



Development of risk-based trading farm scoring system to assist with the control of bovine tuberculosis in cattle in England and Wales



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ABSTRACT

Identifying and ranking cattle herds with a higher risk of being or becoming infected on known risk factors can help target farm biosecurity, surveillance schemes and reduce spread through animal trading. This paper describes a quantitative approach to develop risk scores, based on the probability of infection in a herd with bovine tuberculosis (bTB), to be used in a risk-based trading (RBT) scheme in England and Wales. To produce a practical scoring system the risk factors included need to be simple and quick to understand, sufficiently informative and derived from centralised national databases to enable verification and assess compliance. A logistic regression identified herd history of bTB, local bTB prevalence, herd size and movements of animals onto farms in batches from high risk areas as being significantly associated with the probability of bTB infection on farm. Risk factors were assigned points using the estimated odds ratios to weight them. The farm risk score was defined as the sum of these individual points yielding a range from 1 to 5 and was calculated for each cattle farm that was trading animals in England and Wales at the start of a year. Within 12 months, of those farms tested, 30.3% of score 5 farms had a breakdown (sensitivity). Of farms scoring 1–4 only 5.4% incurred a breakdown (1-specificity). The use of this risk scoring system within RBT has the potential to reduce infected cattle movements; however, there are cost implications in ensuring that the information underpinning any system is accurate and up to date.

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1. Introduction

Bovine tuberculosis (bTB) is an infectious disease of cattle caused by the bacterium *Mycobacterium bovis* (*M. bovis*). The disease has proved expensive and difficult to eradicate in livestock once the disease has been introduced into a new area. This is due to long incubation periods, moderate sensitivity of diagnostic tests, presence of spatially dependent disease transmission factors including infected wildlife reservoirs in certain areas, and the further complication of undetected infected cattle being traded between farms. One method of targeting resources in animal health eradication programmes is to apply risk-based concepts which may

include risk-based surveillance or risk-based trading (RBT) with the categorisation or risk scoring of farms most likely to be affected.

Risk-based surveillance enables higher efficiency (benefit-cost) than traditional systems from the application of exposure and risk assessment methods (Stärk et al., 2006). Risk-based surveillance systems for bTB have been developed for Minnesota US, Scotland and Ireland using a variety of methods to target herds according to risk, taking into account the most likely transmission pathways present in those territories (Ribeiro-Lima et al., 2015; Bessell et al., 2013; Wolfe et al., 2010). There is normally a small group or individual risk manager, in industry or government, who is responsible for the implementation of surveillance schemes and identifying those premises or animals to be tested. The level of resources and training of the risk manager may permit development of complex methodologies and ranking systems, using a broad range of risk factors including spatial factors (climate and population density), host factors, and management factors (biosecurity and risk practices) (Oidtmann et al., 2013). With unrestricted risk-based trading schemes there may be as many risk managers as there are batches of cattle being sold, where a rapid view of the information, consideration and subsequent decision needs to be made by cattle

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purchasers. Due to these requirements such schemes need to be (1) practical: risk categories need to be presented in a simple, standardised and unambiguous way enabling rapid identification of different risk levels, (2) transparent: farmers need to be able to understand how risk scores are estimated and be able to gain sufficient information from those scores to make an informed choice at purchase, and (3) based on accurate and available data: in order for any scheme to work the information used must be robust, with categories and the relative rankings reflecting the risk that animals originating from that herd are infected (Defra, 2013; Kennedy, 2003).

Approaches taken to ranking herds may be based on subjective judgement or more quantitative methods including risk factor analysis, based on within-herd prevalence, or other risk assessment activities. There are significant variations in national approaches that have been applied to classify herds within current animal health RBT schemes, even within programmes focused on the control of the same disease. For example, there are multiple herd scoring systems for Johne's disease (*Mycobacterium avium* subspecies *paratuberculosis*) including prevalence based systems, categorisations derived from quantitative risk assessment, and expert judgement classifications (Geraghty et al., 2014). For bTB several eradication programmes have implemented RBT schemes based on the number of years that a herd tests clear of disease. The Australian scheme coupled this herd classification with a ban on the movement of cattle from high risk farms/zones to low risk farms/zones, where zones were classified by a maximum permissible between herd prevalence (Cousins, 2001). In New Zealand, trade can occur between farms of differing bTB risk; however, the farm status is based on the lowest of all animals in the herd, deterring the purchase of lower status cattle.

The aim of this research was to develop a quantitative approach for England and Wales to classify cattle herds on the probability of being infected with bovine tuberculosis (bTB), which could be used within a risk-based trading scheme. A final aim to estimate the impact of selected scoring systems on infected movements is presented in the accompanying paper.

2. Material and methods

There were five key stages in developing the risk-based trading scoring system:

- (1) Estimation of the probability of bTB infection for each farm in England and Wales.
- (2) Identification and inclusion of risk factors (that could be practically applied in a scoring system) significantly associated with the probability of bTB infection using a generalised linear model.
- (3) Selection of a method to present the risk scoring system.
- (4) Calculation of the points contributing to the risk score using the mean odds ratios; and,
- (5) Assessment of the performance of the scoring system in the sensitivity analysis.

The results of the sensitivity analysis were then used to optimise the selection of risk factors to be retained in a risk scoring system.

2.1. Study population and data sources

The study population was active cattle herds in England and Wales recorded on cattle surveillance databases (SAM RADAR bTB reception database (SAM)) between July 2009 and June 2010, which amounted to 60,233 herds. Surveillance data for each herd was downloaded on the 1st April 2013 of all bTB tests undertaken

between July 2005 and June 2010. The single intradermal comparative cervical tuberculin test (SICCT) is used for all routine surveillance. The test frequency varies with annual herd testing in high incidence areas in England and throughout Wales and quaterly in low incidence areas of England. Data extracted from external data sources included cattle movements to slaughter and movements on/off herd by year by County Parish Holding (CPH) identifier from Cattle Tracing System (CTS) (BCMS, 2013). Herds were not separated at holding level due to limitations in extracting movement data to that strata.

2.2. Estimated probability of bTB infection per herd, $P(\text{Inf})$

The estimated probability of bTB infection per farm in England and Wales was generated by modifying a freedom from infection (FFI) model (AHVLA, 2011). This Bayesian model was previously developed to estimate the probability that a given herd was free of infection given its test and disease history and the probability of introduction of infection (Martin et al., 2007; Cameron and Baldock, 1998a,b). This model framework has been adapted and described in full for estimating the probability of cattle herd bTB incidents using Scottish bTB surveillance data (Bessell et al., 2012). The underlying premise of the model is that the probability of infection on farm can be estimated based on the farms testing history and on the probability of introduction since that time. The model inputs required are herd size, the frequency and number of animals in the herd historically tested together with test results, animal-level sensitivity of the diagnostic test performance (Downs et al., 2011), an initial prior infection status of farm and the probability of introduction of bTB infection into herd during each time period. The probability that a herd is infected with bTB at time t , $P(\text{Inf})$, was estimated using this approach which is presented with the relevant formula in Supplementary materials. Several modifications using English and Welsh surveillance were made and are detailed as follows.

The probability of bTB infection in herd at the starting time point (time = 0) for each farm was estimated by the bTB incidence rate at that time point. The probability of introduction of bTB infection into the herd during each subsequent time period was based on observed bTB incidence rate updated annually from June 2005.

The bTB incidence rate was defined as the rate of new herd bTB incidents in the period of interest relative to the sum of the time the herds (time at risk or TAR) were at risk of infection (and officially tuberculosis free). New herd bTB incidents may occur as a result of herd tests (tests conducted on the majority of animals in the herd) and individual animal tests during the time period of interest. The TAR is the sum of time the herd was at risk of infection from the last negative herd test up to the most recent negative herd test in the period of interest. It excludes periods of time the herd was restricted as result of a bTB incident (see Appendix to Downs et al., 2013). The background incidence rate calculated for this study was each herd was the overall incidence rate for the 200 herds that were geographically closest.

When an infection was detected in a herd due to a positive bTB test either during field surveillance, or through post-mortem inspection in the abattoir, the probability of freedom from infection, $1 - P(\text{Inf})$, was reduced to zero. At this point, the farm was subject to cattle movement restrictions until the confirmed cases were removed and at least one (although usually two) successive short interval skin tests were undertaken with negative test results. During this entire period the probability that the herd was free from infection remained at zero to indicate the herd remained infected. When movement restrictions were lifted, the probability that the herd was free from infection was reset to the original prior but limited to a maximum value of 62% for the following 24 months using evidence for the probability of bTB recurrence of infection (Karolemeas et al., 2011).

Table 1
Summary statistics of the full model derived from regression analysis and the points allocated in the baseline risk scoring system. Only grey highlighted factors are included in the selected risk scoring system explored in the risk assessment.

Risk factor	Full model Mean odds ratio [5th, 95th confidence interval]	Baseline Risk points ^a
Initial value for all farms		+1
Years since bTB breakdown		
0–2 years	8.4 [7.9, 8.9]	+3
3–5 years	4.5 [4.2, 4.8]	+2
6–10 years	2.1 [1.9, 2.3]	+1
>10 years	1.5 [1.3, 1.7]	Not included
Cattle movements from high risk area		
>0 in the last 5 years	1.6 [1.5, 1.6]	+1
Herd size (0–10 head)	1.6 [1.5, 1.8]	Not included
Region: West England	3.7 [3.5, 3.9]	Not included
Region: Wales	2.2 [2.1, 2.4]	Not included

^a Where Risk points=Round (Mean odds ratio $\times \frac{\text{Score from additional factors (4)}}{\text{Maximum odds ratio risk (8.4+1.6)}} + 0$). Breakdown inclusive of confirmed (OTFW) or unconfirmed (OTFS) cases.

Using the modified model, together with the Excel Add-on @Risk (version 6.1), the probability that each herd was infected with bTB, $P(\text{Inf})$, was calculated stochastically for each year, assuming that the on-farm variability of infection with bTB can be described by the binomial process. A burn-in period from 1st June 2005 was used, with the probability of bTB infection for each CPH in England and Wales estimated for the final year 1st June 2009–1st June 2010.

2.3. Identification and inclusion of risk factors in full model

A literature review was conducted to identify those risk factors cited in the literature as being associated with the occurrence of bTB on farm. In total 41 different risk factors were identified in the literature (refer to Supplementary materials). Each risk factor was examined against inclusion criteria for further consideration in the model. The inclusion criteria were studies of relevance to England and Wales and the availability of good quality data to estimate the risk factor for each farm. Climatic variables were excluded as being intractable by either farmer's actions or regulation, and the breed, age and sex of animals on farm were excluded as individual animal-based traits. Applying these criteria, 35 risk factors were removed. The six risk factors remaining for further analysis were identified as (1) herd history of suspected bTB (Official TB Free Status Suspended (OTFS)), (2) herd history of confirmed bTB (Official TB Free Status Withdrawn (OTFW)), (3) local bTB prevalence, (4) movement history onto farm, (5) herd size, and (6) herd type. Herd size was defined as the number of cattle on farm on 1st January 2010. Where this data was absent, the average from July 2009 to June 2010 was used. For movements, the term "high risk" and "low risk" were spatially defined. For England, "low risk" areas were those located in a surveillance zone where testing was carried out once every 4 years. Movements from all remaining areas were defined as "high risk". For Wales, there was one "low risk" area: Gwynedd, with the remaining areas in Wales defined as "high risk".

The estimated probability that each herd was infected with bTB, $P(\text{Inf})$, described previously, was used as the response variable. Each risk factor was incorporated into a generalised linear model of the binomial family, with a logit link function. Preceding the model building, investigations were carried out to determine the critical intervals for continuous variables and the most relevant groupings for categorical variables by placing each variable in a univariate model and calculating the statistical significance of the defined categories. This was completed to select the most appropriate variable to enter the initial base model where variables were possibly collinear or confounding. The model was developed in the R programming language, using the *glm* function (R-2.14.1 (December Snowflakes)). The model provided estimates of the coef-

Table 2

Results of stakeholder questionnaire to rank different methods of presenting the risk scoring system.

	Ranking of score presentation			
	Most useful	Useful	Not useful	No response
Traffic lights (e.g. red amber and green)	4	5	2	2
Text (e.g. high, medium and low)	1	5	2	5
Number (e.g. 5–1)	9	2	2	0

ficients associated with each potential risk factor and odds ratios (OR) were calculated by taking the exponential of the coefficient.

Backwards stepwise regression was used to determine the most appropriate model (using the *step* function in R-2.14.1), starting with a model containing all of the variables significantly associated with the probability that each herd was infected with bTB, $P(\text{Inf})$, at the univariate stage (i.e. a P -value <0.25). The different models were compared using Bayes information criterion (BIC) to determine which one was the best fit. This provides a likelihood measure for a finite set of models where a higher penalty is applied for increasing the number of parameters in the model than using the Akaike information criterion (AIC). Calculations were made for the pseudo R^2 statistic ((defined as $1-L_M/L_0$), where L_M is the log likelihood of the full model and L_0 is the log likelihood of the model with no predictors, i.e. the null model) (McFadden, 1973). The risk factors selected and corresponding odds ratios in the full model are presented in Table 1 column titled full model. The performance of variations in the application of the full model, with removal of certain risk factors, was investigated in the sensitivity analysis.

2.4. Method of representing the risk in a trading scheme

There are a number of ways in which risk scoring systems are presented. Parts of the food industry use traffic light colours (green, amber and red) to indicate the levels of salt, sugar and fat in foods. Hotels and internet sites use stars to rate products, whilst terms (low, medium and high) and numbers have been used in other risk-based trading frameworks. Discussions were held during 2012–2013 with the England Risk-Based Trading Working Group (Defra, 2013), and other cattle industry stakeholders in England and Wales on the different formats to declare the risk scores, including a 1–5 score, 1–10 score and colour scheme (green, amber and red) representing low, medium and high risk scores. Participants in England were asked individually to rank a number of methods to represent the risk in a trading scheme as most useful, useful or not useful. The results of 13 individual respondents are shown in Table 2. From these discussions and responses to the questionnaire, a final presentation scheme consisting of a numerical risk score

Table 3
Matrix of used definitions of true positive, false positive, false negative and false positive.

		Risk score	
		High risk Score 5	Lower risk Score 1–4
Farms with tests in the outcome year ^a	Tested positive	TP	FP
	Tested negative	FN	TN

TP: True positive, FP: false positive, FN: false negative, TN: true negative.

^a Positive inclusive of confirmed (OTFW) or unconfirmed (OTFS) cases.

with 5 divisions from 1 to 5 was selected with increasing score corresponding to increasing risk. All farms were scored initially at 1 with additional points added if other risk factors were present.

2.5. Calculating the risk score points from the odds ratios

To estimate the additional points for the presence of other risk factors, we used the calculated mean point estimate of the odds ratios presented in Table 1 to weight the selected risk factors and rounded each to an integer, to ensure the maximum score was a total of 5 points. The points allocated within the risk score would vary depending on the risk factors odds ratio values included in the overall score, and the presentation of the scoring (e.g. 1–10 or 1–5). An example of the calculation to estimate the contribution of four different factors (highlighted in grey) with additional points needing to equal 4 (a 5 point system where all farms have one point initially) is shown in Table 1 in the column titled Baseline risk points.

2.6. Sensitivity analysis and selection of a baseline scoring system

We investigated the performance of the scoring system using bTB surveillance data. Removal of risk factors identified from the full model allowed comparison of the most simple system involving one risk factor measure (score A) to a more complex scoring system approaching the full model (score D). The ability of the scoring system based on data from 2005 to 2010 to predict those farms that tested positive in the following year in 2011 (skin test positive, gamma interferon positive and cases identified at slaughter house) was compared. As shown in Table 3, the risk scoring system was assigned as the gold standard since it contains our best estimate of true infection status of the farms, with the test results (from field and slaughterhouse surveillance) in the follow-

ing year assigned as the test. Risk scores were defined as either high risk score (score 5) or a lower risk score (score 1–4) with this cut off agreed as most informative with stakeholders. The following equations were used to estimate the sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) for each scoring system:

$$\text{Sensitivity} = \frac{TP}{TP + FN}, \text{ Specificity} = \frac{TN}{FP + TN}, \text{ PPV} = \frac{TP}{TP + FP}, \text{ NPV} = \frac{TN}{TN + FN}$$

In addition, we compared the outputs from simulating the scoring system in a risk assessment (described in the accompanying paper).

3. Results

3.1. Risk scoring system

The risk factors identified by the logistic regression and the relative importance in the form of odds ratios are provided in Table 1 (results for univariate analysis provided in Supplementary materials). The pseudo R^2 statistic of the full model was only 30% which may reflect a high level of variation in the estimated probability of bTB infection on farm and/or incomplete specification of explanatory factors. The risk factors included in the model were re-evaluated in terms of practical implementation of a risk-based scoring system containing that combination of measures. Breakdowns longer than 10 years previously were removed due to the extended period of assessment required, with the consequence that a farm having ever incurred a breakdown would be permanently assigned a higher score. Secondly, once all other factors had been considered in the full model the remaining risk was best represented by inclusion of small farm sizes (1–10 head). From the univariate analysis and previous studies, increasing herd size is associated with increasing risk of bTB on farm. The univariate analysis found a protective effect of small farm sizes with an odds ratio of 0.7 [0.67, 0.74] for farms of 0–10 animals, although this effect did not persist in the multivariate analysis and the variable was therefore not included as a risk factor to calculate risk scores. The inclusion of region was further explored in the sensitivity analysis.

3.2. Sensitivity analysis and selection of a baseline scoring system

The results from comparing the performance of scoring systems A–D with the removal and addition of risk factors identified in the full model are displayed in Table 4, together with the num-

Table 4
Classification of farms into score 1–5 using various RBT schemes; validation statistics and percentage reduction in infected movements for each scheme.

	Risk-based trading scoring systems			
	A (Simplest)	B	C (Baseline)	D (approaching full model)
Ability of risk scores to predict test results in outcome year				
Sensitivity	29.7%	29.7%	30.3%	30.0%
Specificity	95.1%	95.1%	94.6%	93.8%
PPV	55.1%	55.1%	49.4%	39.5%
NPV	87.0%	87.0%	88.7%	90.8%
Percentage of farms in England and Wales classified to each score				
5	15.9%	15.9%	14.0%	11.3%
4	0%	0%	8.1%	11.6%
3	0%	7.3%	4.4%	25.5%
1 or 2	84.1%	76.8%	73.5%	51.6%
Estimated impact on reducing infected animal movements ^a				
Mean	30.2%	34.7%	36.6%	37.6%

Scoring system A: year since breakdown (0–2 years).

Scoring system B: years since breakdown (0–2, 3–5 and 6–10 years).

Scoring system C (baseline): years since breakdown (0–2, 3–5 and 6–10 years) and high risk movements in the last 5 years (>0).

Scoring system D: years since breakdown (0–2, 3–5 and 6–10 years) and high risk movements in the last 5 years (>0), location of farm (Wales, West England).

^a Estimated using risk assessment for Statutory scenario, 90% compliance level.

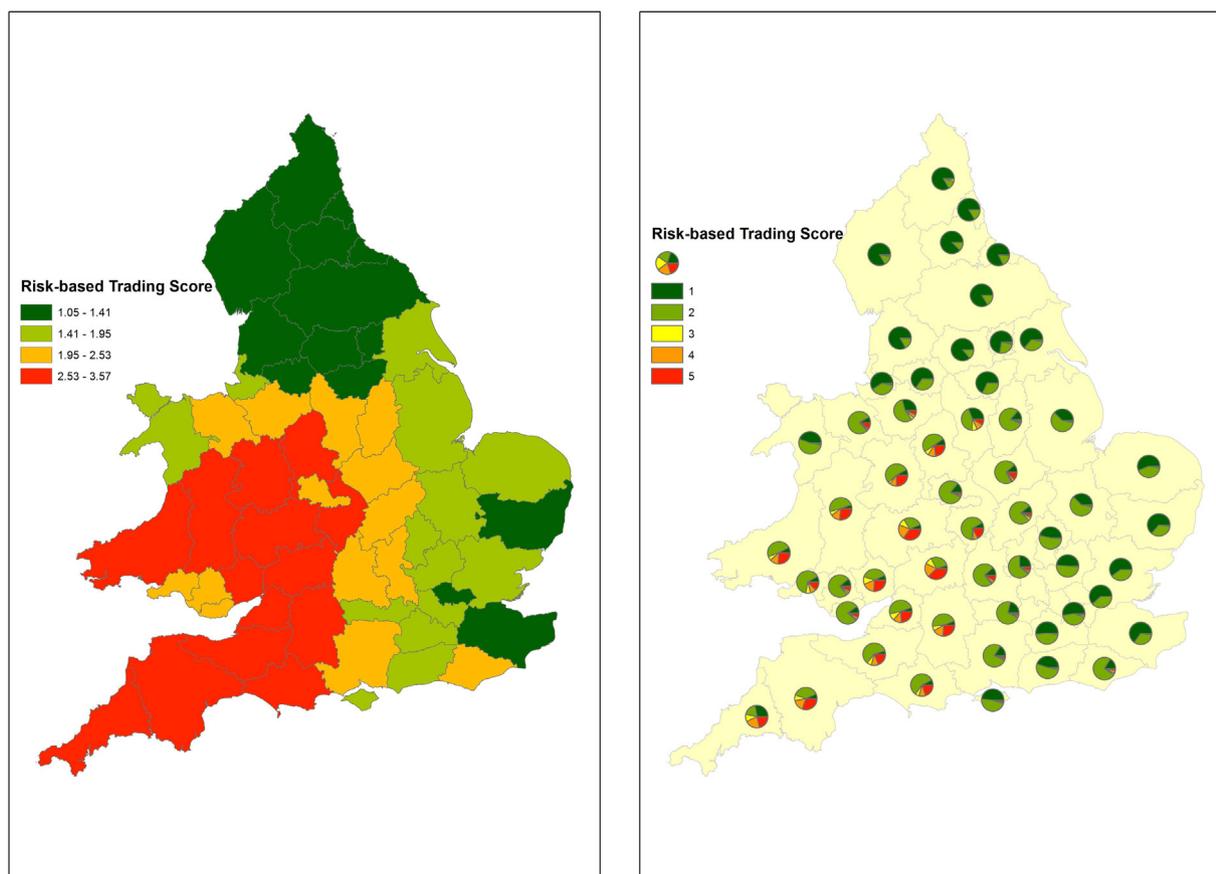


Fig. 1. Estimated average risk score (numerical 1–5) for each county based on individual farm scores in England and Wales^a, and individual pie charts per county illustrating the proportion of farms per risk score.

^aThe cut-off values assigned from quantile classification of the data. A quarter of the total data points are in each category.

ber of farms classified by score for each RBT system. In general, lower score farms have a high probability of subsequently testing negative. For example, in the baseline scoring system only 5.4% of those farms scoring 1–4 tested positive in the following year (1-specificity). In contrast 30.3% of farms scoring 5 tested positive in the following year (sensitivity) within that score system. Results are also provided where the different scoring systems have been used in a stochastic risk assessment (described in the accompanying paper). The risk assessment estimates the impact of risk-based scoring systems on reducing the percentage of infected cattle traded annually using historic movement data recorded between July 2010 and June 2011. [Table 4](#) provides the mean percentage reduction in infected movements from simulating each scoring system using the risk assessment where a theoretical compliance of 90% of farmers is used (statutory scenario).

The simplest scoring system A is based solely on whether a farm has incurred a breakdown in the last two years. Under system A there is an estimated reduction in infected movements of 30.2%. Including breakdown data up to ten years previously in scoring system B, increases the estimated reduction to 34.9%. These systems would be the simplest to implement with the data required available from one database. Inclusion of high risk batch movements in scoring system C increases the mean reduction in infected movements to 36.6% and produces the highest score system sensitivity value of 30.3%. Increasing the complexity of this scoring system with additional risk factors approaching the full model selected by the regression analysis, for example, D does not increase the sensitivity of the scoring system.

When selecting the baseline scoring system, ideally the system would have the highest sensitivity, specificity, NPV and PPV whilst limiting the financial impact on cattle trades and with a particular weighting to those scoring systems reducing the movement of infected animals. However, in view of the use of the scores to inform purchasers, of these measures the sensitivity and 1-specificity of the scoring system are likely to be the most important, i.e. the probability of a score 5 farm testing positive in the following year, and the probability of a score 1–4 farm subsequently testing positive. Additionally the scoring system assigning the highest percentage of farms in England and Wales as low risk (score 1 and 2) may encourage the highest uptake in a voluntary scheme thereby indirectly increasing the effectiveness of a scheme. [Table 4](#) presents the relative estimates of these statistics. Variations of this risk-based scoring system could be further explored in terms of the cost of implementation (not considered in this study); however, the most favoured simplified scoring system C, with the highest sensitivity, comprised of the number of years since the last farm tested positive (up to 10 years previously), together with any movements from areas deemed to be high risk. The risk points for each of these factors are shown in [Table 1](#). [Fig. 1](#) displays the resulting geographical distribution of the selected risk scoring system, with the average per county in England and Wales and the distribution of farms achieving each score per county. From viewing the results for the high risk area in England and Wales, it can be seen that there are significant proportions of farms are assigned at the two lowest risk scores (score 1 and 2) under the baseline scoring system. These farms may be particularly likely to participate within a voluntary trading scheme if established.

4. Discussion

The aim of this research was to develop a practical, transparent risk score for each herd in England and Wales with a ranking that reflects the risk that animals originating from that herd are infected. The quantitative approach developed is reliant on results from a logistic regression to identify the factors to be included and weighting within the scoring system. Specific inclusion criteria were applied to the factors that could be included, namely that the factors were practical, standardised, transparent to farmers, and could be verified if required.

Using this approach, the full model identified previous bTB breakdown history with the highest relative odds ratio, with farm location, and herd movements from high risk area associated with an increased probability of being infected. These results are consistent with other studies conducted. [Bessell et al. \(2012\)](#) identified breakdowns in lower risk areas in Great Britain were associated with number of animals bought from high incidence areas, and in high risk areas with a history of disease and probability of badger occurrence using a multilevel logistic regression model.

Bessell and others also found that at the national level large herds and fattening herds are more likely to have an occurrence of a bTB breakdown. Herd size has been consistently and positively associated with the probability of a bTB incident or breakdown ([Goodchild and Clifton-Hadley, 2001](#); [Medley and Green, 2013](#)) and was demonstrated in the univariate results of this analysis. One explanation frequently given for this has been that the number of contacts and hence the probability of transmission increases with the number of animals in an epidemiological group ([Conlan et al., 2012](#)). Herd size was not positively related to the probability of infection in the final full model in this analysis and the absence of an association is difficult to explain. Sensitivity (and specificity) of a test at the herd level is determined by test performance at the animal level, herd size, the number of animals tested (sample size) and also the number of test-positive animals needed to classify the herd as positive (design prevalence) ([Wagner et al., 2013](#)). Herd level sensitivity increases as the number of test positive animals required to classify a herd as infected decreases. Only one test positive animal is required to classify a British herd as infected with bTB i.e. the probability of classifying a herd as infected maximized but also the probability of a false positive classification maximized. The Freedom From Infection (FFI) model assesses the probability of infection, given diagnostic test performance but not the probability of detection. If small herds are relatively less likely to be detected and classified as infected through field surveillance (because the probability of a false positive is lower) then herd size may be negatively associated with the probability of infection (based on the FFI model) as observed in the multivariate analysis. Alternatively, small herd size may describe some type of variability positively associated with bTB risk which is not captured by other variables or controlled for in the full model, perhaps related to a difference in the management of smaller farms, e.g. biosecurity, feed or other management practices.

The full model selected by the regression analysis had a relatively low pseudo R^2 with the risk factors explaining 30% of the variation about the mean. The pseudo R^2 statistic for the model including all the variables in the dataset was 55%, suggesting that there was still a reasonable amount of variability in the data that was unaccounted for by the model describing the probability of bTB infection on farm. This may reflect the misclassification in the specification of dependent and independent variables and/or the absence of significant risk factors from the analysis due to the specific inclusion criteria applied for application within a RBT scheme. Several groups of risk factors were excluded from the model including climatic variables, animal characteristics (e.g. breed and age), and the presence of infected wildlife reservoirs. During discussions

with stakeholders the non-inclusion of any wildlife related risk factors was raised, in particular the absence of any risk factors relating to badger presence. Badger occurrence has been associated with the risk of bTB breakdown and transmission from badgers to cattle is an important cause of breakdowns in high incidence areas ([Bessell et al., 2012](#); [Godfray et al., 2013](#)). However, data of sufficient coverage and quality for the period of time of the analysis was not available. The high level of variation in the estimated probability of bTB infection on farm identified in this study has also been previously found for bTB analyses by other researchers ([Karolemeas et al., 2011](#); [Wolfe et al., 2010](#)).

The outcome variable used in this analysis was the “probability of infection”—the complement of the outcome from the FFI model which is the “probability of freedom from infection”. This outcome differs from others commonly used which are based on the presence or absence of a bTB incident or breakdown or existence of reactors. The latter depends on detection of infection and therefore the performance of a diagnostic test whereas the former, probability of infection (based on the FFI model output), attempts to measure whether infection is actually present given the *performance of diagnostic tests* and historical test information. It is well accepted that there is significant undetected infection which is contributing to the epidemic ([Conlan et al., 2012](#)) so it is a strength of the RBT scoring system that it is based on a prediction model for infection and takes into account surveillance system sensitivity as opposed to detected infection. However, the evaluation of performance of the risk scoring system was based on the sensitivity and specificity of the score to predict farms test results in the following 12 months. This was due to the absence of any appropriate ‘gold standard’ to determine those farms that were infected rather than the subset that were infected farms detected. Giving a more sensitive diagnostic test the number of true positives would increase and false negative decrease. Therefore, the sensitivity of the RBT scoring system may be underestimated at 30.3% by using this test comparator, but may result in an overestimate for the specificity, reducing the value from 94.6%.

The baseline scoring system proposed is not perfect, as would be expected given the difficulties in predicting future herd bTB incidents and the exclusion of some risk factors which cannot be practically incorporated in an RBT scheme at this time. There is a need for further work to improve the practical implementation of the risk scoring system and provide more incentives for farmers to participate, in the case of voluntary schemes, whilst not unnecessarily disrupting trade. The baseline risk scoring system presented in this paper uses movements from a high risk area as a risk factor. However, the use of a specific area penalises farmers by location. If the scoring system was implemented, it would be advisable that the ‘movements from high risk areas (HRA)’ risk factor was replaced by ‘movements from high risk farms (HRF)’. In this way, farms which may have worked hard to ensure a low risk status would not be penalised for being located in a high risk region with buyers not incurring a higher risk score by purchasing stock from them. Initial trials have estimated the reduction in infected movements, using the accompanying risk assessment, comparing scoring systems based on movements from HRA versus movements from HRF. Preliminary results indicate a scoring system with points added for on-movements from HRF (score 5) provides a slightly better performance but within model convergence values as the baseline scoring system presented. Additionally, actions taken by farmers to reduce their risk of bTB were not included in the analysis due to limited data available, for example, the degree of risk reduction from implementing specific biosecurity measures, or which farms are members of certain assurance schemes. Furthermore, any scheme must enable and encourage progression towards the lower risk categories. Whilst the full model selected the longest timeframes available for both animal movement history and occur-

rence of breakdowns, a reduction in the time a farmer is penalised for certain actions or events may be worthwhile. For example, cost-benefit analysis and social research may provide insight to where acceptable reductions in the sensitivity of the scoring system can be made if considerably greater uptake of the scheme by farmers could be demonstrated.

So, is a risk-based trading scheme a possibility in England and Wales? Such policy decisions will depend on the expected costs and benefits that such a scheme would provide, the debate of which this paper feeds into. For the baseline scoring system identified here, as evidenced from the sensitivity and the estimated impacts on reducing infected animal movements as indicated in Table 4, a trading scheme, on its own, will not completely prevent the spread of bTB from cattle movements, however, it may, in certain areas, contribute to the aim of reducing RO (reproduction number) indicating spread of infection to below one in combination with other measures. As discussed in the accompanying paper, key to high performing risk-based trading schemes is farmer confidence and participation in such schemes and the education of farmers—particularly with the concept that a clear test for bTB does not provide 100% confidence that an animal is free from bTB due to the relatively low sensitivity of the tuberculin skin test. In 2013 a voluntary system in England was initiated where purchasing farmers are being urged to ask sellers the date of the last pre-movement test, date of last herd test and date of TB free status in a step towards starting the conversations needed.

5. Conclusions

In this paper we have described a quantitative method for designing risk scores for use in a bTB risk-based trading scheme. A review of the literature was conducted to identify relevant risk factors associated with the probability of bTB on a farm. Logistic regression was applied to those risk factors that were deemed to be available for a risk-based scoring system and estimated odds ratio values used to weight them in a scoring system. The input data required for the risk score to be calculated must be available for all farms and needs to be accurate and kept up to date. The approach could be useful for the quantitative development of risk-based scoring systems for other livestock pathogens where the inter-dependency of numerous risk factors exists.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.prevetmed.2015.11.020>.

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