Foresight

Infectious Diseases: preparing for the future

OFFICE OF SCIENCE AND INNOVATION

T8.6: Future Risks of Foot and Mouth Disease Spread in the UK

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Abstract:

Foot and Mouth Disease (FMD) is a significant hazard to UK agriculture. The 2001 epidemic led to the loss of six million animals. This report models future FMD risk for the UK. It takes account of the trend towards fewer but bigger cattle and pig farms with little change in the number of sheep farms. It is found that the decreasing number of farms and the increasing number of livestock on the remaining farms approximately cancel each other out. Hence, ignoring other confounding factors, the risk of a foot and mouth outbreak is predicted to be similar in 2015 to the risk today. However, it is possible that the risk of disease transmission will increase in some areas such as Cornwall and East Anglia. In addition, it is possible that an alternative strain of the disease will be more damaging than the type seen in 2001 and in earlier epidemics.

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Future risks associated with FMD spread

This project looks at the likely risks associated with a foot-and-mouth disease (FMD) epidemic in the near future, focusing on 2015 as a case study. The FMD epidemic of 2001 was a huge blow to the farming industry, leading to the loss of over 6 million livestock. During and since 2001, a variety of models have been used to assess the optimal use of control strategies for combating future FMD epidemics (Keeling 2005). However, none of these approaches considered the impact of the changing farming landscape. Here we use current trends in the farming industry (generally characterised by a reduction in the number of farms, but an increase in the number of livestock per farm) to create a plausible landscape for 2015. This environment is used as the susceptible population through which a future FMD epidemic can spread. Using the parameters from 2001, we estimate the number of secondary cases per index case in this new landscape and compare these with the predictions from 2001.

1. Projecting livestock distributions for Great Britain

Constructing a risk map of the likely impact of future FMD epidemics requires forecasts of future animal distributions, and how the number of livestock farms and associated holding sizes would change. A dataset of animal distributions in June 2000 was compiled as part of a Wellcome Trust project on FMD by the University of Edinburgh. This was developed using data from the June 2000 agricultural census (DEFRA 2005), which includes details of the numbers of animals of different species on each holding as well as co-ordinates for the principal building for each farm holding.

The dataset records 139,204 livestock farms in England, Scotland and Wales, with a total of 39,580,902 sheep, 9,501,222 cattle and 6,317,457 pigs. These data were used as the baseline for the forecasts and provide the landscape on which models of the 2001 epidemic are simulated.

The UN Food and Agriculture Organisation (FAO) has compiled projections of animal numbers for 2015 and 2030 (FAO 2003). These were not figures for individual countries, so the figures for industrialised economies were used to calculate a change of –2.2% in cattle numbers, +2.5% in sheep numbers and +2.38% in pig numbers between 1999 and 2015. These estimates were then used to project the total number of animals in the UK in 2015. The FAO (2003) report used to project animal numbers did not make projections of changes in numbers of holdings, and no publications could be found with these details. Additionally, there are no published forecasts of how animal distributions will change across the UK, so forecasts were made non-spatially by calculating overall figures for the UK and then applying these figures uniformly to the UK.

In order to forecast the change in the number of holdings stocking a particular species, historical data from the agricultural census were plotted and the trends extrapolated to 2015. Data for England were available for 1990, 1995 and 2000, after which time an annual census was taken (DEFRA 2005).

However, data for 2001, 2002 and 2003 showed a marked, short-term effect of the 2001 FMD outbreak, so only the data from 2004 could be used. These trends were extrapolated to 2015 and the analyses are presented in Figure 1; projected animal numbers are in Table 1.

***Figure 1**: Trends in sheep, cattle and pig numbers using data for England from the UK Agricultural census, extrapolated to 2015.*

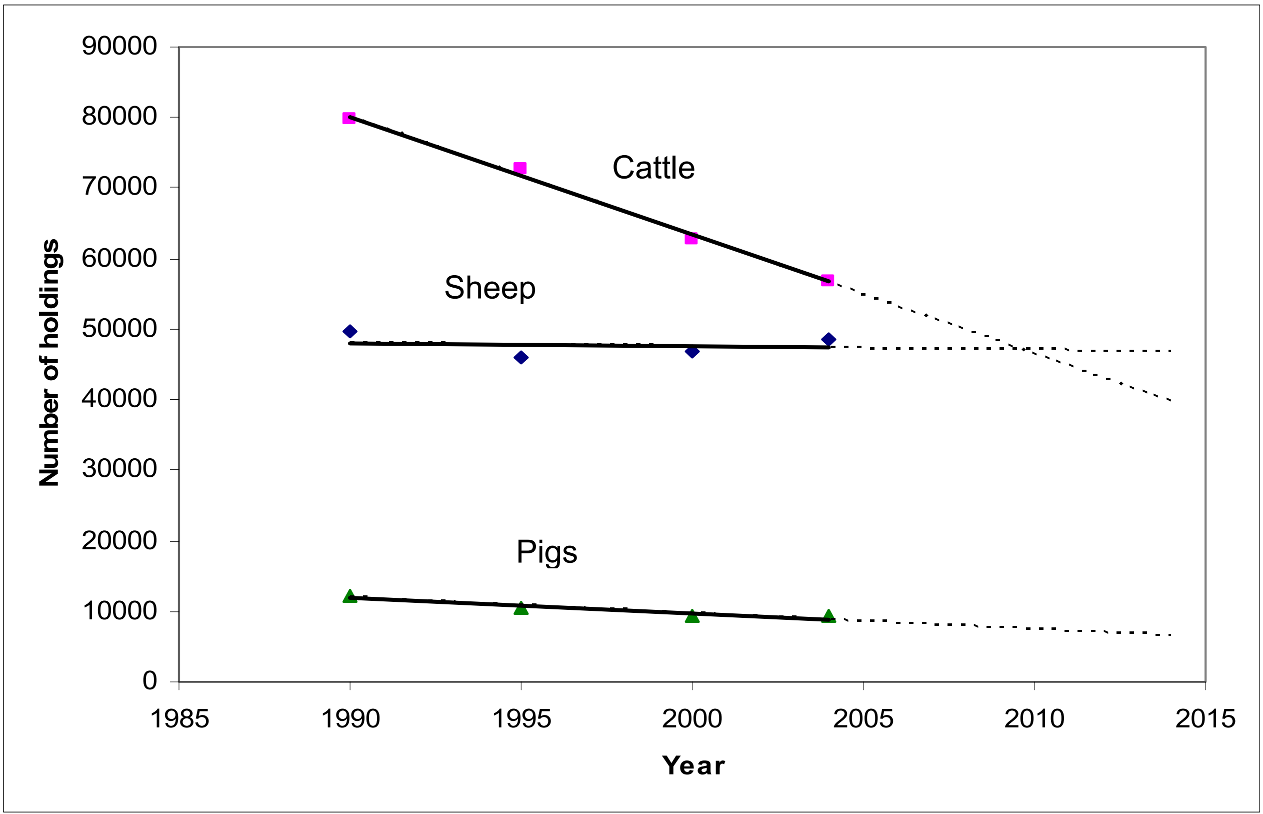

Table 1: Numbers of animals and numbers of holdings in 2000 and projections to 2015

	Animal numbers			Holdings			Animals per holding		
	2000	2015	% change	2000	2015	% change	2000	2015	% change
Sheep	39,580,902	40,570,425	+2.5	82,786	82,774	0	478.1	490.1	+2.51
Cattle	9,501,222	9,296,946	–2.2	94,712	57,626	–39.2	100.3	161.3	+60.8
Pigs	6,317,475	6,467,831	+2.4	12,063	8,271	–31.4	523.7	782.0	+49.3

These projections show that, for cattle and pigs, there will be a substantial reduction in the numbers of holdings stocking these species. However, there will be a large increase in the numbers of animals on the remaining holdings.

Using the projections for the percentage change in the numbers of holdings in Table 1, 60.8% of farms with cattle and 68.6% of farms with pigs were randomly sampled. Due to the large numbers of holdings, multiple sampling would not make a marked difference in the geographical distribution of livestock, therefore only one sample was taken. The numbers of animals on farms sampled were adjusted using the data in the final column of Table 1. Farms not sampled were adjusted to have no animals of that species. The sampling was such that, if a farm was a mixed sheep, cattle and pig farm in 2000, it may, for instance, keep its sheep and pigs but not its cattle. The resulting change in animal distributions is an increase in very large cattle and pig holdings and a decrease in the number of small and medium-sized farms. The projections suggest little change in the distribution of sheep. The changes in the distributions of large holdings are illustrated in Figures 2–4.

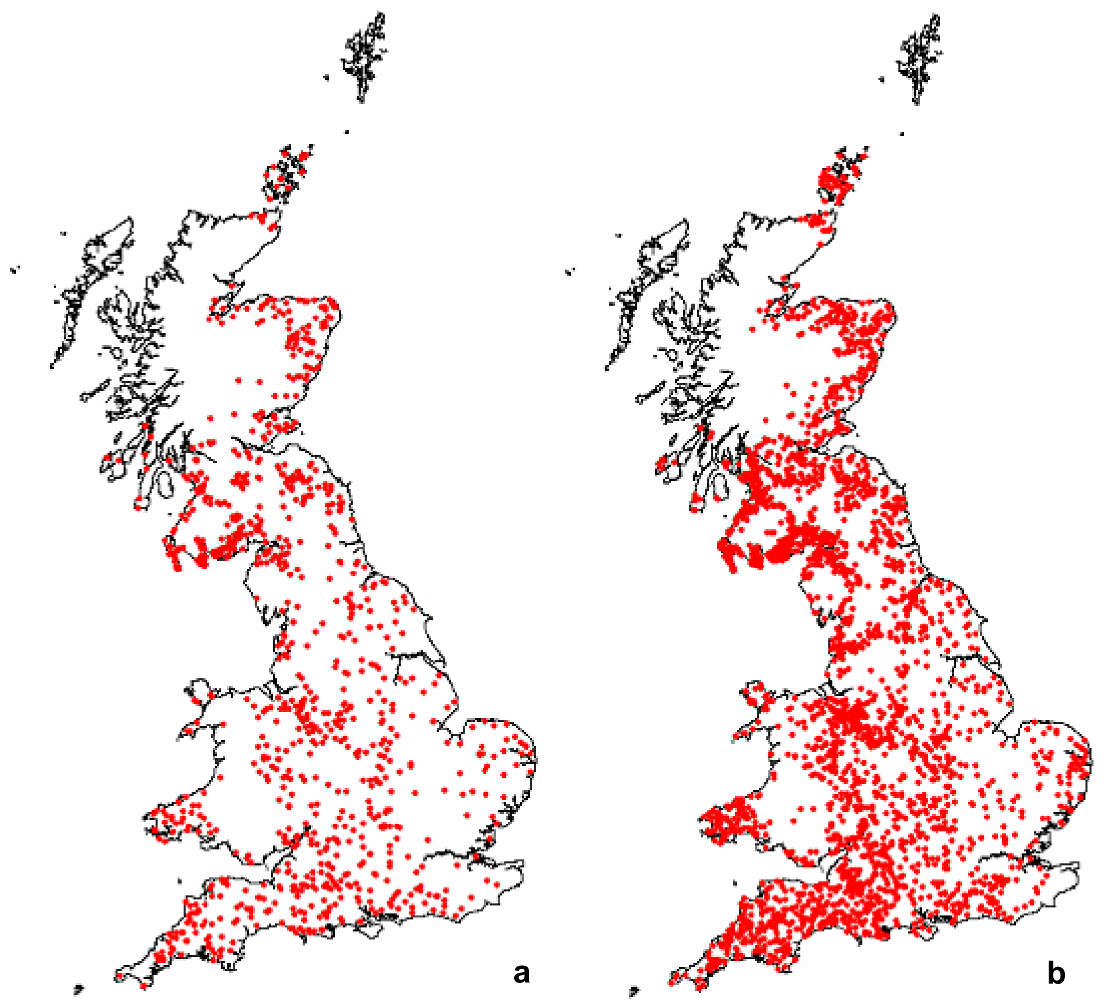

Figure 2: ***(a)*** *The largest 1% of cattle farms (this is 924 farms with >524 head of cattle) in June 2000.* ***(b)*** *Projected distribution of 2,636 farms with >524 head of cattle in 2015.*

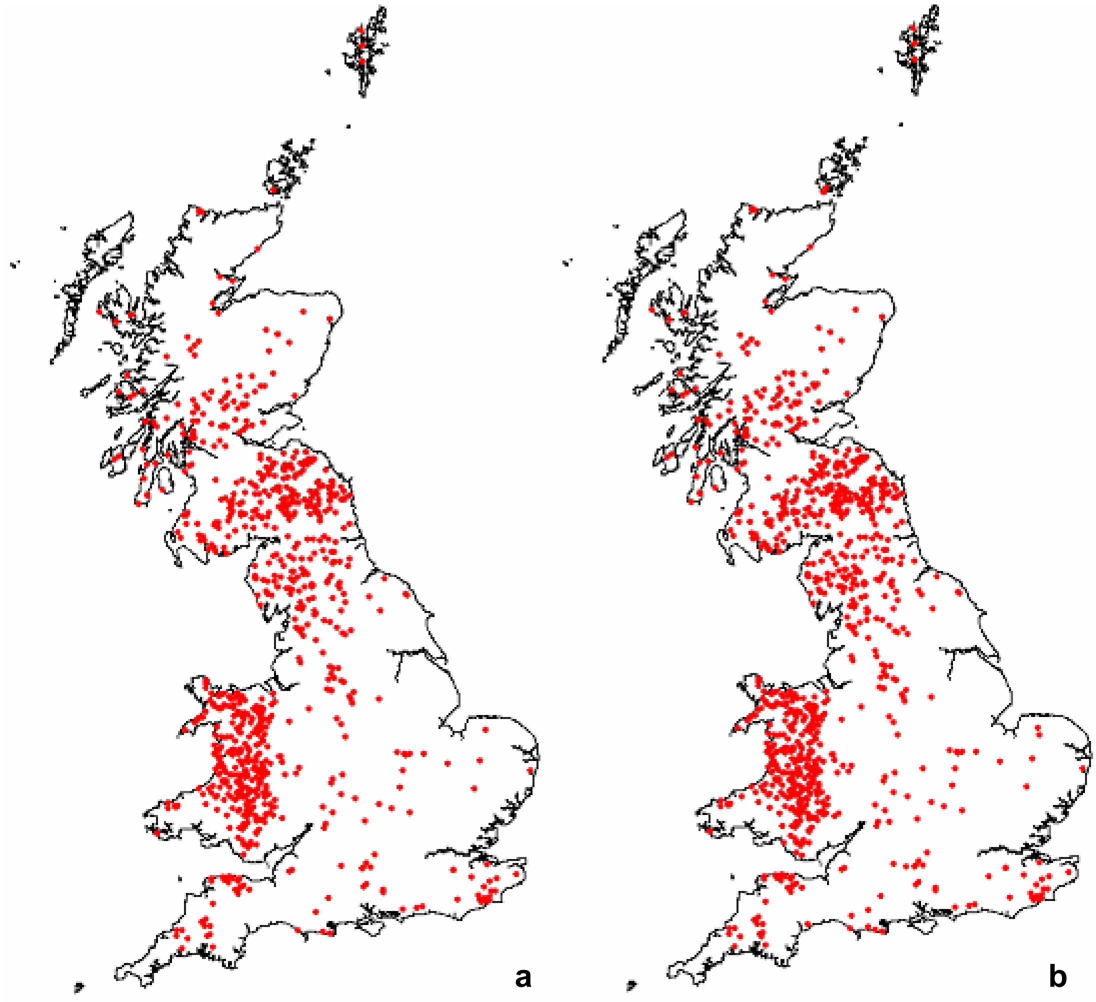

***Figure 3**: (**a**) The largest 1% of sheep farms (this is 828 farms with >3,497 head of sheep) in June 2000. (**b**) Projected distribution of 901 farms with >3,497 head of sheep in 2015.*

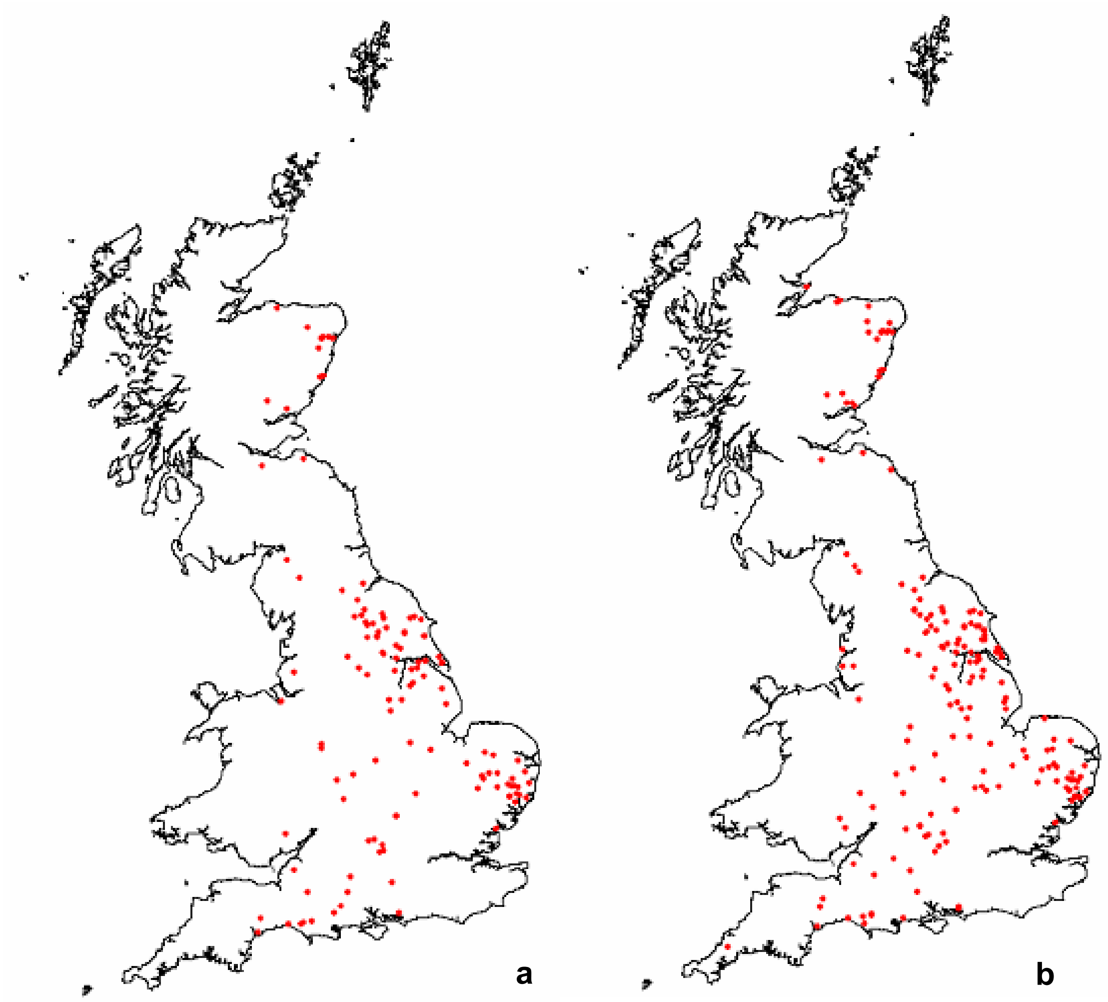

***Figure 4**: (**a**) The largest 1% of pig farms (this is 121 farms with >6,298 head of pigs) in June 2000. (**b**) Projected distribution of 182 farms with >6,298 head of pigs in 2015.*

2. Dissemination from an initial source

We are now in a position to utilise the type of model exploited for modelling the 2001 FMD epidemic to ascertain the expected number of secondary cases for every possible primary case. The probability that farm *j* is a secondary case, given that farm *i* is the primary case is given by:

$$P_{ij} = 1 - \exp\left(-pS_jT_iK(d_{ij})\right)$$

where d_{ij} is the distance between farms *i* and *j*, *K* is the transmission kernel (which measures how infection risk decreases with distance and is estimated from the 2001 data after movement restrictions were enforced – early in 2001, long-range movements through markets dominated the spatial dynamics but these were soon curtailed to prevent wider dissemination of infection), *p* is the duration of the infectious period in days, and S_j and T_i are the susceptibility and transmissibility of farms *i* and *j* based on their number of livestock:

$$S_j = \sum_{species} s_{species} n_{j,species} \qquad T_i = \sum_{species} t_{species} n_{i,species}$$

where *s* and *t* refer to the susceptibility and transmissibility per animal (taking into account farming practices) and *n* refers to the number of animals of a given type on a given farm (Keeling et al. 2001). Thus, farms with a greater number of animals are both at more risk of contracting the disease and more risk of subsequently spreading infection.

The expected number of secondary cases caused by primary infection of farm *i* (known as the reproductive ratio) is therefore:

$$R_i = \sum_j P_{ij}$$

This parameter *R* encompasses both the heterogeneity of farms (in terms of their livestock number and composition) and the heterogeneity of the landscape in terms of the distribution of farms.

We can now use *R* to study the relative spatial dynamics of FMD, comparing 2001 with our predictions for 2015. If *R* is >1, then in the first generation a primary case will produce more than one secondary case; therefore, if these secondary cases also have *R*-values of >1, the epidemic will grow. In contrast, if *R* is <1, it is likely that the epidemic will fail. Thus, analysis of a map of average *R*-values aggregated from the farm-level calculations can inform us about those regions of the country where an epidemic is likely to succeed or fail (Figure 5).

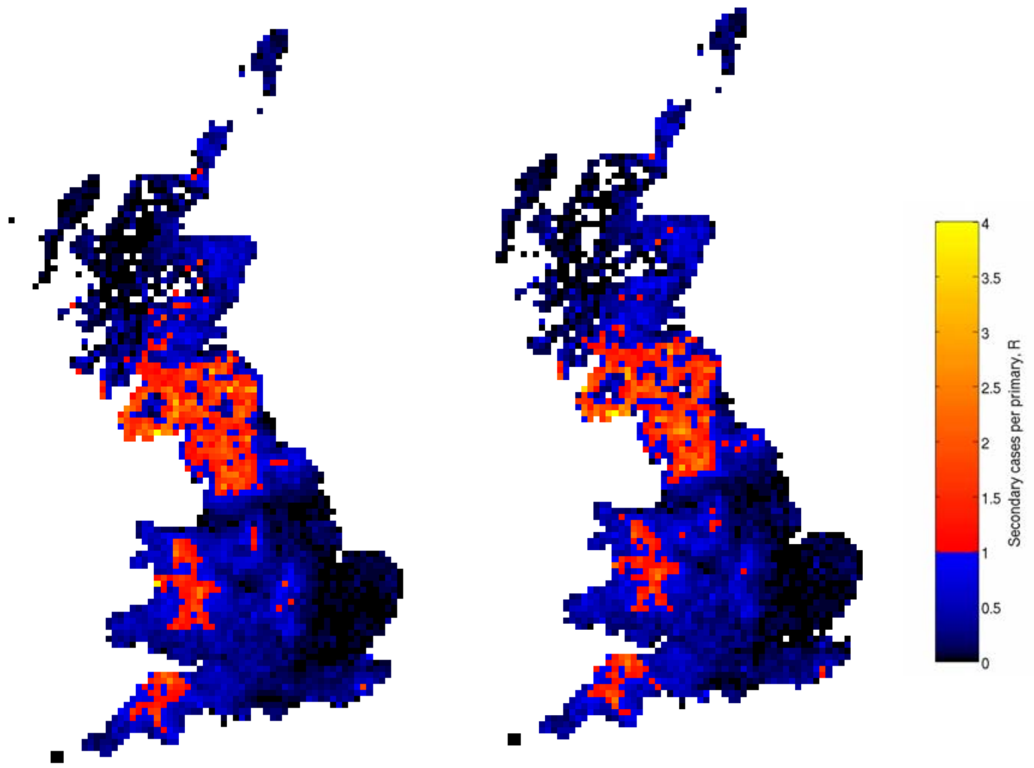

Figure 5: *Average R values from individual-based farm-level analysis aggregated into 10km $\times$ 10km squares for 2001 (**a**) and 2015 (**b**). Average values of R of <1 are shaded black–blue, values of >1 are shaded red–yellow.*

It is clear from Figure 5, that, using our simple characteristic of transmission potential, by 2015 the risk associated with FMD is much the same as for 2001 despite the changes to the farming landscape. Why is there so little change in the potential for an FMD outbreak? Although we predict that there will be a significant decrease in the number of farms in the UK, there will be relatively little change in the total density of livestock across the whole of the UK. Therefore, because the transmission kernel decays rapidly with distance ($K(d) \propto d^{-2}$), the effect of the increasing separation between farms cancels out the increase in the average farm size.

To further understand the predicted change in the farming landscape, we consider the ratio of the average *R*-values in each 10km square for 2001 and 2015. Here, regions of increased *R* are colour-coded red–yellow, with areas of decrease *R* colour-coded black–blue.

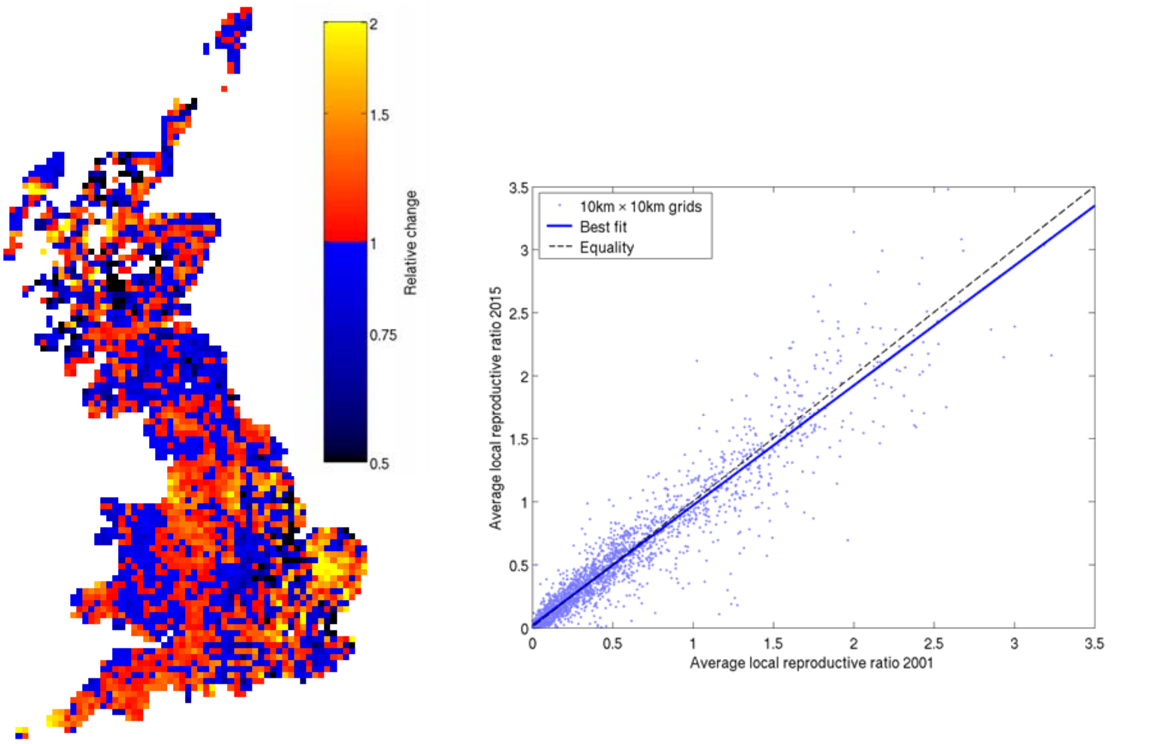

***Figure 6**: Detailed comparison between the R-values predicted for 2001 and 2015. (**a**) Map of relative R-values showing regions of increased (red-yellow) and decreased (black-blue) risk. (**b**) Plot of individual R-values at each location, showing a predicted slight decrease.*

From Figure 6 we observe that, in general, the pattern of change is fairly randomised, although East Anglia and Cornwall see a systematic increase in *R*-values; in these regions *R* has moved from well below 1 to close to 1. Although this trend may be of concern if it continues past 2015, the predicted values of *R* in these regions are still too low to cause concern.

Finally, to account for the local transmission of infection, we calculate the number of tertiary (rather than secondary) cases. This additional, computationally intensive, calculation allows us to estimate the effects of local spatial saturation that may act to reduce transmission, and the compounding effects of heterogeneity which may act to increase transmission. The expected number of tertiary cases is defined as:

$$R_i^2 = \sum_j (1 - P_{ij}) \left[1 - \prod_{k \neq i, j} (1 - P_{ik} + P_{ik}(1 - P_{kj})) \right]$$

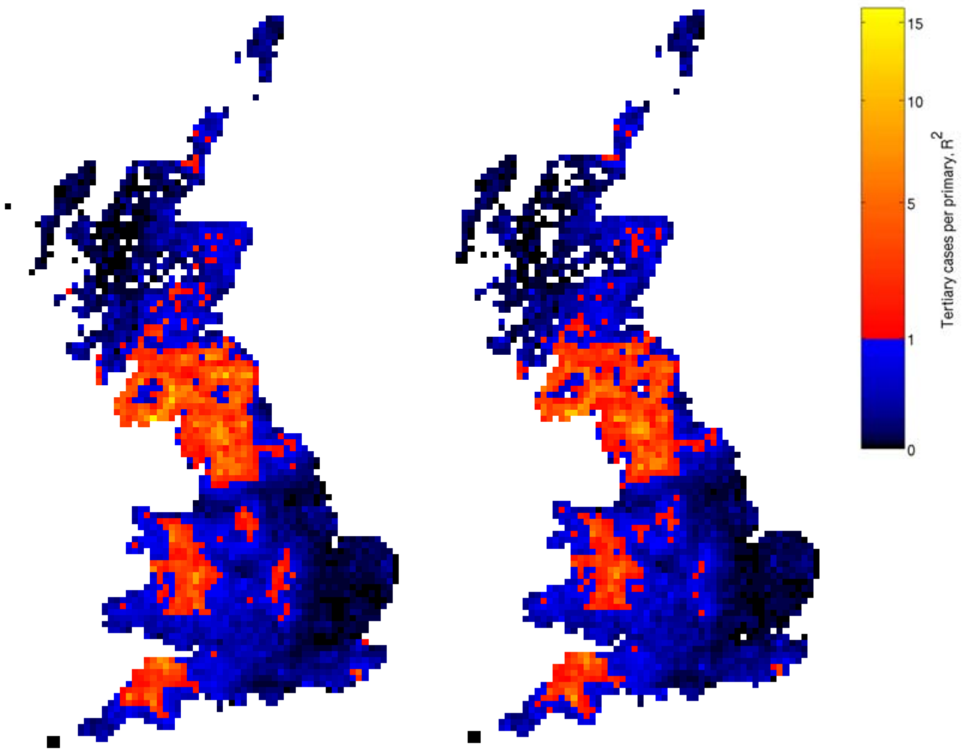

Figure 7*: Average number of tertiary cases per primary case, R^2, in 10km $\times$ 10km squares for 2001 (**a**) and 2015 (**b**). Average values of R^2 of <1 are shaded black–blue, values of >1 are shaded red–yellow. The shading scale used square roots to the value to obtain a better match to the standard reproductive ratio.*

The tertiary cases show a similar pattern to the secondary cases (Figure 7) and, again, the difference between 2001 and 2015 is minimal. Thus, we can conclude that at least the first two epidemic generations in 2015 would follow a similar pattern to those predicted for 2001.

3. Discussion

Our results clearly show that a continued decrease in the number of farms and an increase in the number of animals per farm will have little impact on the risk of FMD spread. This is presumably due to the conserved nature of the livestock density and the form of the transmission relationship. However, there are several factors that may impinge on the accuracy of this prediction:

1. Throughout the calculations of disease spread we have used the transmission, susceptibility and kernel parameters derived from the 2001 epidemic. While this approach provides our best guide to the behaviour of FMD within the UK, it should be realised that there may be considerable variation in parameters between strains. In addition, with a change in the farming landscape the transmission kernel may also vary. For example, the distance between nearest farms may be a determining factor that will change as the number of farms decreases.

This change in kernel would be particularly evident during the ‘silent spread’ phase before the epidemic is detected and when movement of animals is unrestricted. Therefore, while these simulation results provide a best estimate, there are numerous uncertainties involved in extrapolating our knowledge of the 2001 epidemic to 2015.

2. Our equation for the susceptibility and transmissibility of a farm is proportional to the number of livestock. In practice, this simple linear relationship is unlikely to hold. Indeed, ongoing research indicates that a saturating power law (with an exponent of <1) is a better approximation. However, for the predicted farming landscape of 2015, a linear relationship provides a more pessimistic picture and thus acts as an upper bound to the associated risk.

3. Finally, we used the number of secondary cases per farm averaged over 10km squares as our measure of risk of spread. In practice, we are really concerned with accessing the risk associated with large epidemics, for which the number of secondary cases is a crude surrogate. In addition, taking a simple average value (within each 10km square) does not fully represent the nature of the infection process or the need to be risk-averse. Calculating the number of tertiary cases goes some way to accounting for the biases, although there is still the issue over using a simple average. Only multiple, comprehensive simulations of the entire epidemic process, starting with each possible source farm, can provide the level of detail needed. However, the computational demands of such simulations are beyond the scope of this project, and the associated results would be difficult to display in a simple format.

References

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