Eurostat (Eurostat 2017a), which denotes all trade of any product from  
221 any country in the world to any other. We subset the data by product code so that we only include trade in  
222 live cattle not for slaughter. Using the methodology described in Appendix A, we infer the distribution of  
223 the imported cattle amongst regions in each country. To do this, we use trade data at the regional level for  
224 the UK, from 2012-2015 obtained from TRACES, to estimate predictors for determining the proportion of  
225 cattle going to each region. This is under the assumption that UK regional trade data is similar to regional  
226 trade data in the rest of Europe. Based on data availability at a regional level, we analysed the number of  
227 cattle farms in each region and the proportion of those which are dairy as predictors. Our model in  
228 Appendix A identifies both as important predictors for predicting the proportion of cattle trade to each  
229 region. Data on cattle farms across Europe, including how many are dairy, are provided by Eurostat  
230 (Eurostat 2017a). Thus, we use this COMEXT data, alongside the model for distribution of cattle imports  
231 across regions, in our calculations for risk both at the country and regional level.

232 Since we have the TRACES data at a farm level for the whole of Area B, we can use it to calculate regional  
233 risk instead of inferring distribution of cattle amongst regions based on the country trade data. However, as  
234 it is much more likely for the risk assessor to only have access to the country level data, we highlight in the  
235 main text the use of country level data for computing regional risk. It also highlights the differences that  
236 occur between the two datasets. We plot the country risk based on TRACES data in Appendix B and



237 compare this to country risk using COMEXT data to assess whether these differences impact significantly on  
238 the risk calculations.

### 239 **Prevalence of LSD around the world ( $p_k$ )**

240 We use 2016 data from the EU-funded SPARE project (Simons et al. 2017), which estimates prevalence of  
241 disease around the world using OIE data on the number of outbreaks and the number of cases per  
242 outbreak of the disease in the past 10 years. These data were provided to us in the form of distribution  
243 parameters, thus giving a distribution of prevalence of LSD for each country. We use these distributions to  
244 represent our uncertainty in the prevalence in one year for each country. The data do not assume that a  
245 country is free of the disease if it has not notified the OIE of any cases because it takes into account under  
246 reporting and the occurrence of notified cases in bordering countries.

### 247 **Probability of import detection ( $p_D(g)$ )**

248 Although our locations  $g$  can be either countries, regions or even farms, it is unlikely to know the  
249 probability of import detection of infected hosts on the finer scales. Even on a country level it may be  
250 difficult to determine, especially for diseases which do not have a specific test on import. Therefore, for this  
251 case study we set  $p_D(g) = 0$  to indicate no testing of imports occurs and perform a scenario analysis for  
252  $p_D(g) = 0.5$  for all countries. Approximately 30-50% of animals with LSD will show severe clinical signs,  
253 with more showing mild symptoms, and thus may be detected by physical examination (Weiss 1968, Ali et  
254 al. 1990, Carn and Kitching 1995b). A health certificate signed by an official veterinarian is the only health  
255 requirement for movement between different EU countries, although individual countries within the EU  
256 may have their own regulations. For example, the UK tests on import (and quarantines animals until results  
257 are confirmed negative) for LSD from high-risk countries. However, we do not know the procedures of  
258 other countries in Europe and therefore we maintain that an import detection of 0.5 is in a realistic range  
259 for LSD.

### 260 **Number of susceptible hosts ( $S(g)$ )**

261 For the country level assessment of risk, the data is based on cleaned data from the OIE from 2014 which  
262 gives the numbers of cattle and farms in each country (World Organisation for Animal Health (OIE) 2017).  
263 This is to be consistent with the prevalence data which uses OIE data in its methodology. Since OIE data on  
264 number of cattle is rare at the regional level, we use data from Eurostat for the numbers of cattle and farms  
265 in each region in 2016 (some countries are for 2015 due to a lack of 2016 data) for the regional risk  
266 assessment (Eurostat 2017a). Most countries that provide data to Eurostat do so at a NUTS 2 level  
267 (approximately the size of counties), whilst the UK and Germany provide their data on the NUTS 1 level  
268 (larger regions consisting of multiple counties). We, therefore, calculate regional risk of infection depending  
269 on the scale of regional data on susceptible hosts provided to Eurostat. We calculate the average number  
270 of cattle on a farm in each country/region to represent the number of susceptible animals the imported

271 animals will be in contact with. Although we have data on trade to individual farms (determined by their  
272 postcode), we do not have detailed information about those farms, such as the number of cattle. Thus, we  
273 use the regional average number of cattle per farm for the relevant region. We do not include differences  
274 in the types of farming and husbandry systems that may occur throughout the various countries, however,  
275 if data is available for LSD or in a different case study, this could be included by changing the underlying  
276 formula for  $R_0$ .

### 277 **Lumpy Skin Disease data ( $c, \beta, r$ )**

278 There is a great deal of uncertainty over which transmission routes are most important for LSD, the contact  
279 rates along those routes, the minimum infective dose required for each route and the probability that the  
280 infective dose would be met. Therefore, it would be exceedingly difficult to produce reliable estimates for  
281 contact rates ( $c$ ) and the probability of transmission ( $\beta$ ) separately. Instead, we combine the contact rate  
282 between animals and probability of transmission into a transmission rate ( $\xi$ ) and use results from a  
283 statistical analysis of an outbreak on a single farm (Magori-Cohen et al. 2012) which estimated transmission  
284 rates. This study, followed up by personal communication with the authors, determined that vector  
285 (mechanical) and direct transmission were key transmission routes, with rates of 0.026 and 0.006 per day,  
286 respectively. In Magori-Cohen et al. (2012) the mechanical transmission term from cow to cow is  
287 represented by the formula  $\xi SI$  rather than using frequency-dependent transmission therefore we use the  
288 same formula to represent mechanical transmission. Magori-Cohen and authors (personal comm.) provided  
289 us with estimates of the uncertainty for the two transmission rates through 95% confidence intervals,  
290 [0.013, 0.052] and [0.003, 0.012] for mechanical and direct transmission, respectively. Since mechanical  
291 vector transmission is thought of as the most important mode of transmission for LSD (Carn and Kitching  
292 1995b) we use the upper and lower confidence interval bounds for this parameter in a sensitivity analysis  
293 to estimate our uncertainty in the risk calculations due to our uncertainty in transmission rate. We assume  
294 that across the whole of Europe there are suitable vectors which are able to transmit LSD virus. This is a fair  
295 assumption considering the wide range of species that have been implicated as potential mechanical  
296 vectors. The number of days that cattle will exhibit viremia, as well as shedding of virus from nasal, oral and  
297 conjunctival secretions, has been estimated to be between 6-18 days (Carn and Kitching 1995a,  
298 Tuppurainen et al. 2005, Babiuk et al. 2008). However, virus has been detected by PCR in skin nodules on  
299 cattle up to 42 days post inoculation (Babiuk et al. 2008) and up to 159 days in the semen of experimentally  
300 infected bulls (Irons et al. 2005). We assume a 15 day infectious period ( $r$ ) to represent the shorter viremic  
301 period and perform a sensitivity analysis for a 42 day infectious period to incorporate the effects of  
302 potential longer skin nodule infectivity.

303 All of our calculations are performed in R (R Core Team 2016). We take random draws from the prevalence  
304 distribution to estimate the prevalence in each country but reject those samples which fall outside the 5

305 and 95 quantiles due to long tails of this distribution. This is based on the methodology from the SPARE  
306 project which provides the prevalence data. We then randomly draw the number of infected animals  
307 entering a country, as described earlier. In total, we use 10,000 iterations. Executing the calculations  
308 described earlier, the model outputs a distribution of the risk of infection. To present the results the mean  
309 and variance of this distribution are provided. The default scenario considered is a 15 day infectious period,  
310 a mechanical transmission rate of 0.026 and no detection on import. Modifications to the default scenario  
311 are considered in the sensitivity and scenario analyses and are clearly stated; otherwise it can be assumed  
312 that the parameters are those of the default scenario.

## 313 **Results**

314 We reiterate here that we define the risk of infection as the probability of one or more initial infections in  
315 the native susceptible population in Area B. In nearly all simulations, we find that virtually all locations will  
316 have a probability very close to or indistinguishable from 1 if an infected animal is imported to the farm and  
317 obviously a probability of 0 if no infected animal is imported. Therefore, each simulation of the risk is  
318 essentially a Bernoulli distribution. Combining all the simulations together produces a distribution akin to a  
319 scaled Binomial distribution. Hence, the mean and variance of the risk can be interpreted similarly to the  
320 mean and variance of a Binomial distribution. The variance is a representation of our total uncertainty  
321 arising from the model and input parameters and is only driven by the distribution for prevalence.

322 The mean annual probability of initial infection per location, at a country level assessment for the default  
323 scenario is plotted in Figure 2. Many countries in Europe import only from countries which have an  
324 estimated zero prevalence, according to our prevalence data within each country. Therefore, they have  
325 negligible risk of having one or more native susceptible animals becoming infected due to importing an  
326 infected animal. Croatia, with a mean probability estimated at 0.87, has the highest annual risk, followed by  
327 Italy (mean risk 0.72), Hungary (mean risk 0.62), Spain (mean risk 0.6) and Slovenia (mean risk 0.448). This  
328 indicates a probability of 87% for at least one infected native host in Croatia in 2016. We also plot the  
329 variance in this estimate of risk of infection. There is little uncertainty in our estimate of risk for Croatia,  
330 indicating that the high risk assessment holds true regardless of the stochastic nature of prevalence within  
331 countries. On the other hand, uncertainty is high for Italy, Spain, Hungary and Slovenia, with variance  
332 between 0.2 and 0.25.

333 The mean probability of infection due to trade at a regional level also highlights Croatia, Italy and Hungary  
334 as countries with the highest risk (Figure 3). However, now it is possible to observe that this risk is focussed  
335 in specific regions of these countries. Croatia has high risk across the whole country whereas Italy has  
336 highest risk in the northern regions, and in Hungary the highest risks are in the southern part of the  
337 country. Similarly, the variance of this risk is plotted on a regional scale. Some countries, for example

338 Romania and Germany, have regions with both low probability of infection and low variance in this  
339 probability, as well as other regions which have low mean probability but a higher variance. This allows for  
340 better understanding of where to focus surveillance activities.

341 Risk of initial infection at an individual farm level (Figure 4) indicates that the majority of trade within Area  
342 B with countries that have non-zero prevalence occurs in Croatia, hence why Croatia had such a high risk at  
343 a country and regional level. The two farms with the highest probability of infection are in Croatia including  
344 one farm with a risk of 0.65. However, Spain follows closely behind with the next 3 highest risk farms with  
345 probabilities of infection between 0.51 – 0.54. Some countries which are assessed as having negligible risk  
346 due to not importing from infected countries (according to the COMEXT dataset, Figure 2), have individual  
347 farms in the TRACES data doing so, e.g. France and UK, Figure 4. This is due to differences that occur  
348 between the two different trade datasets (see Appendix B). However, the regional and individual farm risk  
349 maps agree on the regions with highest risk in Italy, Germany, Poland and Hungary. The plot of variance in  
350 the risk of initial infection at an individual farm level indicates much uncertainty in the risk assessment  
351 centred in Croatia, in contrast to the country and regional level risk assessments which indicated lower  
352 uncertainty in Croatia's risk. Although each farm has high uncertainty as to whether infection is likely to  
353 occur in a native host, the combination of multiple farms with high risk culminates in more certainty that  
354 infection would occur. Hence, the result of many farms with high risk and high uncertainty results in high  
355 risk with little uncertainty at a regional or country level.

#### 356 **Sensitivity Analysis**

357 We performed sensitivity analysis on the two main parameters that have uncertainty, the length of the  
358 infectious period in cattle (15 or 42 days) and the mechanical (vector) transmission rate (in the range 0.013-  
359 0.052). Varying either of these parameters within these values does not make a noticeable difference to the  
360 results. The high transmission rates, the ability for hosts to infect any of the susceptible hosts on the farm  
361 and the long infectious period, lead to high  $R_0$  values at each location, even when these parameters vary.

#### 362 **Scenario Analysis**

363 A risk assessment at a country level when the import detection probability is increased from 0 to 0.5 for all  
364 countries indicates, as expected, a decrease in the overall probability (Figure 5). Although import detection  
365 approximately halves the number of imported infected animals, it does not halve the value of risk. This is  
366 because in many simulations no infected animals enter due to low prevalence, which will not change when  
367 import detection does occur. In general, the values for risk are reduced most for countries with low to  
368 medium risk with, for example, Germany, the Netherlands, Romania and Poland reducing their probability  
369 of infection by 30 – 50%. In contrast, import detection is not as successful for countries with higher risk,  
370 with Italy and Croatia only reducing their risk by 13% and 7% respectively. This is due to high import rates

371 from countries with non-zero prevalence, so that with 50% detection many infected animals could still  
372 enter the country.

## 373 **Discussion**

374 Our risk assessment was performed at various spatial scales, both to show the flexibility of the framework,  
375 and to understand more clearly how LSD risk is distributed across Europe. In comparison to the risk of  
376 infection calculation at a regional or country level, the individual level informs whether higher risk arises  
377 due to a large number of farms with low to medium risk, or due to a small number of farms with high risk.  
378 For example, only a few individual farms in Spain import but they have a high risk of LSD, whereas in Italy  
379 and Hungary many farms import from countries with non-zero prevalence but they have low to mid risk  
380 (Figure 4). This is particularly pertinent for Spain, in this case, as at a country level its risk is lower than a  
381 few other countries. This could lead to less overall surveillance than those countries when in reality there  
382 are a few farms with very high risk. This level of detail is not possible in the regional and country level risk  
383 assessment. We reiterate that our regional risk assessment involves the assumption that the distribution of  
384 animal imports amongst regions will be similar between the UK and the rest of Europe. Our model for trade  
385 distribution (see Appendix A) found that the number of farms and the proportion that are dairy are  
386 significant determinants of cattle being imported into different regions of the UK but this may not be the  
387 case for other European countries. Comparing Figure 3 and Figure 4 we can see that while most countries  
388 have similar areas of risk predicted at a regional level and at an individual farm level, this is not true for  
389 Spain. The regional areas at risk are predicted to be in the north west of Spain but according to the TRACES  
390 dataset, Figure 4, the individual farms at risk are in the north east. This is likely due to Spain not importing  
391 according to our model for trade distribution amongst regions. However, for most countries our results are  
392 consistent across the spatial scales. Whilst individual farm risk provides the most detailed information,  
393 when time is short or data are not available, country and regional risk assessments provide a useful and  
394 relevant measure of risk.

395 This risk assessment for LSD is focussed on 2016, coinciding with the outbreak in the Balkans, and highlights  
396 Croatia as the country with the highest risk. However, our risk assessment did not take into account any  
397 control measures, other than import detection, which countries may have implemented during this  
398 outbreak. In fact, Croatia started to vaccinate its cattle population for LSD in August 2016, achieving 100%  
399 coverage by November 2016 (European Food Safety Authority (EFSA) 2017). This risk assessment, alongside  
400 Croatia's close location to infected countries, suggests that Croatia was wise to vaccinate to avoid infection.  
401 In fact, the FAO have released a position paper (FAO 2017), following a number of confirmed cases of LSD in  
402 2017, suggesting full-scale vaccination policies in countries with high risk in Eastern Europe, regardless of  
403 whether they have had infected cases, in order to reduce the likelihood of another outbreak. This is to

404 avert the spread of the disease and reduce the need for a total stamping-out policy, which can significantly  
405 affect farmers, especially smallholders. As in other models of the spread of infectious diseases (Keeling and  
406 Rohani 2007), our model can include the role of vaccination by reducing the number of susceptible animals  
407 in Area B that may come into contact with the imported infected species. This reduction would be based on  
408 available data on the proportion of animals that are vaccinated at each location in Area B. Vaccination  
409 could also lower the transmission rates, as vaccinated cattle may be less susceptible to the disease, or it  
410 could reduce infectivity of cattle by shortening the length of the infectious period, both of which can be  
411 easily changed in our model.

412 However, vaccination against LSD may not be suitable or recommended for all countries due to the fact it is  
413 a live vaccine with no test to distinguish infected from vaccinated cattle (Tuppurainen and Oura 2012). As  
414 an alternative, increasing the probability of detection on import does reduce the risk from trade imports.  
415 However, the effects of import detection are not equivalent across countries, and the countries with  
416 highest risks would need higher probabilities of successful detection to be able to reduce their risk by the  
417 same proportion.

418 Italy, Hungary, Spain and Slovenia had higher risk than many other countries, demonstrating the potential  
419 for LSD to lead to local infections in cattle populations across Europe due to trade. However, this risk  
420 assessment assumed that a suitable active vector is always present in all locations – this may not be the  
421 case in more northern countries in Europe, or during certain times of the year. This could significantly  
422 reduce the risk estimates in more northerly countries as the transmission rates through direct contact are  
423 significantly smaller than through mechanical vector contact (Carn and Kitching 1995b, Magori-Cohen et al.  
424 2012). Croatia, Italy and Spain have similar Mediterranean climates to Greece, where infection has  
425 occurred and spread, indicating disease suitability in that climate for at least part of the year provided  
426 vectors are present.

427 This case study did not assess the risk of initial infection through vector movement across borders or other  
428 unregistered trade/movement, such as illegal trade or movement of people, including refugees who may  
429 bring cattle with them. Undoubtedly, this would increase the risk in those countries which are neighbouring  
430 infected countries, such as Croatia, Bosnia and Herzegovina, Hungary and Romania, depending on the  
431 political climate, wind events, presence of vectors and temperature requirements of vectors. Furthermore,  
432 if transtadial and transovarial transmission of LSD is shown to occur in many tick species (Tuppurainen et al.  
433 2011), this may be an important transmission pathway to consider for spread of LSD.

434 The difference in risk for LSD across Europe is primarily driven by prevalence in export countries and the  
435 number of cattle imported, whereas specific disease parameters and the differences between  
436 countries/regions in the average number of susceptible animals on a farm did not have much impact on risk

437 estimates. This finding is expected to be similar for most diseases, although different formulas for  $R_0$  to  
438 estimate disease transmission within each area could affect it, especially if the  $R_0$  parameters are  
439 dependent on environmental factors, which vary between areas. The lack of consensus on which vectors of  
440 LSD are the most influential in spreading the disease (via mechanical transmission) mean that we are not  
441 able to vary  $R_0$  with location based on how the vectors respond to environmental variables. Therefore, our  
442 LSD case study is not able to include details surrounding a key element of transmission. However, as the  
443 difference in risk is primarily driven by the import trade and as the greatest risk is located in countries  
444 which are likely to have similar climates to those which had outbreaks in 2016, we believe our results  
445 provide a robust estimation of risk across Europe for 2016.

446 Our generic framework can be adapted for different modes of transmission by changing the formula used  
447 for  $R_0$ . This provides flexibility to consider other case studies which involve different transmission  
448 pathways, such as vector-borne transmission, environmental and contaminated feed and water sources.  
449 Furthermore, the generic framework can also be used for different types of movement in to Area B, such as  
450 unregistered movement. Movement of terrestrial wildlife, migratory birds and local and windborne travel  
451 of vectors can be included in to the framework through the parameter  $N_k(g)$  in the same way as the  
452 import of animals by trade. The difference is that the estimation of  $N_k(g)$  will likely be based on a model of  
453 animal movement instead of a global database, such as we used for trade in the LSD case study. Similarly,  
454 we estimated the number of susceptible animals using databases on the number of animals on farms in  
455 each country, but for other pathways a more useful measure could be the number of animals in a 10km<sup>2</sup>  
456 area extracted from density maps of animals, depending on the data used for movement of animals.  
457 Importantly, however, the framework itself remains unchanged for these different pathways of disease  
458 introduction.

459 The accuracy of our framework to predict the risk of initial infection for different diseases will depend  
460 greatly on the quality and quantity of data available for the disease and relevant animal species. Even  
461 though the framework is applicable to all disease introductions as outlined above, it may not always be  
462 possible to calculate the risk of initial infection if there is insufficient data available. If exact data required  
463 by the model are not available, it is possible to use proxy data, although this increases the uncertainty  
464 associated with the results. For example, it is possible to use cattle density as a proxy for vector density but  
465 there may be greater uncertainty over the reliability of the proxy data at low and high densities. In general,  
466 a focus on a risk ranking of countries is likely to produce more reliable predictions rather than  
467 concentrating on the risk estimates themselves. Missing or inaccurate data can always bias the results,  
468 even if under-reporting factors or models are used to estimate the true values. This can be seen in  
469 Appendix B, Figure B2, in which the risk estimates at a country level are compared using either the Comext  
470 dataset or the TRACES dataset, indicating that there are clear differences between these datasets.  
471 However, it is not possible to state with any certainty which is the better dataset to use. Similarly, reliable

472 estimates for prevalence of a disease in all countries throughout the world are difficult to obtain. The data  
473 we use for prevalence from Simons et al. (2017) is based on OIE notified cases, the best freely-available  
474 source for worldwide animal disease outbreaks. But it is judicious to remember that the resulting data on  
475 prevalence is the result of a model with uncertainty and assumptions. We provide a risk assessment for LSD  
476 based on the best available data. Conversely, the generic framework we present is applicable for all data  
477 sources and can be re-used as better data becomes available.

478 A major advantage of a framework that promotes the computation of risk at various spatial scales is that it  
479 allows for the identification of hotspots of disease, and hence it can guide policy decisions regarding the  
480 implementation of more specific and directed surveillance of potential infection. Enhancing surveillance  
481 methods has the potential to reduce time to detection of infection thus reducing the likelihood of  
482 widespread outbreaks, as well as decreasing the costs of, and time spent, on surveillance. Clearly countries  
483 with a range of low, medium and higher risks should target surveillance within those regions appropriately.  
484 On the other hand, countries with low risk may also want to have surveillance in place but this may be too  
485 costly to implement across the whole country. In this case, the variance in the risk can provide additional  
486 information for directing surveillance. Additionally, the generic framework can also be expanded to include  
487 a method for risk of spread from the hotspots of infection. Combining the risk of initial infection with risk of  
488 spread would allow the risk assessor to determine not only which locations have highest risk of infection  
489 occurring from outside sources but also, of those locations, which are most likely to spread the disease  
490 further within Area B. Our generic framework provides a method for the calculation of risk of initial  
491 infection for the introduction of any pathogen from any Area A to Area B, and specifically it allows these  
492 calculations to be made across many different spatial scales depending on the question in mind and the  
493 data available to the risk assessor. This is a powerful tool that can be used to determine not only which  
494 diseases are of most concern for different countries, but also where to focus surveillance within countries  
495 for different pathogens.

## 496 **Acknowledgements**

497 The authors wish to sincerely thank Dr Robin Simons and Dr Amie Adkin, APHA, (funded through the Animal  
498 Health and Welfare ERA-NET consortium (<https://www.anihwa.eu/>) under SPARE 'Spatial risk assessment  
499 framework for assessing exotic disease incursion and spread through Europe') for providing the prevalence  
500 distribution parameters for lumpy skin disease in 2016. The authors also wish to thank Dr Rachel Jinks,  
501 APHA, for useful discussion on the statistical methods used in Appendix A. This project has received funding  
502 from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No  
503 643476.



## 504 **Conflict of Interest**

505 The authors declare that there is no conflict of interest.

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592

## 593 Tables

594

595 Table 1 Data required to calculate the risk of initial infection for the generic framework.

Parameter	Specific Data	Further Details	Potential Data Sources
Movement from Area A to Area B ( $N_k(g)$ )	Trade/Registered Movement	Trade in livestock or registered movement of hosts from regions in Area A to locations in Area B. Reason for movement helpful to determine final location of host. For illegal trade an underreporting factor is necessary or estimates for locations with no reported data.	UN Comtrade data Eurostat COMEXT data Trade Control and Expert System (TRACES)
	Import Detection ( $p_D(g)$ )	The probability that locations in Area B will detect infection in animals imported through trade.	Published literature
	Movement of wild animals	Average home range size or distance routinely travelled by wild animals. This may be affected by weather events. For birds, this would include migration routes together with time of year.	Published literature
	Location and abundance of	Approximate spatial distribution and numbers of wild animals in Area A.	Published literature

	wild animals in Area A		Global Biodiversity Information Facility (GBIF)
Prevalence ( $p_k$ )	Prevalence of the disease in Area A	Preferably for the same regions in Area A as the movement data.	OIE Animal Disease Notification System FAO EMPRES-i
Susceptible Hosts ( $S(g)$ )	Size of farms in Area B	When importing to farms this determines how many susceptible hosts will be in contact with the infected imports. Depending on spatial scale, this could be the number of hosts on a specific farm, or the average number of hosts on farms in a region.	OIE Eurostat
	Spatial distribution of wild animals or people	To determine where and how many susceptible hosts the imported hosts will have contact with	Published literature Global Biodiversity Information Facility (GBIF)
Specific host and disease data ( $c, \beta, r$ )	Length of the infectious period ( $r$ )	This could be affected by whether disease is detected at locations in Area B once symptoms appear and if they perform culling or eradication measures.	Published literature OIE for control measures
	Average lifespan of species $i$ and $j$ in Area B ( $r$ )	This could be affected by climate data.	Published literature
	Probability of transmission ( $\beta$ ) between species $i$ and $j$		Published literature
	Contact rates ( $c$ ) between species $i$ and $j$	This could be affected by climate data.	Published literature

597 Table 2 Parameter values and data sources used in the lumpy skin disease case study for the default  
 598 scenario. Different values used in the sensitivity and scenario analyses are provided in square brackets.

Parameter	Description	Value	Source
Movement from Area A to Area B ( $N_k(g)$ )	Legal trade	-	Country & Regional level: Eurostat Comext data (Eurostat 2017a)  Farm level: TRACES data (TRACES 2017)
Prevalence ( $p_k$ )	Prevalence of the disease in Area A	-	EU-funded SPARE project (Simons et al. 2017)
Susceptible Hosts ( $S(g)$ )	Average (Country or regional level) or specific (farm level) number of animals on a farm	-	Eurostat data (Eurostat 2017a)
Import Detection ( $p_D(g)$ )	Probability of detecting infected animals on import	0 [0.5]	-
Infectious period ( $r$ )	Length of infectious period in days	15 [42]	(Carn and Kitching 1995a)
Transmission rate ( $\xi$ )	Direct transmission  Mechanical transmission via vectors	0.006  0.026 [0.013 – 0.052]	Magori-Cohen et al. (2012)

599

600

## 601 **Figure Legends**

602

603 Figure 1 The 5 steps of the risk pathway for the generic spatial risk question “What is the risk of infection of  
604 a pathogen in Area B due to the presence of that pathogen in Area A?” The term “unit” in Step 1 refers to a  
605 generic source of infection such as species, products or feed, provided that they could be in contact with  
606 native susceptible hosts.

607

608 Figure 2 The mean annual risk of infection (A) and the variance of this risk (B) are plotted in shades of  
609 purple across Europe, calculated at the country level. Countries in yellow have negligible risk due to only  
610 trading with countries that have zero prevalence, according to our prevalence data. Countries which had  
611 notified cases in 2016 are in red. Comext trade data is used.

612

613 Figure 3 The mean annual risk of infection (A) and the variance of this risk (B) are plotted in shades of  
614 purple across Europe, calculated at the regional level. Countries in yellow have negligible risk due to only  
615 trading with countries that have zero prevalence, according to our prevalence data. Countries which had  
616 notified cases in 2016 are in red. Countries in grey have insufficient data for calculating risk. Comext trade  
617 data is used.

618

619 Figure 4 The mean annual risk of infection (A) and the variance of this risk (B) are plotted in shades of  
620 purple across Europe, calculated at the individual farm level. Individual farms are only plotted if they trade  
621 with a country that has non-zero prevalence. In (C) and (D), the mean and variance, respectively, of the  
622 annual risk of infection are again plotted, but zoomed in to the areas outlined by rectangles in (A) and (B).  
623 Regions in yellow have negligible risk due to farms within those regions only trading with countries that  
624 have zero prevalence, according to our prevalence data. Countries which had notified cases in 2016 are in  
625 red. Countries in grey have insufficient data for calculating risk. TRACES trade data is used.

626

627 Figure 5 The percent that mean risk is reduced by when the probability of detection is increased from 0 to  
628 0.5 is plotted in shades of purple across Europe, calculated at the country level. Countries in yellow have  
629 negligible risk due to only trading with countries that have zero prevalence, according to our prevalence  
630 data. Countries which had notified cases in 2016 are in red. Comext trade data is used.

631

1 A generic framework for spatial quantitative risk  
2 assessments of infectious diseases: lumpy skin disease case  
3 study

4 Supplementary Material

5  
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9  
10 **Appendix A**

11 **Distributing cattle amongst regions**

12 The country trade data that we use only indicates which country is importing the cattle, and not the region  
13 within that country. This hinders us from performing risk assessment at the regional level. To estimate the  
14 distribution of cattle amongst each region given the number that enter the country, we extrapolate based  
15 on Great Britain (GB), in which we are able to access a higher resolution of data. We use the Trade Control  
16 and Expert System (TRACES) database, which collects data on trade of live animals from both within and  
17 outside Europe (TRACES 2017). Importantly, it provides detailed information, such as addresses, when the  
18 import country is the country through which you have access to the database. Therefore, we collate this  
19 data from 2012-2015 to calculate the proportion of imported animals to each region relative to the total  
20 number of imports to GB overall. We perform a generalised linear regression with a logit transformation on  
21 the number of imports into each region versus the number which are imported into all GB regions  
22 (hereafter referred to as the proportion of imports). The null hypothesis is that cattle imported to GB are  
23 randomly distributed amongst regions. We use the following predictors: the number of farms in each  
24 region, and the proportion of farms in each region which are dairy farms, both of which are accessed on a  
25 NUTS 1 level through Eurostat (Eurostat 2017). Pearson's correlation coefficient indicates no correlation  
26 between the number of farms in each region and the proportion which are dairy farms. We compare the  
27 models with each and all of the predictors using Akaike's Information Criterion (AIC) to choose the best  
28 fitting model.

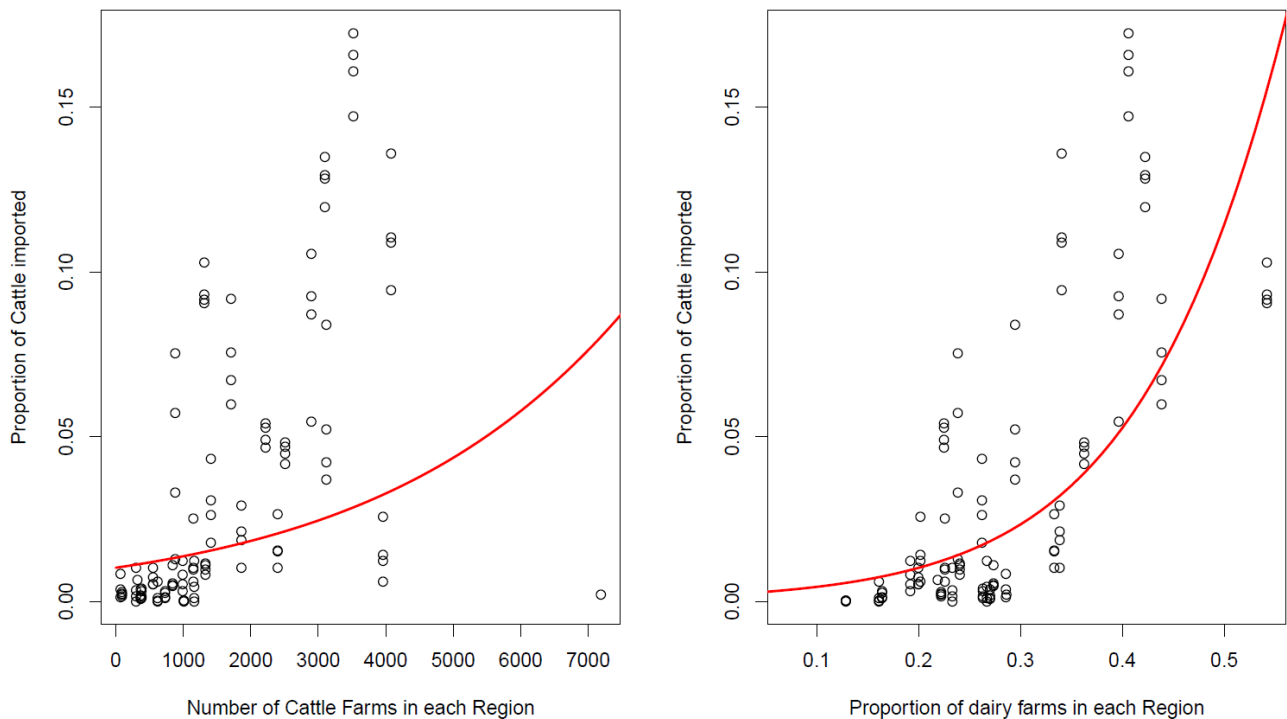
29 Including the two predictors, the number of cattle in each region and the proportion of cattle farms that  
 30 are dairy farms, as well as the interaction term is the best model by AIC to describe how imported cattle to  
 31 GB are distributed amongst regions of GB, with all coefficients statistically significant. An increase in the  
 32 proportion of dairy farms in a region always leads to an increase in imports, but this is not true for the  
 33 number of farms (Table A, Figure A 1). If the number of farms increases but none of them are dairy, imports  
 34 go down but this relationship changes when the dairy proportion increases. Regions with large numbers of  
 35 farms and high proportion of dairy farms will import the most cattle.

36

37 Table A Model results from the generalised linear model with a logit transformation. In the model,  
 38 PropImport indicates the proportion imported to each region, Farms and Dairy and the number of farms  
 39 and the proportion of dairy farms in each region, respectively. \*\*\* indicates a p-value less than 0.001.

Model: $\text{PropImport} \sim \text{logit}(\beta_0 + \beta_1 * \text{Farms} + \beta_2 * \text{Dairy} + \beta_3 * \text{Farms} * \text{Dairy})$			
Variable	Estimate	Std. Error	P-value
Intercept ( $\beta_0$ )	-5.61	$2.23 \times 10^{-2}$	***
Farms ( $\beta_1$ )	$-3.52 \times 10^{-4}$	$1.15 \times 10^{-5}$	***
Dairy ( $\beta_2$ )	3.87	$6.94 \times 10^{-2}$	***
Farms*Dairy ( $\beta_3$ )	$2.44 \times 10^{-3}$	$3.54 \times 10^{-5}$	***

40



41

42 Figure A 1 The proportion of cattle imported in to each region plotted against each predictor. The curve of  
 43 best fit is plotted in red against each predictor while the other predictor is held at its mean value.



44

45

46 Now we have this model for how to distribute cattle amongst regions for GB, we use it to estimate the  
47 proportion of imports into each region of each country across Europe in 2016. To calculate the predicted  
48 proportion, we input the number of cattle farms and the proportion of dairy farms for each region in each  
49 country and then normalise the predicted proportions, as the sum of all the regional predicted proportions  
50 of a country should sum to 1. We then multiply each proportion by the total number of imports to the  
51 country to get the number of imports to each region. Finally, we round these numbers off to the nearest  
52 integer for whole animals, ensuring that the total is still equal to the total imported to the country as a  
53 whole.

54

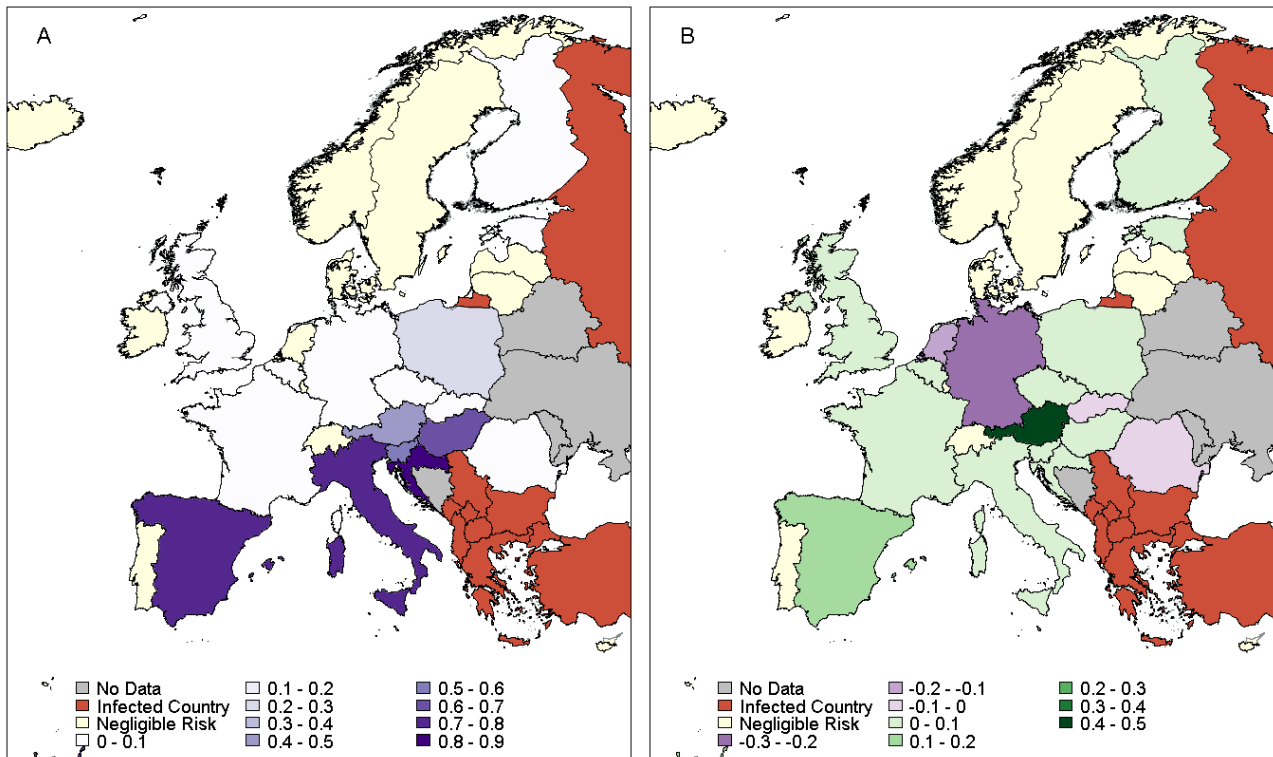
## 55 **Appendix B**

### 56 **Comparing Data Sources**

57 The trade data that we use in the main text to compute country and regional risk is COMEXT, a source of  
58 freely available trade data listing all products traded between countries in 2016. However, we also had  
59 access to the TRACES data, a primarily EU-based trade system, which provided us with data on all cattle  
60 traded in 2016 to the EU, including the postcode of the final destination. We used this for our calculation of  
61 risk at the individual farm level. However, as these are different data sources, it is not clear how accurately  
62 they match up and whether they would lead to very similar results. We consolidate the TRACES data into  
63 the total imports into each country as a whole in order to compute the risk assessment at a country level  
64 with TRACES data (Figure B 1A). This can then be compared with the risk assessment using the COMEXT  
65 data (Figure 2) to produce Figure B1B.

66 Figure 4 and Figure B 1 demonstrate the presence of data in the TRACES (postcode) data that is not in the  
67 COMEXT (country) data. In particular, some countries now have a risk estimate whereas in the COMEXT risk  
68 map they were recorded as having negligible risk due to not trading with any infected partner. Mostly this  
69 arises from a single farm (see Figure 4, e.g. France, UK, Finland). However, the most notable country that  
70 changes from negligible risk is Austria, with a probability of infection now of 0.45. Other countries also have  
71 higher probabilities, most notably Spain, while Germany's risk estimate is significantly smaller. The  
72 Netherlands has negligible risk according to the TRACES data whereas COMEXT predicts a probability of  
73 infection in the range 0.1-0.2.

74 Clearly, there are differences between the two different data sources in terms of how much trade occurs  
 75 with partner countries. However, looking at the level of risk throughout Europe overall, both datasets  
 76 predict a very similar ordering of countries with the highest risk. Both outline Croatia as the only country in  
 77 the highest risk bracket, with Italy, Hungary and Spain having the next highest risks. It is not possible to  
 78 determine which of the two data sources is more reliable. We choose to focus on the COMEXT dataset in  
 79 the main text due to its freely available nature, with the use of TRACES restricted to when we have no other  
 80 dataset available at that resolution.



81

82 Figure B 1 In (A) the mean annual risk of infection is plotted in shades of purple across Europe, calculated  
 83 at the country level, when the trade data is from TRACES. In (B) the difference between the mean risks  
 84 calculated using TRACES (Figure B1A) or COMEXT data (Figure 2A) is plotted across Europe. Positive values  
 85 (in green) indicate TRACES predicts a higher risk. Negative values (purple) indicate COMEXT predicts a  
 86 higher risk. Countries in yellow have negligible risk due to only trading with countries that have zero  
 87 prevalence, according to our prevalence data. Countries which had notified cases in 2016 are in red.  
 88 Countries in grey have insufficient data for calculating risk.

89

## 90 References

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