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Can Ingoing Contact Chains and other cattle movement network metrics help predict herd-level bovine tuberculosis in Irish cattle herds?

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ABSTRACT

We used logistic regression to investigate whether the risk of an Irish cattle herd undergoing a bovine tuberculosis (bTB) breakdown increased with the size of the Ingoing Contact Chain (ICC) of previous herd to herd cattle movements, in a sequence up to eight moves back from the most recent, direct, movement into the herd. We further examined whether taking into account the bTB test history of each herd in the chain would improve model fit. We found that measures of cattle movements directly into the herd were risk factors for subsequent bTB restrictions, and the number of herds that animals were coming from was the most important of these. However, in contrast to a previous study in Great Britain, the ICC herd count at steps more remote than direct movements into the herd did not result in better fitting models than restricting the count to direct movements. Restricting the ICC counts to herds which had previously or would in the future test positive for bTB resulted in improved model fits, but this was not the case if only the previous test status was considered. This suggests that in many cases bTB infected animals are moving out of herds before being identified through testing, and that risk-based trading approaches should not rely solely on the previous test history of source herds as a proxy for future risk. Model fit was also improved by the inclusion of variables measuring bTB history of the herd, bTB in neighbouring herds, herd size, herd type, the movement network measures “in strength” and “betweenness”, altitude, modelled badger abundance and county. Rainfall was not a good predictor. The most influential measures of bTB in nearby herds (a proxy for neighbourhood infection) were the proportion of herds with a history of bTB whose centroids were within 6 km, or whose boundaries were within 4 km, of the index herd. As well as informing national control and surveillance measures, our models can be used to identify areas where bTB rates are anomalously high, to prompt further investigation in these areas.

1. Introduction

Bovine tuberculosis (bTB) is endemic amongst the cattle population in the UK and The Republic of Ireland (henceforth “Ireland”), both of which have bTB eradication programmes; all herds are tested on an annual basis and, if they test positive, are put under “restriction”, i.e. prevented from selling or otherwise moving animals out to other herds, until further testing indicates they are likely to be clear of the disease (Sheridan et al., 2014; Allen et al., 2018; More, 2019). In both countries, mechanisms of transmission of infection to a herd are believed to include contact between cattle from other herds, both across farm boundaries and from movement between herds, contact with infected wildlife

populations, especially badgers (*Meles meles*), and, possibly, exposure to the main causative organism, *Mycobacterium bovis*, residing in the wider environment (More and Good, 2015; Broughan et al., 2016). However, the relative contribution of each of these factors is poorly understood and may vary from location to location.

Many studies have shown an association between inward cattle movements and bTB risk in Irish herds (Clegg et al., 2008, 2015; White et al., 2013; Byrne et al., 2020). One approach used to investigate this in Ireland (Clegg et al., 2008, 2015) has been to identify cases where herd breakdowns (the period during which herds test positive) could reasonably be attributed to the introduction of an infected animal from another herd; they looked for animals which tested positive at the initial

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breakdown which had i) been introduced into the herd at some time after the most-recent, clear (i.e. negative) full-herd test and ii) had moved from a herd where subsequent herd-level testing suggested it may have been exposed to bTB.

However, there are problems with this approach. On the one hand, ‘potential for exposure’ is assumed to correspond to being infected, which is unlikely always to be the case, potentially leading to over-estimation of risk. Conversely, the potential for residual infection through animals infected at the time of introduction but subsequently passing the first full-herd test (Wolfe et al., 2009; More, 2019) is not taken into account, potentially leading to an underestimate of risk. In Ireland, any herd that is not currently under restriction for bTB is typically tested only once per annum, using the Single Intradermal Comparative Cervical Tuberculin (SICCT) test, known as the “CITT” under Commission Delegated Regulation (EU) 2020/689, thus offering the potential for infected animals to move out of a herd before being discovered. Furthermore, depending on the stage of infection, a large proportion of infected cattle may test negative on the SICCT (Clegg et al., 2011; Nuñez-García et al., 2018) and indeed a significant number of bTB infected animals end their lives without ever having tested positive (Frankena et al., 2007; Conlan et al., 2012).

In addition, infected animals that test positive may do so in a different herd to the one where they acquired infection, whether because they were a false test-negative in that herd or because they moved herds between becoming infected and being tested. In either case, it is often not possible to be confident of the direction of transmission: whether an introduced animal passed the infection to animals already present within the herd, or vice versa. Once an animal does test positive it is sent to slaughter, so the effect of introducing a known infected animal to a naïve herd cannot be studied. As a result, it is usually not possible to be certain if, when, and from where, bTB was brought into a herd through cattle trading.

Another approach, different to querying the movements and infection status of individual animals, is to examine the strength of association between a herd’s bTB status and metrics of movement into it, such as the number of animals introduced over a certain period. Such approaches have proved informative both in Ireland (e.g. Byrne et al., 2020) and elsewhere (e.g. Ribeiro-Lima et al., 2015; Palisson et al., 2016; Pozo et al., 2019). A limitation of studies adopting such an approach has been that they have generally not taken into account the fact that some moves carry more risk than others because some selling herds are themselves more likely to host a bTB infection. To address this, Fielding et al. (2019), working on bTB transmission in Great Britain (GB), used a network-derived metric, the in-going contact chain (ICC), to take account not only of direct movement into a herd but also previous indirect movements through other herds. They further refined this approach by taking into account whether herds which occurred previously in the chain were located in areas identified as of high, medium or low risk for bTB and found that connections to more farms in the England High-Risk Area up to three movements away from the root farm increased the odds of a bTB incident, while connections with more herds in the England Low-Risk Area up to eight movements away decreased the odds.

The aim of our study is to expand on the approach adopted by Fielding et al. (2019), henceforth referred to as “the GB study”, using a logistic regression model to examine how movement network metrics such as ICCs relate to herd-level bTB status in Ireland, and whether an improved model, more suited to Ireland, can be produced. As part of this process, we used three exogenous inputs not considered in the GB study: rainfall, altitude and, using the output produced by Byrne et al. (2014a), the estimated probability of the presence of a badger social group. To our knowledge ours is the first study to examine the relationship of any of these three drivers on herd-level bTB incidence across all of Ireland. We included rainfall and altitude as one might expect that survival of *M. bovis* in the farm environment might vary with these two factors. Furthermore, Jin et al. (2013) found a positive association between

rainfall and bTB incidence across 2666 herds in Wicklow but did not test whether this relationship might be driven by a positive association between rainfall and altitude. We included the badger metric as badgers play a role in the epidemiology of bTB in Irish cattle (Ní Bhuachalla et al., 2015), and localized studies in Ireland have found associations between estimated measures of badger abundance and bTB in cattle (Olea-Poppelka et al., 2006; Byrne et al., 2014b), although Madden et al. (2021) used a metric derived from the badger data in a grid based spatial analysis on bTB incidence across Ireland, finding no significant association. Ours is also the first bTB study to examine differences in infection risk between three types of beef production common in Ireland; suckler (where beef calves are born into the herd), fattener (where animals are bought in to be fattened relatively late in their life, and then sent to slaughter), and stores (where animals are brought into the herd when young, reared for some time, and then sold on or sent to slaughter).

2. Methods

In the foregoing text we firstly describe the data used in the analysis in two sections: i) “data sources”, where we describe where each of the data sets came from and what processing we conducted on it to allow it to be used to calculate variables for each herd, and ii) “variables used in the analysis”, where we list each of the variables used as inputs to the models.

2.1. Data sources

- **bTB data.** The bTB test history of each herd in Ireland, comprising results of the SICCT, gamma interferon tests and slaughterhouse inspections, was obtained from the national database (the Animal Health Computer System (AHCS) of the Irish Department of Agriculture and the Marine (DAFM)). Using these data, we were able to calculate whether, and for what time, each Irish herd was restricted on the basis of a bTB case.
- **Herd locations and land parcels.** DAFM’s Land Parcel Information System (LPIS), 2018, (Zimmermann et al., 2016) was used to delineate the extent of the land occupied by each cattle herd. Following Tratalos et al. (2020), the Easting and Northing coordinates of the centroid (central point) for each herd were also derived from these data, with the exception of approximately 5% of herds which were not recorded in the LPIS system, which were mapped by randomly assigning a location within the Electoral Division they were located in. The mean size of Electoral Divisions is 20.6 km².
- **AIM data.** The births, movement records and end of year herd profiles for all Irish bovines during the period 2010–2019 were acquired from the DAFM’s Animal Identification and Movements (AIM) database. Analyses conducted on 2016 movement data from the same source are described in more detail in Tratalos et al. (2020) and McGrath et al. (2018). These data were used to estimate movement network variables as well as herd type and size.
- **Modelled badger abundance.** We used the mapped output from Byrne et al. (2014a), which estimates probability of the occurrence of a badger social group (strictly a main sett), at 100 m resolution, as a proxy for badger abundance.
- **DEM data.** Altitude at the centroid of the herd, using a digital elevation model (DEM) of Ireland.
- **Precipitation data.** Mean annual precipitation, 2015–2018, in millimeters, at 1 km grid resolution, were obtained by Met Éireann, the Irish Weather Forecast Service (<https://www.met.ie/monthly-rainfall-and-temperature-grids/>).

2.2. Variables used in the analyses

The data previously described in the data sources section were used to compute the following variables for the models. *Italic font indicates variable names reported in the results, whereas bold font indicates data*

sources described in the previous section.

2.2.1. Dependent variable

TB_{18–19}. The dependent variable was a binary measure of whether a herd was restricted during 2018 or 2019 based on the **bTB data**.

2.2.2. Independent variables

The following independent variables were used to model bTB risk. As outlined previously, these variables aimed to match those of the GB study, with the addition of those measuring rainfall, altitude and the probability of the presence of badgers.

- *TB_{13–17}* was, like the dependent variable, based on the **bTB data** and was a binary variable measuring whether the herd had previously been bTB restricted at any time between 2013 and 2017.
- *Herd size* was calculated from the **AIM data**, measured as the mean of the number of animals in each herd on 1st January, 1st May and 1st September of each year, 2018–2019
- *Herd type* was estimated for each year, 2018 and 2019, using a modified version of the methodology used by Brock et al. (2021). The AIM data was used to classify herds as *Dairy*, *Suckler*, *Beef*, *Fattener*, *Stores*, *Mixed*. Seasonal (N = 251) and Trader (Dealer) (N = 292) herds were excluded from the analysis. In cases where herd type differed between the two years, the type was selected randomly from one of them. *Herd type* was modelled as dummy (binary categorical) variables for each herd type, with *Mixed*, herds employing both dairy and beef production systems (Brock et al., 2021), as the reference category.
- *In strength*, the number of individual bovine animals entering the herd. We calculated the mean value per annum, over the period 2015–2017, based on the **AIM data**.
- *Trades in*, a binary metric measuring whether any animals had entered the herd between 2015 and 2017, based on the **AIM data**.
- *Betweenness*, which measures how often a herd is on the shortest path between each herd to herd combination in the trade network (Freeman, 1977); it was a directed measure, and we weighted each connection using the inverse of the number of animals involved in each trade, matching the methodology of the GB study. We calculated the mean value per annum, over the period 2015–2017, based on the **AIM data**.
- *Rainfall*. Using the **precipitation data**, mean annual precipitation, 2015–2018, in millimeters, was calculated at the herd centroid. In some cases, herd locations along the coast fell outside the coverage of the rainfall grid, and in these cases the nearest neighbouring value was used.
- *Altitude*. Calculated at the location of the herd centroid from the **DEM data**.
- *Badger Metric*. To measure the likelihood of the occurrence of a badger social group coming in contact with the herd we took the maximum value of the **modelled badger abundance** within the footprint of the herd's land parcels as represented in LPIS.
- *ICCs*. ICCs were calculated using the same approach as the GB study. For each month, January 2016–December 2017, each ICC was traced back up to 8 steps within the previous 12 months. For any given source herd, the minimum number of steps was calculated across all 24 of these monthly ICCs. Using this approach, we obtained, for each study herd and each ICC step, a) the number of source herds in the ICC at this or fewer steps from the study herd, as well as b) the total number of herds, with a history of bTB between 2013 and 2017, at this or fewer steps from the study herd and c) the total number of herds, with a history of bTB between 2013 and 2019, at this or fewer steps from the study herd. We used the same approach to measure bTB history as used for the dependent variable (*TB_{18–19}*). These data were highly skewed, and we took account of this in the modelling process by testing the effect on the model fit of using untransformed, square root transformed and natural log + 1

transformed data, as well as creating categorical variables for membership of each quartile in the frequency distribution (this last approach was the one used in the GB study). In the case of the log transformation, 1 was added to the raw data before transformation, to avoid calculating logs on zero values. In the foregoing text, these variables are named with reference to their transformation (*U*: Untransformed, *Lg*: Natural Log + 1, *Q*: Quartiles, *SR*: Square root), the ICC step (1–8) and whether the ICCs were calculated for all source herds (*All*) or just those with a history of TB across 2013–2017 (*TB_{13–17}*) or 2013–2019 (*TB_{13–19}*); for example, *ICC4_Ut_TB_{13–19}* represents the untransformed version of the ICC at step 4 restricted to herds with a history of TB between 2013 and 2019.

- *Measures of proximity to infected herds*. We used three alternative approaches to measure the proportion of nearby herds with a history of restriction for bTB during the period 2013–2017, each based on the assumption that any positive association between bTB infection in a herd and in each of its neighbours would be likely to decline with distance. 1) The first approach matched that of the GB study and used distance between herd coordinates to calculate the proportion of previously restricted herds within each of 5 straight line distance bands: 2 km, 4 km, 6 km, 8 km and 10 km. 2. The second method used these same four distance thresholds but used the LPIS data and calculated distance from farm boundary to farm boundary, with the addition of a metric calculated using neighbouring herds only (measured as ≤ 1 m apart). 3. Finally, we calculated a similar set of metrics with respect to the number of steps (i.e. herds) an infection would have to travel through in a land route from one herd to another, again using the ≤ 1 m criterion to designate neighbours; on the basis of this we calculated the minimum number of steps to a herd with a history of restriction. In the foregoing text, these variables are named with the prefix “*Prox*” followed by the method of measuring the effect of distance (*XY* method 1., *LPIS*: method 2, *Steps*: method 3) and then any distance threshold applied (0 km, 2 km, 4 km, 8 km, 10 km); for example, *Prox_XY_6km* used the herd coordinates to measure distance, with a cut-off point of 6 Km.
- *County*. The county location of each herd (n = 26) was obtained by reference to its eight character herd number, where the first letter identifies the county the herd is registered in (https://en.wikipedia.org/wiki/Counties_of_Ireland).

2.3. Statistical analysis

Employing the *glm* function in R 4.1.1 (<https://www.r-project.org/>), we used the dependent and independent variables described in the previous sections in multivariable logistic regressions, with herd restriction for bTB (*TB_{18–19}*) as the dependent variable.

These regressions were calculated for a set of study herds. These study herds consisted of all Irish herds for which i) we had LPIS data, as some of our exogenous variables were calculated with reference to each study herd's land parcels, and ii) had been in existence throughout the period 2013–2019, so that variables derived from data occurring across this period, such as *TB_{18–19}* and *TB_{13–17}*, would not be affected by missing data. For the continuous variables selected in these models we estimated standardised odds ratios (OR) using the same method as the GB study – calculating the increase in likelihood in moving from the 10th to 90th percentile of each variable.

We examined whether multicollinearity was an issue in the models using Pearson correlation and through an examination of the Variance Inflation Factor (VIF) calculated by the “*check_collinearity*” function in the Performance Analytics Package of R (<https://github.com/brave-rock/PerformanceAnalytics>; <https://www.rdocumentation.org/packages/PerformanceAnalytics/versions/2.0.4/topics/PerformanceAnalytics-package>).

We used ArcMap 10.6 to create 5 km resolution grids of the mean value of the response residuals (real minus predicted values), to reveal

any spatial patterns in the performance of the models, and examined whether there was any spatial autocorrelation in these residuals using Moran's I (Moran, 1950).

2.3.1. The base model

We first built a regression model using *Herd size*, *Herd type*, *In strength*, *Trades in*, *Betweenness*, *Rainfall*, *Altitude*, *Badger Metric* as independent variables. We examined each of these in turn and removed any variable whose exclusion brought about an improvement in model fit, as indicated by a lower Akaike Information Criterion (AIC) (Stoica and Selen, 2004). We used this model as a basis to develop three further models, as described in the next two sections.

2.3.2. Simple, history and proximity, and county models

The measure of whether the herd had a history of bTB (*TB_{13–17}*) and the *measures of proximity to infected herds* might be expected to play roles similar to autoregressive variables – temporal in the case of the former and spatial in the latter. Therefore, although these variables represented the possibility of residual infection in the herd and spread of bTB from nearby herds, respectively, they might also be expected to act as proxies for a range of drivers which might have been imperfectly measured by other, existing, inputs to the models, and therefore subsume some of any improvement in model fit which would otherwise be attributed to these other drivers. In view of this, we created a simple model, which consisted of the Base Model with the addition of an ICC variable, and a “History and Proximity Model” model, which additionally included the *TB_{13–17}* and *measures of proximity to infected herds* variables. Similarly, using the county location of a herd might reveal spatial patterns in the data due to the presence of missing variables but might also capture some of the explanatory power of other factors which are already taken account of in the other variables, but are imperfectly measured. We therefore created a third set of models using the same set of variables as used in the History and Proximity Model with the addition of the *County* variable, which we will refer to as the “Counties Model”. In the case of the *measures of proximity to infected herds* in the History and Proximity and Counties models we included only a single measure from amongst those we calculated, selected using AIC as a measure of best fit and parsimony.

2.3.3. ICCs

For all three models (the Simple Model, the History and Proximity Model, the Counties Model) we added the ICC variable that produced the best fit. As part of this process, we tested whether transforming the ICC data, using square root or log, or using quartiles as categorical variables would improve the fit. We then tested whether the removal of any of the other variables in the model would result in a reduction in the AIC. Finally, we tested whether adding any of the previously rejected variables could improve the fit of this model, again using AIC to find the most parsimonious model.

As a sensitivity analysis, we reran the selected models replacing the ICC terms with equivalent ICC variables, calculated including only those source herds which were not direct neighbours (≤ 25 m) of the sample herd. We also examined the effect on model fit of inclusion of each of the various transformations of these ICC variables, in the same way as described in the previous paragraph for the ICCs which included neighbouring herds. We conducted this sensitivity analysis because, after a bTB breakdown in the sample herd, neighbouring herds would typically be tested at an earlier date than required by the usual annual bTB testing interval, and we wanted to make sure that any relationships between bTB test status in the sample herd and future test status in the source herds found in its ICC was not influenced by this.

3. Results

3.1. The base model

There were 90,257 study herds, of which 8285 were bTB restricted with reference to the dependent variable (*TB_{18–19}*). This compares to 124,222 herds existing at any time between 2013 and 2019, as measured by at least one bTB test being recorded for the herd during that period.

The only variable rejected from the base Model was *Trades in*, the binary measure of whether animals had entered the herd, as its inclusion alongside the other cattle movement variables resulted in an increase in the AIC.

3.2. Simple, history and proximity, and counties models

Outputs for the three final models (“Simple”, “History and Proximity” and “Counties”) are shown in Table 1. *Herd size*, *Altitude*, *Badger Metric*, and *In-strength* all showed positive associations with *TB_{18–19}* (Odds Ratio > 1), whereas *Betweenness* showed negative associations. *Rainfall* showed a negative association in the Simple Model, a positive one in the Counties Model and was not included in the final History and Proximity Model, as it resulted in an increase in the AIC. Amongst the *Herd type* categories, relative to the reference category of *Mixed*, *Dairy* showed higher risk and *Beef* and, especially, *Stores* lower risk, with *Fattener* at a similar risk to the reference group. Summary statistics for the variables in these models are presented in Table 1 and 2 of the Supplementary Material.

In the History and Proximity Model, the best fitting *measure of proximity to infected herds* was provided by the coordinates-based measure at 6 km (*Prox_{XY_6km}* in Table 1) whereas in the Counties Model it was from the measure based on a 4 km distance between herd boundaries: *Prox_{LPIIS_4km}*. For both these models the variable for prior bTB in the herd, *TB_{13–17}*, brought about the greatest reduction in AIC of all the exogenous variables. Fig. 1 shows the effect on the AIC of substituting each of the *measures of proximity to infected herds* in the final selected models.

In the Counties Model, County Monaghan carried the highest OR (2.7, 95% CI = 2.3–3.1) and the most notable difference between the spatial distribution of the residuals from the Counties Model and those from the History and Proximity Model was in this county (Table 1, Figs. 2 and 3).

3.3. The contribution of ICC variables

Introducing any of the ICC variables at Step 1 (ICC1), representing direct inward moves from other herds, in all cases brought about improvements in fit as measured by the AIC (Fig. 4 and Supplementary Material Fig. 1). For the Simple and History and Proximity models, relative to models with no ICC variable, improvements in fit were also brought about through the introduction of ICC variables at steps 2 – 8 (ICC2–ICC8), but this was not always the case for the Counties Model (Fig. 4). ICC1 in all but one case produced a better fit than ICCs at remoter steps, the exception being “*Qt_{All}*” in the Simple and History and Proximity models. For all three models (Simple, History and Proximity and Counties), the best fitting treatment of the ICC1 variables was *SR_{TB_{13–19}}*: a square root transformation, combined with taking into account test results for source herds for 2013–2019 (as opposed to not taking test history into account, or using only the years 2013–2017) (Fig. 4).

Reintroduction of the previously rejected *Trades In* (the binary movement variable), in models including *SR_{TB_{13–19}}*, improved the AIC slightly in all three models, but for a negative coefficient; there was therefore no compelling reason to reintroduce it. It should also be noted that if both of the other movement related variables (*ICC1_{SR_{TB_{13–19}}}* and *In-strength*) were excluded, the coefficient for *betweenness* changed from negative to positive, although its inclusion resulted in a higher AIC.

Table 1

Logistic regressions for bTB in Irish cattle herds (N = 90,257). Three models are shown; in all three the dependent variable measures whether the herd was restricted during 2018–19. The History and Proximity and Counties models (b and c) include an exogenous variable for whether the herd has been restricted in the period 2012–2017 (*TB_13–17*) and variables for the proportion of nearby herds which have been restricted in the period 2013–2017 (*Prox_LPIS_4km* and *Prox_XY_6km*); the Counties Model in addition has the county a herd was located in as an explanatory variable – odds ratios for individual counties are shown in Fig. 2. CL = 95% Confidence Limits. For continuous variables Odds Ratios and CLs have been standardised to represent the change in odds between 10th and 90th percentile. AIC: Akaike Information Criterion. Change in AIC shows the increase in the AIC of the model if the variable is removed from the final model. Individual variables are described fully in the Methods section.

Parameter			a) Simple Model				b) History and Proximity Model				c) Counties Model			
	10th pc.	90th pc.	Odds Ratio	2.5% CL	97.5% CL	Change in AIC	Odds Ratio	2.5% CL	97.5% CL	Change in AIC	Odds Ratio	2.5% CL	97.5% CL	Change in AIC
<i>TB_13–17</i>							3.355	3.187	3.533	2026.6	3.29	3.123	3.465	1924.7
<i>Prox_LPIS_4km</i>	0.074	0.295									2.251	2.09	2.425	446.9
<i>Prox_XY_6km</i>	0.058	0.255					2.021	1.909	2.14	558.6				
<i>Herd size</i>	8.5	168.5	2.649	2.415	2.907	440.5	1.992	1.815	2.186	216.2	2.524	2.285	2.789	342.4
<i>Herd type</i>						489.3				338.4				375.7
Mixed			Baseline				Baseline							
Beef			0.798	0.727	0.877		0.813	0.737	0.896		0.76	0.688	0.84	
Dairy			1.236	1.121	1.362		1.16	1.05	1.283		1.168	1.055	1.292	
Fattener			1.007	0.906	1.119		1.003	0.899	1.12		1.048	0.938	1.171	
Stores			0.368	0.321	0.422		0.414	0.36	0.476		0.413	0.359	0.476	
<i>Badger Metric</i>	0.427	0.839	1.272	1.181	1.369	39.1	1.11	1.029	1.198	5.3	1.109	1.025	1.199	4.6
<i>Altitude</i>	25	165	1.281	1.21	1.357	68.3	1.127	1.064	1.194	14.4	1.136	1.055	1.224	9.2
<i>Rainfall</i>	925	1579	0.88	0.824	0.94	12.7					1.101	0.993	1.222	1.3
<i>In Strength</i>	0	48	1.041	1.018	1.065	10.9	1.046	1.02	1.072	13.9	1.081	1.055	1.108	42.4
<i>Betweenness</i>	0	403,863	0.992	0.988	0.995	34.7	0.994	0.991	0.997	19.2	0.994	0.99	0.997	19.7
<i>ICC1_SR_TB_13–19</i>	0	10	1.722	1.626	1.822	336.7	1.474	1.428	1.523	161.7	1.325	1.247	1.408	79.8
County														668.8
Null Deviance: 55,357.81			AIC: 50,749.5				AIC: 47,597.7				AIC: 46,928.9			
			rea Under ROC: 0.706				Area under ROC: 0.769				Area under ROC: 0.78			

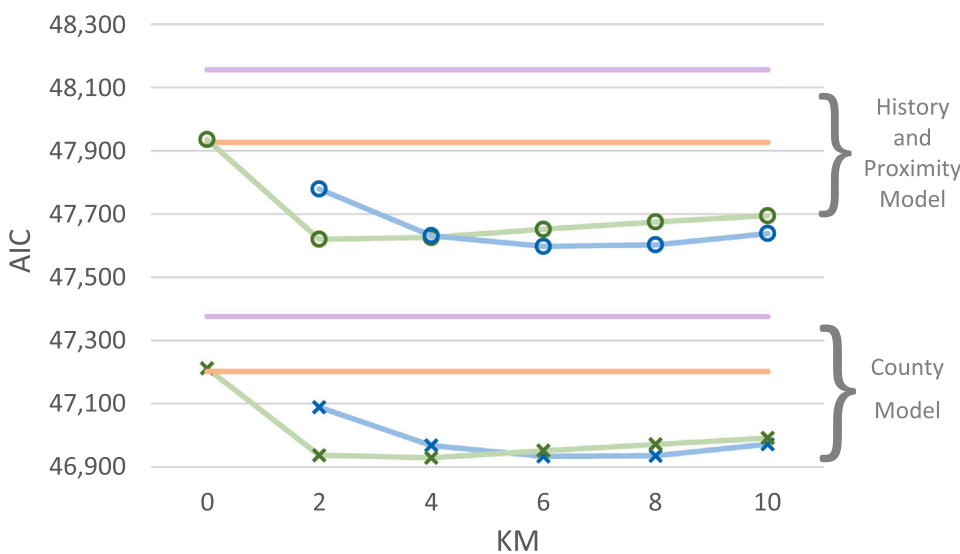


Fig. 1. AIC of models using three different measures of bTB history (restricted at any time during the period 2013–2017) in nearby herds (green, blue and orange lines) and for a model with no such measure (purple line). The colours of the green, blue and orange lines distinguish the way that distance was measured, which in the case of the blue and green lines represent the proportion of neighbours within 1 m (green line only), 2 km, 4 km, 6 km, 8 km and 10 km, with each distance threshold shown as a point on the line. Points on the blue line represent these distances as measured between herd centroids, those on the green line as measured by the shortest distance between land parcels belonging to a herd. The orange lines show AICs for models incorporating the neighbourhood effect as the number of herds an animal would have to travel through to reach a herd with a history of bTB and therefore represent a single value for each line. Similarly, the purple lines represent models with no neighbourhood measure and therefore the AIC does not change across the x-axis. Results for the History and Proximity and Counties models are shown separately; each of these

models is described in detail in the methods section.

3.4. Comparison of the three models

The Counties Model had a better fit than the History and Proximity Model as measured by the AIC and the area under the ROC Curve and in turn the History and Proximity Model had a better fit than the Simple Model (Table 1). Both *TB_13–17* and the measures of proximity to infected herds played a major contribution to this difference (Table 1). The standardized odds ratio for the *ICC1_TB_13–19* variable was 1.72 in the Simple Model, 1.47 in the History and Proximity Model and 1.33 in the Counties Model, which was smaller than that for herd size (2.65, 1.99 and 2.52) and of similar importance to that for the herd type categorical variables, which ranged from 0.37 (*Stores*) to 1.24 (*Dairy*) across the

models (confidence intervals for all standardized odds ratios are given in Table 1). The other movement-related variables played a smaller role: the standardised odds ratio for *Betweenness* was 0.99 in all three models and that for *In Strength* ranged from 1.05 to 1.08. Standardised odds ratios for *Altitude* were 1.28 in the Simple Model and approximately 1.13 in both History and Proximity and Counties models. For the badger abundance variable (*Badger Metric*), the standardised odds ratio was 1.28 in the Simple Model and 1.11 in the History and Proximity and Counties models. By far the greatest variation for a single variable across the three models was for *Rainfall*, whose standardized odds ratio was 0.88 in the Simple Model and 1.1 in the Counties Model, whereas was not selected in the History and Proximity Model.

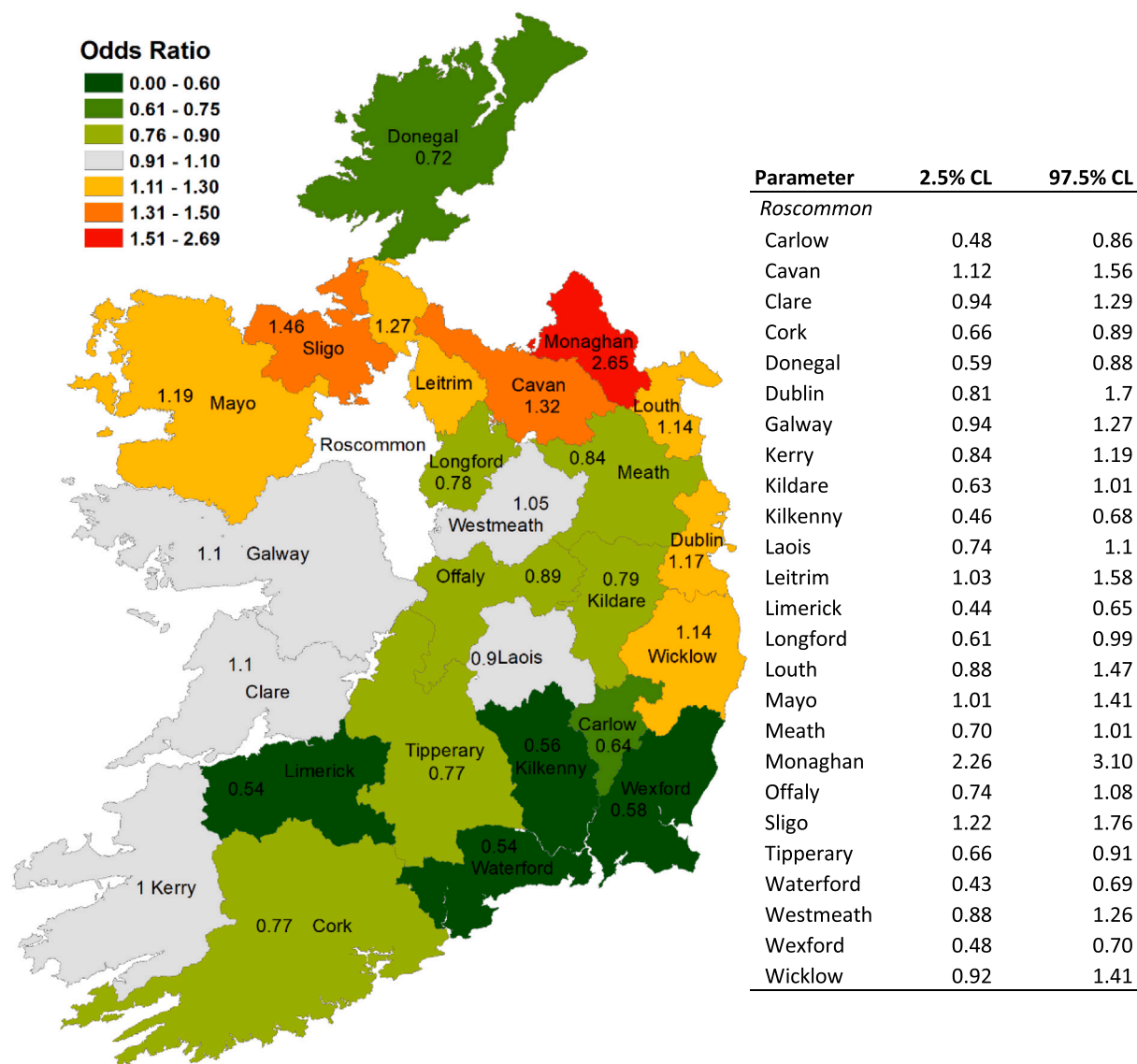


Fig. 2. Odds ratios for each county in Ireland derived from the Counties Model, a logistic regression model of bTB restriction amongst Irish cattle herds, 2018–2019. The reference county was Roscommon. Confidence intervals for the odds ratios are shown in a separate table (right). See.

The VIF for the variables in the Simple and History and Proximity models showed that multicollinearity was not a major issue in either, with no VIF values higher than 3.1. However, this was not the case in the Counties Model, where five variables carried VIF values above 4 - *County* (108.5), *ICCI_SR_TB_13–19* (28.6), *In Strength* (31.7), *Altitude* (20.8) and *Herd Type* (6.8) (Supplementary Material, Table 3). Amongst continuous variables found together in any of the models, highest R values were between *In Strength* and *ICCI_SR_TB_13–19* (0.66), between *Badger Metric* and *Herd Size* (0.44) and between *Badger Metric* and *Prox_LPIS_4km* (0.27). Betweenness was only weakly correlated with the other movement variables: *in strength* (0.21) and *ICCI_SR_TB_13–19* (0.16). Rainfall was negatively correlated with all other variables apart from altitude ($r = 0.16$), and mostly strongly with *Prox_LPIS_4km* ($r = -0.3$). More detail on the VIF statistics can be found in Table 3 of the Supplementary Material.

Based on a simple visual comparison between the spatial distributions of the raw data and model fits (Fig. 3), the History and Proximity Model performed better than the Simple Model at predicting the spatial patterns in the data but both models broadly succeeded in predicting the higher probabilities of restriction which occur in certain areas toward of the South and East of Ireland, as well as The Burren (an upland area of

karst geology identifiable as a bTB hotspot halfway up the west coast). Both models smoothed the local variation amongst grid cells seen in the real data. Adding *County* to the model (i.e. in the Counties Model) in some areas further reduced the degree to which spatial patterns were evident in the residuals (Fig. 3). However, Moran’s I showed that positive spatial autocorrelation remained in the residuals (correlation values: Simple = 0.041, History and Proximity = 0.031; County = 0.020; all three were highly significant ($P < = 0.01$)).

The sensitivity analysis excluding neighbouring herds in the calculation of the ICCs produced similar results to those already reported (compare Table 1 with Supplementary Material Table 4 and Fig. 4 with Supplementary Material Fig. 2).

4. Discussion

The motivation for our study was to examine whether the calculation of ICCs could shed light on the epidemiology of bTB in Irish cattle herds. In contrast to the GB study we found that using information on the ICC chain at steps further back than the most recent one did not produce the best fitting models. It should be borne in mind however that the final model in the GB study incorporated measures of the location of source

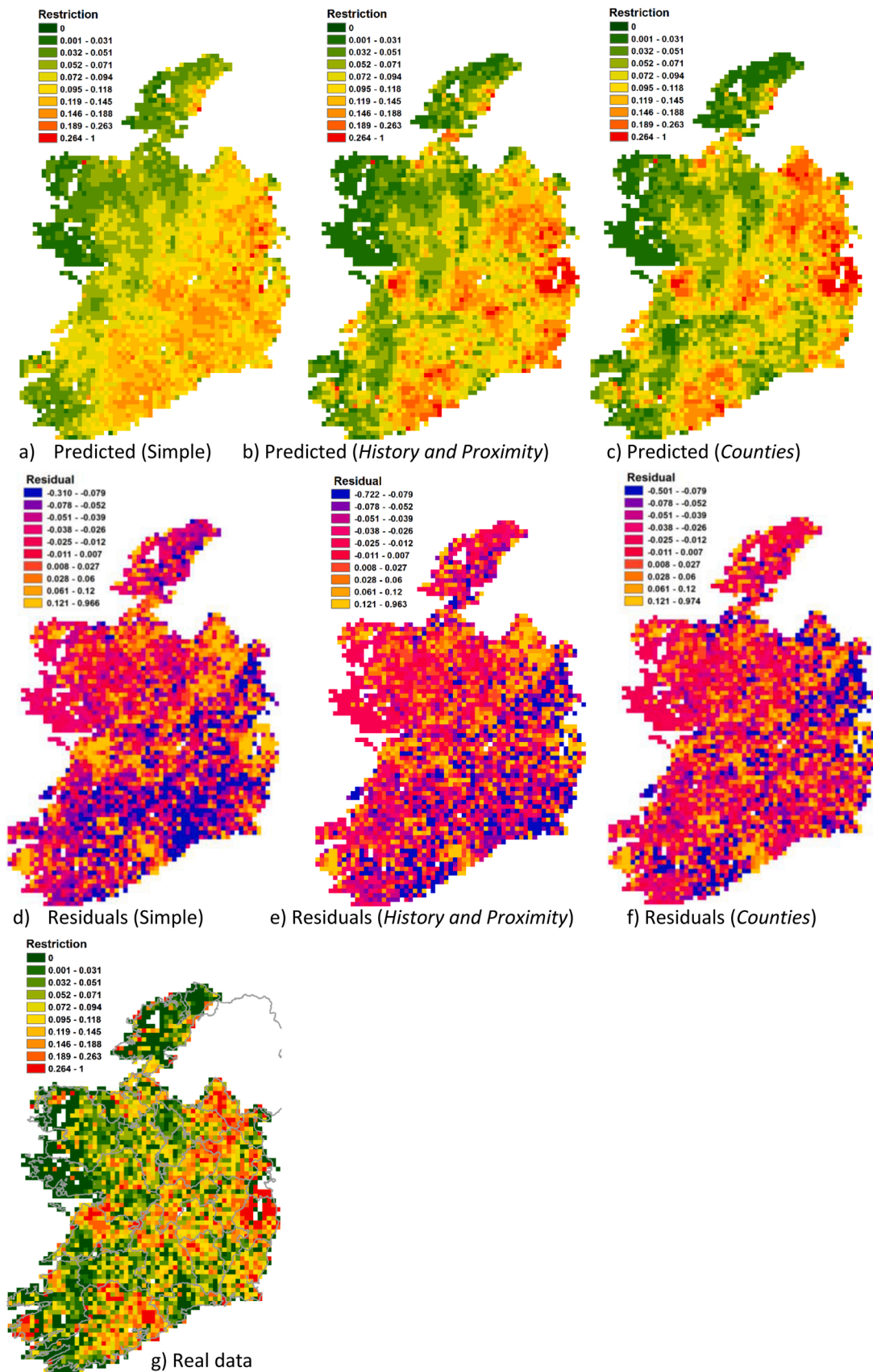


Fig. 3. Rates of bTB restriction amongst Irish cattle herds in 2018 and 2019 at 5 km resolution (g), alongside equivalent probabilities estimated by three logistic regression models (the Simple, History and Proximity and Counties models, a to c, described in the methods section) and their response residuals (observed minus predicted, d to f).

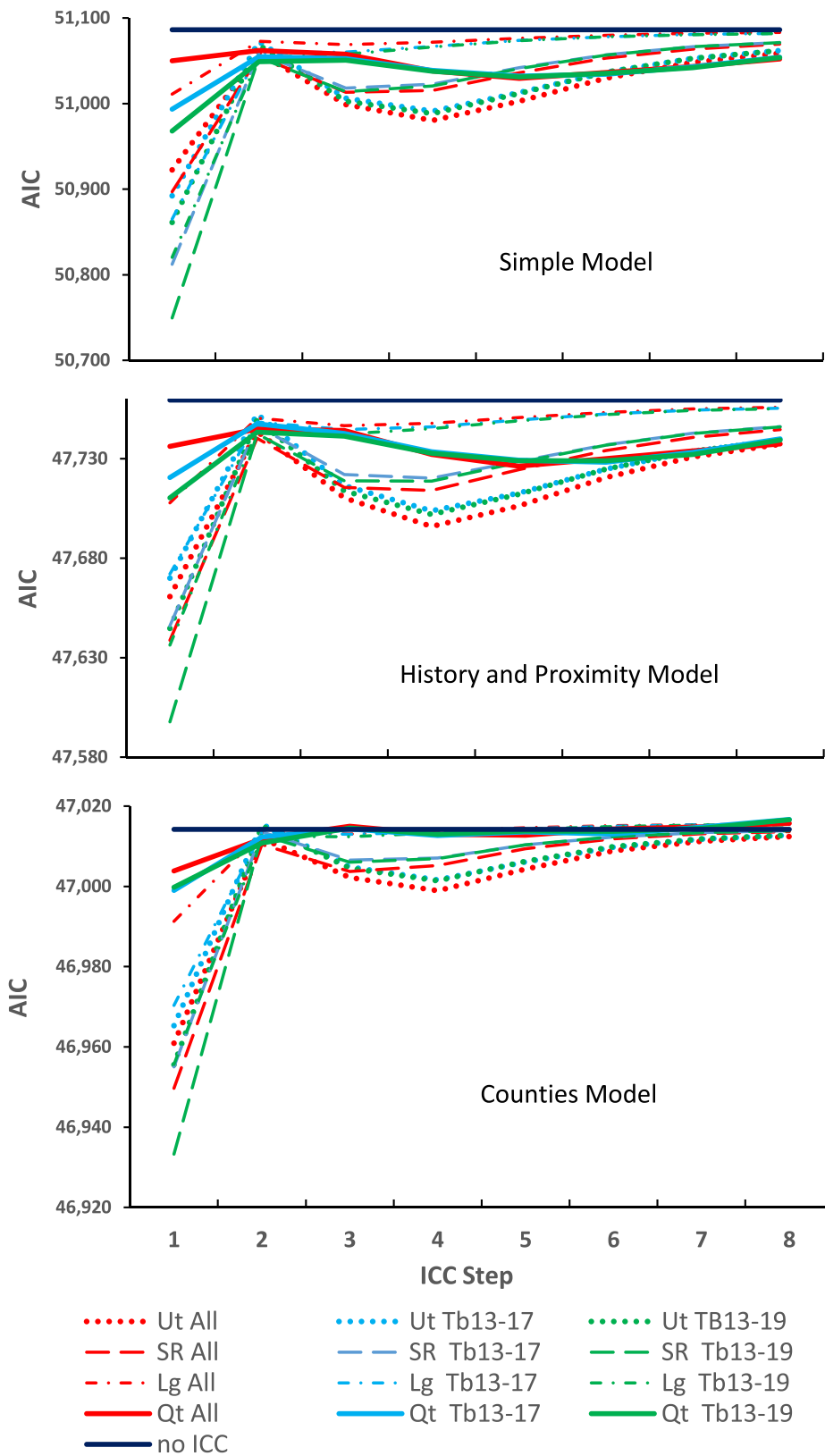


Fig. 4. Effect on the model AIC of adding each of 4 transformations (including untransformed) on three different criteria for including herds in the ICC calculation, up to 8 ICC steps removed from the receiving herd. Transformations included Untransformed (Ut), Square Root (SR), Log (Lg), and Quartile (Qt). Criteria for including herds in the ICC calculation included All herds (“All”), only counting herds restricted for Tb between 2013 and 2017 (“Tb13–17”), and ICC size only counting herds restricted for Tb between 2013 and 2019 (Tb13–19). These data are also present in the [Supplementary Material](#) (Fig. 1). The horizontal black line represents the AIC if no ICC variable is included in the model.

herds in the UK (in high, medium or low bTB areas) rather than their bTB history. Such an approach was not used in our study, as bTB infection is spread more evenly across Ireland than it is in GB. Instead we use the bTB test history of the herds during two periods – 2013–2017, which is the 5 years before the period measured by the dependent

variable, and an extension of this, 2013–2019, also covering the period measured by the dependent variable. We found that taking into account testing history from 2013 to 2019 produced better fitting models than disregarding this information, but that restricting this information to the period 2013–17 only did so for the Simple Model. An implication of this

is that we should not rely too heavily on past test results, as a measure of risk, in targeted surveillance or risk based trading.

It should be noted, however, that our results do not show that herds previously infected with bTB pose no higher risk than those which have not, but rather that our estimation of risk needs to take into account those herds which have not previously tested positive but may be harbouring undetected disease, and indeed may go on to test positive after animals have moved from them. It should also be noted that when we incorporated test results from 2018 to 2019 into our estimation of bTB test history we were thereby using more years of data to estimate risk, and it was the increased sampling period, rather than, specifically, the inclusion of years after the movement data, that gave better fitting models. However, this seems implausible, as the five year period 2013–2017 already seems long enough to capture bTB test results as a measure of likelihood of testing bTB positive at any given time. It would not be a suitable test of this to compare a measure for 2013–2017 with one for 2015–2019 (i.e. both a five year periods) as such a long period was chosen because moving animals out the herd is not allowed during bTB breakdowns and therefore a sufficient amount of time needs to elapse for a herd testing positive for bTB to at least go through their restriction period and start to sell potentially infected animals. bTB breakdowns and their associated movement restrictions during our study period had a mean duration of 179 days and a median of 147 days (IQR 136 – 189 days). The majority of these otherwise high-risk herds will have become truly bTB free during their period of restriction and will take some time to acquire it and subsequently test positive again.

To arrive at a better approximation to the high, medium and low risk areas used by the GB study, further work could identify whether regional level risk scores could be calculated, for example by estimating the incidence of bTB within a certain radius of all source herds, or using the county-level bTB prevalence of the source herds. However, a problem with this approach, which may also apply to the results shown in the GB study, is that herds tend to trade with other herds relatively close by (Tratalos et al., 2020) and, given the high degree of spatial dependence found in this and other studies (e.g. Madden et al., 2021), are likely to show a tendency to be trading with other herds with similar levels of bTB to themselves, and therefore any association between high bTB prevalence in a given herd and in the locations of its trading partners may reflect this.

Our results indicate that bTB in a herd is more strongly associated with the number of herds it takes animals from (ICC at step 1) than it is with the number of animals moving into it (*In Strength*; Table 1). Furthermore, *In Trades*, the measure of whether a farm purchased animals or not, a measure also used in the GB study, did not merit inclusion in our final models. The network variable selected for the final model, *Betweenness*, carried a negative coefficient, which was unexpected and was not the case in the GB study. However, the standardized odds ratio for *betweenness* was close to 1, and, when the other movement related variables (*ICCI_SR_TB_13–19* and *In Strength*) were excluded, its coefficient was positive. In the context of our study, “betweenness” measures the proportion of shortest paths between other herds in the network that a herd belongs to, taking into account the number of animals involved in each movement. In the light of this, perhaps the negative coefficient is revealing that, for a given level of inward movement (measured by *ICCI_SR_TB_13–19* and *In Strength*), herds which have a lot of throughput, connecting many other herds with each other through trade in many animals, are more likely to have animals in the herd for a short period of time and therefore may be less likely to acquire bTB.

Our models generally support previous findings that bTB in Irish herds was related to herd type, herd size, previous history of bTB, bTB in neighbouring herds and cattle movements (White et al., 2013; Byrne et al., 2014b, 2020; Clegg et al., 2015; Broughan et al., 2016).

Our study used a broader range of measurements than previous studies to identify the role of proximity in the spread of bTB from neighbouring herds. The GB study calculated proximity to neighbouring herds with a history of bTB by measuring the distances between the

geographic coordinates for each herd. We also used this approach but complemented it with two alternative methods: measuring distances between herd boundaries and measuring the number of herds an infection would have to pass through between each herd. As these measures were closely related and therefore highly collinear, we followed the GB study by retaining only the best fitting variable from amongst these groups in the final model. For the Simple and History and Proximity models we found that the best measure of the influence of proximity to infected herds was using a cutoff of 6 km with distance measured between the geographic coordinates of each herd, although this model performed only marginally better than the 4 km one measuring distances from herd boundary to herd boundary, which was in fact the best fitting variable in the Counties Model (Fig. 1). It should be noted that it would be expected that the distance band for the coordinates based measure would be larger than measuring the distance between herd boundaries, as herd centroids will always be some distance from the boundary. Both metrics performed better than counting the number of herds an infection would have to cross (Fig. 1). This suggests that a more sophisticated approach to measuring the distance between herds, such as taking into account the configuration of land parcels occupied by each herd, may not be needed. It should be borne in mind here that many Irish farms consist of numerous parcels of land which are separated from one another, and even where this is not the case, the existence of a shared boundary between two farms does not necessarily mean that cattle on one would come into close proximity with those from the other, depending on how the land in each field is managed (e.g. for silage, crops, other livestock). Our proximity measures may also be picking up spatial autocorrelation explained by missing or poorly measured variables rather than over the fence transmission (or a combination of both phenomena).

Similarly, the very high explanatory power of the previous history of bTB binary variable (*TB_13–17*, Table 1) in the History and Proximity and County models suggests that this variable may be picking up a mixture of residual infection and missing or poorly measured variables. It should be noted that our dependent variable (*TB_18–19*) measured whether a herd was restricted during 2018–19 and this criterion would include herds which were already restricted during the previous year (2017), which also partly explains the high explanatory power of *TB_13–17*.

This study is the first to investigate the role of rainfall and altitude on bTB across Ireland. In contrast to Jin et al. (2015), *Rainfall* was not selected in the History and Proximity Model and carried non-significant negative coefficients when introduced into the final versions of the Counties and Simple models, and also in versions of these models where the altitude variable was excluded. There was, however, a positive association between *Altitude* and bTB in a herd, possibly because of increased survival of the bTB bacillus in cooler environments or because of some aspect of the nutritional status or breed type of animals raised at higher elevations.

Our herd type categories closely matched those of the GB study but with the addition of the *Stores* category and it was interesting that stores herds were associated with lower odds ratios than fattener herds, possibly because the former typically contain younger animals. Dairy herd type was associated with a high odds ratio and beef type with a low odds ratio, which matches results elsewhere, and the fact that this occurred even in models including movement and herd size based variables suggests that this effect is due to more than the fact that dairy herds are typically larger, a characteristic which has previously been suggested as the underlying cause behind high rates of bTB in dairy herds (Conlan and Wood, 2016). The ORs for herd size were much lower than in the GB study, at around 2 (Table 1) versus 19.4 (CI: 17.1–22.1), which may be partly due to typically smaller herds in Ireland (compare 90 percentile 168 versus 280 in the GB study).

The *Badger Metric* was only moderately associated with bTB infection, with a standardized OR of 1.11 (1.03–1.20) in the Counties and the History and Proximity models and 1.27 (1.18–1.37) in the Simple Model

(Table 1). However, these data are themselves based on a model, and therefore may not correlate perfectly with the measure they are designed to estimate (the probability of a given grid square hosting a badger main sett), let alone precisely capture the relative likelihood of badgers transmitting bTB to cattle. Note that the variable we used represented the maximum value, at 100 m resolution, of the badger abundance model output within land parcels hosting each herd. We used the maximum value, rather than the mean or median, as badgers occupy territory based around a main sett, and much of this territory may be suitable to them for other purposes (e.g. foraging) but not suitable for a main sett.

Deer, especially Sika deer *Cervus nippon*, are thought likely to transmit bTB to cattle in some areas of Ireland, notably County Wicklow (Kelly et al., 2021), although they are mostly regarded as a spillover host in other areas. We did not include a measure of deer abundance in our models, mostly because little data exists on this, and there are no published models of deer abundance. Comprehensive deer shooting records exist in Ireland (Kelly et al., 2021), but only at county level, and are arguably just as likely to represent the abundance of human hunters as deer.

Possible further inputs to our model might include measures of the number of distinct batches of animals entering the herd ("contacts" in the terminology of Tratalos et al., 2020), which is a distinct measure from in degree and in strength. However, Tratalos et al. (2020) show that, in Ireland, the in-degree and the number of "in contacts" are highly positively correlated, and we therefore decided not to include a separate variable for the latter. We might also consider an investigation of interaction effects to see if these might address some of the collinearity issues indicated by the VIF analysis. However, these collinearity issues were only evident in the county model, and it is unclear to us what biologically justified interaction terms we could incorporate into our models to address this issue.

The ORs for the exogenous variables were fairly consistent across the three types of models (the Simple, History and Proximity and Counties models) (Table 1). However, even with the inclusion of binary variables for each county (in the Counties Model) there remained areas of Ireland where the models tended to over or under predict (Fig. 3). This suggests that there may be other factors which are driving bTB infection in these areas. These might be farm management practices concerning husbandry, biosecurity and the exclusion of badgers, the presence of bTB in deer and the configuration of habitat types such as woodland and pasture, which might bring about more or less interaction with wildlife. The zoning of areas for control of bTB in badgers through vaccination or culling may also explain some of these patterns.

In this study we have built statistical models of the factors driving bTB prevalence in Ireland at a herd level. However, there is much further work which could be undertaken using our models as a starting point. We have touched on some of these areas elsewhere in our discussion. Such studies could include:

1. Adaptation of the ICC methodology to include alternative measures of how risky each link in the chain is. This has been done in this study by flagging whether each herd in the chain has been under restriction for bTB but this might not be the best measure of true incidence of undetected bTB in the herd. Alternative measures might include calculating the average past and future bTB testing history of herds in the neighbourhood of each herd in the ICC and using that as a measure of the riskiness of the location of each herd or using a model to estimate the riskiness for each herd, based on similar inputs to those in this study and using the resulting risk scores as herd-level weights in the calculation of the ICC.
2. Studies on the possible role of deer as vectors of bTB. Measures of deer abundance or prevalence of bTB in deer could be used as inputs into a model. Areas where the model does not work well could be investigated as possibly due to an unknown bTB host, such as deer.

3. Smaller scale studies on effects of farm management practices such as differences in husbandry methods, biosecurity measures, and wild-life management.
4. In our study we used five of the six broad categories of herd type identified by Brock et al., 2021. However, within these categories 17 sub types have been calculated (e.g. dairy herds using contract rearing are one of these subgroups, Brock et al., 2021). An examination of the relationship between the residuals from our model and the subtype of the herd might allow a better understanding of the riskiness of each of these 17 production types.
5. Detailed investigation of locations and herds where the residuals from our model are particularly high (i.e. herds or areas identified by the model as low risk but with a relatively high incidence of bTB infection), to try to understand what might explain this.

5. Conclusions

The primary aim of our study was to investigate whether risk of bTB infection increased with the size of the ICC, and whether taking into account the bTB infection history of each herd in the chain would further improve prediction of the future bTB status of the receiving herd. We found that using information at steps more remote than direct movements did not result in better fitting models. Measures of cattle movements directly into the herd were risk factors for subsequent bTB restrictions, and the number of herds that animals were coming from was the most important of these. Using information on the previous and future bTB infection status of the sending herds resulted in improved model fits. Aside from factors found to be important in previous studies (such as herd size and herd type) we found that both altitude and modelled badger abundance also held some predictive power and facilitated a better understanding of the spatial pattern of infection risk from neighbouring herds.

We believe our model can be used as a basis for the investigation of other exogenous factors such as the abundance of deer populations and also to identify areas where bTB rates are anomalously high, to prompt further investigation of local factors such as wildlife management, husbandry practices and biosecurity.

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Conflicts of interest

None.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.prevetmed.2022.105816](https://doi.org/10.1016/j.prevetmed.2022.105816).

References

- Allen, A.R., Skuce, R.A., Byrne, A.W., 2018. Bovine tuberculosis in Britain and Ireland – a perfect storm? The confluence of potential ecological and epidemiological impediments to controlling a chronic infectious disease. *Front. Vet. Sci.* 5. <https://doi.org/10.3389/fvets.2018.00109>.
- Brock, J., Lange, M., Tratalos, J.A., More, S.J., Graham, D.A., Guelbenzu-Gonzalo, M., Thulke, H.-H., 2021. Combining expert knowledge and machine-learning to classify herd types in livestock systems. *Nat. Sci. Rep.* 11. <https://doi.org/10.1038/s41598-021-82373-3>.
- Broughan, J.M., Judge, J., Ely, E., Delahay, R.J., Wilson, G., Clifton-Hadley, R.S., Goodchild, A.V., Bishop, H., Parry, J.E., Downs, S.H., 2016. A review of risk factors for bovine tuberculosis infection in cattle in the UK and Ireland. *Epidemiol. Infect.* 144, 2899–2926. <https://doi.org/10.1017/S095026881600131X>.
- Byrne, A.W., Acevedo, P., Green, S., O’Keefe, J., 2014a. Estimating badger social-group abundance in the Republic of Ireland using cross-validated species distribution modelling. *Ecol. Indic.* 43, 94–102. <https://doi.org/10.1016/j.ecolind.2014.02.024>.
- Byrne, A.W., White, P.W., McGrath, G., O’Keefe, J., Martin, S.W., 2014b. Risk of tuberculosis cattle herd breakdowns in Ireland: effects of badger culling effort, density and historic large-scale interventions. *Vet. Res.* 45, 109. <https://doi.org/10.1186/s13567-014-0109-4>.
- Byrne, A.W., Barret, D., Breslin, P., Madden, J.M., O’Keefe, J., Ryan, E., 2020. Bovine Tuberculosis (*Mycobacterium bovis*) Outbreak Duration in Cattle Herds in Ireland: A Retrospective Observational Study. *Pathogens* 9 (10). <https://doi.org/10.3390/pathogens9100815>.
- Clegg, T.A., More, S.J., Higgins, I.M., Good, M., Blake, M., Williams, D.H., 2008. Potential infection-control benefit for Ireland from pre-movement testing of cattle for tuberculosis. *Prev. Vet. Med.* 84, 94–111. <https://doi.org/10.1016/j.prevetmed.2007.11.004>.
- Clegg, T.A., Duignan, A., Whelan, C., Gormley, E., Good, M., Clarke, J., Toft, N., More, S. J., 2011. Using latent class analysis to estimate the test characteristics of the γ -interferon test, the single intradermal comparative tuberculin test and a multiplex immunosay under Irish conditions. *Vet. Microbiol.* 151 (1–2), 68–76. <https://doi.org/10.1016/j.vetmic.2011.02.027>.
- Clegg, T.A., Good, M., More, S.J., 2015. Future risk of bovine tuberculosis recurrence among higher risk herds in Ireland. *Prev. Vet. Med.* 118, 71–79. <https://doi.org/10.1016/j.prevetmed.2014.11.013>.
- Conlan, A.J.K., Wood, J.L., 2016. Testing the dairy difference. *Vet. J.* 217, 134–135. <https://doi.org/10.1016/j.tvjl.2016.07.017>.
- Conlan, A.J.K., Wood, J.L., Clifton-Hadley, R.S., Karolemeas, K., McKinley, T.J., Pollock, E.B., Goodchild, A.V., Mitchell, A.P., Birch, C.P.D., 2012. Estimating the hidden burden of bovine tuberculosis in Great Britain. *PLoS Comput. Biol.* 8, e1002730. <https://doi.org/10.1371/journal.pcbi.1002730>.
- Fielding, H.R., McKinley, T.J., Delahay, R.J., Silk, M.J., McDonald, R.A., 2019. Effects of trading networks on the risk of bovine tuberculosis incidents on cattle farms in Great Britain. *R. Soc. Open Sci.* 7. <https://doi.org/10.1098/rsos.191806>.
- Frankena, K., White, P., O’Keefe, J., Costello, E., Martin, S.W., van Grevenhof, I., More, S.J., 2007. Quantification of the relative efficiency of factory surveillance in the disclosure of tuberculosis lesions in attested Irish cattle. *Vet. Rec.* 161, 679–684. <https://doi.org/10.1136/vr.161.20.679>.
- Freeman, L.C., 1977. A set of measures of centrality based on betweenness. *Sociometry* 40, 35–41. <https://doi.org/10.333543>.
- Jin, R., Good, M., More, S.J., Sweeney, C., McGrath, G., Kelly, G.E., 2013. An association between rainfall and bovine TB in Wicklow, Ireland. *Vet. Rec.* 173, 452. <https://doi.org/10.1136/vr.101777>.
- Kelly, D.J., Mullen, E., Good, M., 2021. Bovine Tuberculosis: The Emergence of a New Wildlife Maintenance Host in Ireland. *Front. Vet. Sci.* 8. <https://doi.org/10.3389/fvets.2021.632525>.
- Madden, J.M., McGrath, G., Sweeney, J., Murray, G., Tratalos, J.A., More, S.J., 2021. Spatio-temporal models of bovine tuberculosis in the Irish cattle population, 2012–2019. *Spat. Spatio-Tempo Epidemiol.* 39. <https://doi.org/10.1016/j.sste.2021.100441>.
- McGrath, G., Tratalos, J.A., More, S.J., 2018. A visual representation of cattle movement in Ireland during 2016. *Ir. Vet. J.* 71. <https://doi.org/10.1186/s13620-018-0129-x>.
- Moran, P.A.P., 1950. Notes on continuous stochastic phenomena. *Biometrika* 37 (1), 17–604. <https://doi.org/10.2307/2332142>.
- More, S.J., 2019. Can bovine TB be eradicated from the Republic of Ireland? Could this be achieved by 2030. *Ir. Vet. J.* 72. <https://doi.org/10.1186/s13620-019-0140-x>.
- More, S.J., Good, M., 2015. Understanding and managing bTB risk: perspectives from Ireland. *Vet. Microbiol.* 176 (3–4), 209–218. <https://doi.org/10.1016/j.vetmic.2015.01.026>.
- Ní Bhuachalla, D., Corner, L.A.L., More, S.J., Gormley, E., 2015. The role of badgers in the epidemiology of *Mycobacterium bovis* infection (tuberculosis) in cattle in the United Kingdom and the Republic of Ireland: current perspectives on control strategies. *Vet. Med.: Res. Rep.* <https://doi.org/10.2147/VMRR.S53643>.
- Núñez-García, J., Downs, S.H., Parry, J.E., Abernethy, D.A., Broughan, J.M., Cameron, A. R., Cook, A.J., de la Rúa-Domenech, R., Goodchild, A.V., Gunn, J., More, S.J., Rhodes, S., Rolfe, S., Sharp, M., Upton, P.A., Vordermeier, M.H., Watson, E., Welsh, M., Whelan, A.O., Woolliams, J.A., Clifton-Hadley, R.S., Greiner, M., 2018. Meta-analyses of the sensitivity and specificity of ante-mortem and post-mortem diagnostic tests for bovine tuberculosis in the UK and Ireland. *Prev. Vet. Med.* 153, 94–107. <https://doi.org/10.1016/j.prevetmed.2017.02.017>.
- Olea-Popelka, F.J., Phelan, J., White, P., McGrath, G., Collins, J.D., O’Keefe, J.J., Duggan, M.G., Collins, D.M., Kelton, D.F., Berke, O., More, S.J., Martin, S.W., 2006. Quantifying badger exposure and the risk of bovine tuberculosis for cattle herds in County Kilkenny, Ireland. *Prev. Vet. Med.* 75 (1–2), 34–46. <https://doi.org/10.1016/j.prevetmed.2006.01.014>.
- Palisson, A., Courcoul, A., Durand, B., 2016. Role of cattle movements in bovine tuberculosis spread in France between 2005 and 2014. *PLoS ONE* 11 (3), e0152578. <https://doi.org/10.1371/journal.pone.0152578>.
- Pozo, P., VanderWaal, K., Grau, A., de la Cruz, M.L., Nacar, J., Bezos, J., Perez, A., Minguez, O., Alvarez, J., 2019. Analysis of the cattle movement network and its association with the risk of bovine tuberculosis at the farm level in Castilla y León, Spain. *Transbound. Emerg. Dis.* 66 (1), 327–340. <https://doi.org/10.1111/tbed.13025>.
- Ribeiro-Lima, J., Enns, E.A., Thompson, B., Craft, M.E., Wells, S.J., 2015. From network analysis to risk analysis—An approach to risk-based surveillance for bovine tuberculosis in Minnesota, US. *Prev. Vet. Med.* 118 (4), 328–340. <https://doi.org/10.1016/j.prevetmed.2014.12.007>.
- Sheridan, M., Good, M., More, S.J., Gormley, E., 2014. The impact of an integrated wildlife and bovine tuberculosis eradication program in Ireland. In: Thoen, C.O., Steele, J.H. (Eds.), *Zoonotic Tuberculosis: Mycobacterium bovis and other Pathogenic Mycobacteria*. Wiley-Blackwell, Iowa, USA, pp. 323–340. ISBN: 978-1-118-47429-7.
- Stoica, P., Selen, Y., 2004. Model-order selection: a review of information criterion rules. *IEEE Signal Process. Mag.* 36–47. <https://doi.org/10.1109/MSP.2004.1311138>.
- Tratalos, J.A., Madden, J.M., McGrath, G., Graham, D.A., Collins, Á.B., More, S.J., 2020. Spatial and network characteristics of Irish cattle movements. *Prev. Vet. Med.* 183. <https://doi.org/10.1016/j.prevetmed.2020.105095>.
- White, P.W., Martin, S.W., De Jong, M.C.M., O’Keefe, J.J., More, S.J., Frankena, K., 2013. The importance of neighbourhood in the persistence of bovine tuberculosis in Irish cattle herds. *Prev. Vet. Med.* 110, 346–355. <https://doi.org/10.1016/j.prevetmed.2013.02.012>.
- Wolfe, D.M., Berke, O., More, S.J., Kelton, D.F., White, P., O’Keefe, J.J., Martin, S.W., 2009. The risk of a positive test for bovine tuberculosis in cattle purchased from herds with and without a recent history of bovine tuberculosis in Ireland. *Prev. Vet. Med.* 92, 99–105. <https://doi.org/10.1016/j.prevetmed.2009.07.012>.
- Zimmermann, J., Fealy, R.M., Lydon, K., Mockley, E.M., O’Brien, P., Packham, I., Smith, G., Green, S., 2016. The Irish Land-Parcels Identification System (LPIS)—Experiences in ongoing and recent environmental research and land cover mapping. *Biol. Environ.: Proc. R. Ir. Acad.* 116B, 53–62. <https://doi.org/10.1353/bae.2016.0025>.