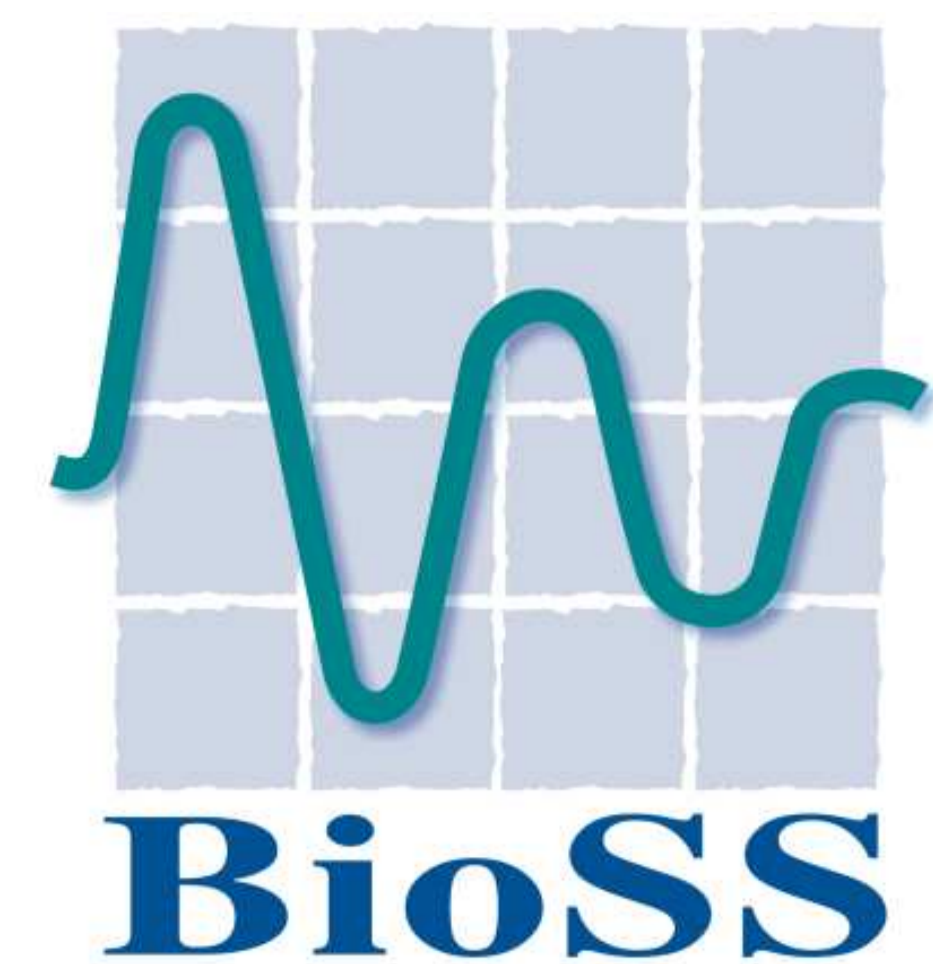


# Statistical analysis of abattoir condemnation figures: generating extra value from administrative data

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## Introduction

Liver fluke is a serious disease of cattle and sheep throughout the world. The fluke which is most common in Scotland (*Fasciola hepatica*) requires damp and warm conditions in order to infect new hosts.

Around 25% of cattle livers are condemned in Scottish slaughterhouses because of pathological changes caused by the presence of liver fluke. Infection imposes welfare costs on the animal and economic costs on the farmer. Infected animals are appreciably less productive. Climate change is expected to increase the numbers of animals affected with liver fluke in Scotland, affecting the viability of livestock enterprises. Parasite resistance to anthelmintic treatment is likely to become more problematic.



Life cycle of *Fasciola hepatica* liver fluke. Mud snail and *Fasciola hepatica* adult showing internal organs.

## Methods

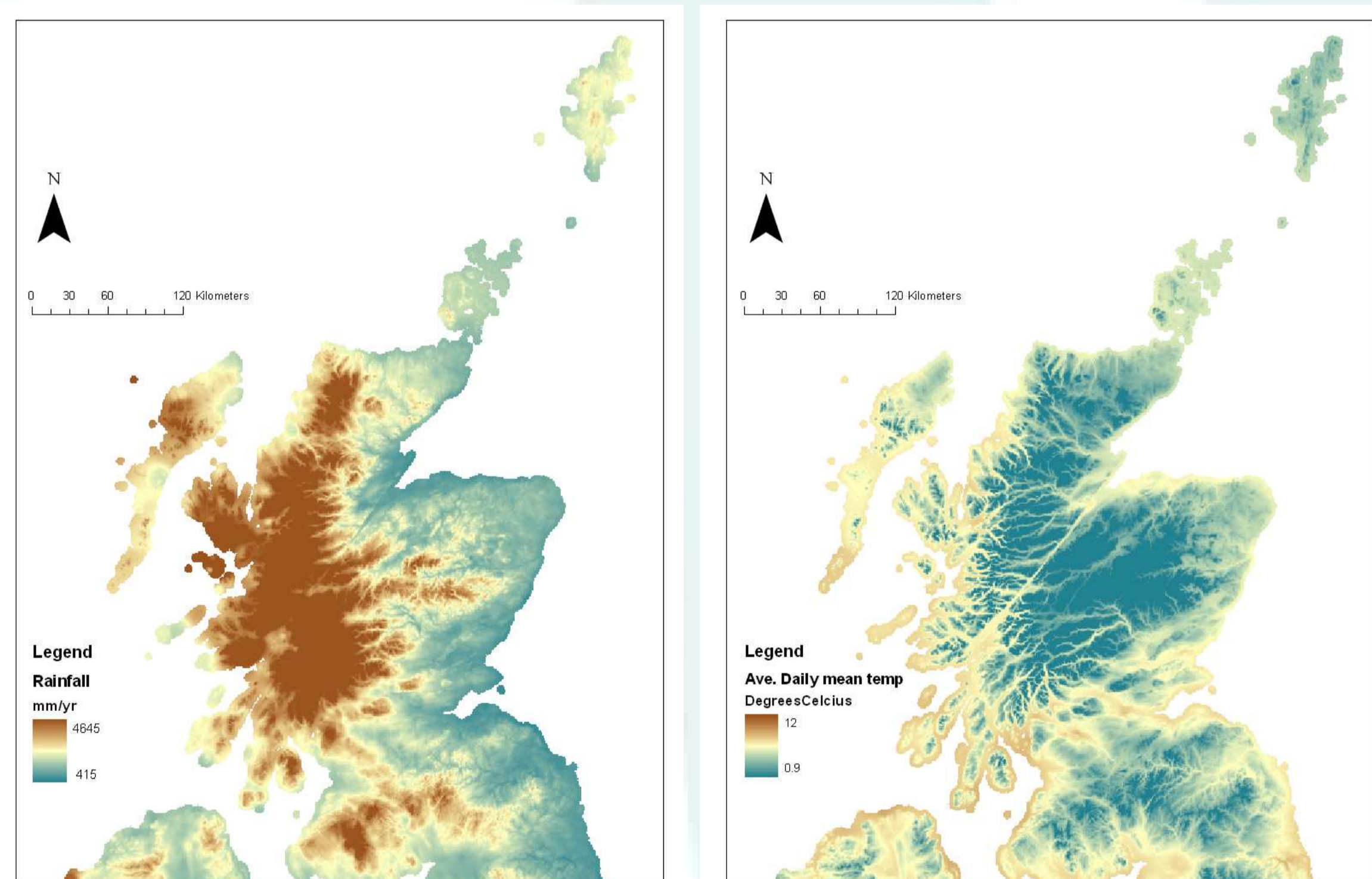
Data for cattle slaughtered at the Dingwall abattoir were available. These gave animal id, whether or not the liver was condemned, age and sex. The UK cattle movement database was used to identify the movement-history for each animal, locating where, when and for how long it had stayed on different farms. A statistical model was developed that allowed us to estimate the risk associated with spending time on each of the farms represented in the data. Essentially the model fits a conditional spatial autoregressive random effect to the risk on each farm, weighted by the number of “risk days” that an animal has stayed on that farm. The model is presented below.

$$\sum \beta_j x_{ij} + \ln(\sum \gamma_k W_{ik}) = \ln(-\ln(1 - p_i))$$

We use a complementary-log-log link;  $\beta$  represents the fixed animal level covariates, whilst  $\gamma$  represents the random conditional autoregressive farm-level coefficients. These latter are then weighted by the number or “risk days”,  $W_{ik}$ . In addition the model can adjust for animal-specific information such as age, farm specific factors and regional characteristics such as mean temperature.

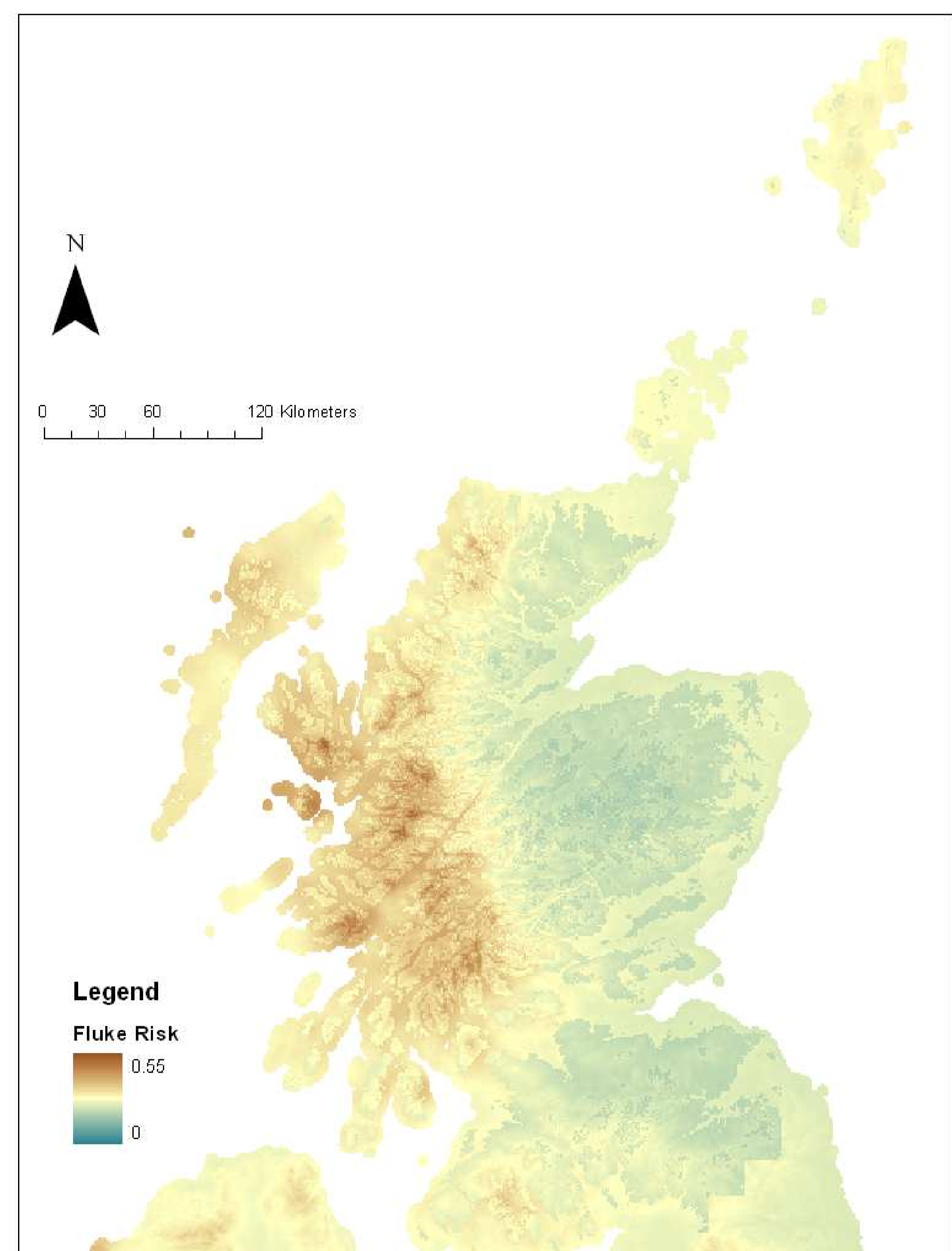
## Results

The model associates fluke infestation with animals spending time on farms that have high average temperatures and/or rainfall. In general, the analysis predicts that risk from liver fluke is higher in the West of Scotland.



Maps of rainfall and temperature over the whole of Scotland as used to predict risk.

Since we are calculating estimates for each farm individually we can examine the unexplained risk associated with each farm. There are marked differences between farms even in the same geographical area (not shown). We can only investigate this local between-farm variability because data from a large number of farms are available.



Predicted risk over the whole of Scotland.

## Conclusions

Liver fluke is typically more common in warm and wet areas. This is reflected in a higher estimated mean infection risk for the West of Scotland. Global warming is likely to increase the severity of the risk across this area, and to expand the “at risk” region. The modeling approach allows regional characteristics to be considered, creating potential for the development and use of predictive models, generating risk maps for liver fluke under different climate projections.

The model utilises only data that is already collected, and should not represent an increase in effort or cost of data collection. The use of sophisticated statistical techniques to combine information from different datasets has allowed us to produce new industry-relevant hazard maps. Environmental change is likely to increase the economic impact of liver fluke in Scotland. Predictive hazard maps will help in the development of mitigation strategies. A plausible strategy to slow the development of resistance to anthelmintic drugs is the restriction of their use to higher-risk areas. Our modeling approach offers a cost-effective way to generate the evidence base for such policies.

## Acknowledgements



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