

Evaluation of bovine tuberculosis surveillance in Jersey and Guernsey

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Executive Summary

While outbreaks of bovine tuberculosis (bTB) continue in many countries within the European Union, the Bailiwicks of Jersey and Guernsey have not had a recorded case of bTB since 1952 and 1937, respectively. The purpose of this study was to analyse current surveillance strategies for both nations in order to provide:

1. A quantitative estimate of the probability that the Bailiwicks of Jersey and Guernsey are bTB free.
2. A recommendation of alternative surveillance strategies that could be used under conditions of confirmed disease freedom.

A review of the available literature suggests that the risk of introduction of bTB into the Channel Islands is likely to be low. It is therefore assumed that any introduction would occur at a rate consistent with the observation of the last known introductions, modified to consider the reduction in prevalence of bTB in cattle over this period. Risk of persistence, if introduced, was analysed using bespoke simulation models that were created utilising recorded births, deaths and animal movements between holdings for the periods of 2003-2013 and 2001-2011 for Jersey and Guernsey, respectively. These models were based on the available data for each jurisdiction and assumed each individual herd was homogeneously mixed, with interactions between herds governed by recorded cattle movements. An examination of the simulated epidemics over time can inform a number of key questions:

- How long would it take for disease to be detected if introduced?
- What proportion of herds and animals would become infected when the disease is detected?
- How do these values change under altered surveillance strategies?

Transmission parameters consistent with the rates seen in low-incidence areas of Great Britain were used as these were assumed to be representative of those likely to be relevant for the Channel Islands. The risk of existing wildlife reservoirs of disease was considered to be negligible. The spread of disease was simulated by introducing a single infected animal into an otherwise wholly susceptible population at the beginning of the simulation period, allowing the infection to spread over time and estimating the following outcome measures:

- The probability of latent bTB cases in each year post introduction
- The size of possible outbreaks if detected
- The probability that the disease would disappear unnoticed.

After the introduction of a single case, in very few instances was the infection found to spread unchecked, with identified outbreak size declining after approximately five years in both jurisdictions. This indicated that endemic bTB is extremely unlikely to become established, even if there were an introduction. Combining the probability (i) above with the probability of introduction per year (calculated as one over the number of years since the disease was last observed) provides an estimate of the upper limit of disease prevalence consistent with the current surveillance strategy. The maximum estimated disease prevalence for both dependencies was found to be 0.0001 and 0.0005, while the overall probability of detecting one test sensitive animal was 0.00005 and 0.0002 in Jersey and Guernsey respectively. Thus it is

extremely unlikely that any past introduction event to the Channel Islands cattle population would have remained undiscovered for any protracted period.

Our analysis suggests that under current testing, both Jersey and Guernsey have disease status that is consistent with freedom according to Article 11.6.2. of the World Organisation for Animal Health (OIE) Terrestrial Animal Health Code. With regards to the European Union Council Directive 98/46/EC amending Council Directive 64/432/EEC, a single infected herd in any of the Channel Islands would be above the limit of 0.1% of herds threshold required for disease freedom. However we can state with confidence that the estimated prevalence is low enough to provide evidence in support of official disease freedom.

The developed simulation model not only allows for evaluation of the current surveillance system, but is also a powerful tool for evaluating alternative surveillance strategies. Two amendments to the current surveillance activities were also considered as previously mentioned:

1. A testing-free abattoir-only surveillance.
2. A reduced number of skin tests based on the number of animals sent to the abattoir.

The majority of instances where disease was undetected across all surveillance schemes involved small, poorly connected herds with few or no animals sent to slaughter. However, these herds had very few or no outward movements to the system at large, mitigating the threat of introduction of bTB to other farms. Simulations that assumed abattoir-only surveillance missed infections at some smaller farms that never sent cattle to slaughter, which sometimes resulted in prolonged persistence. Although current surveillance is adequate in displaying disease freedom, developing a testing regime that reduces the number of skin tests in herds with a greater number of movements to the abattoir may prove the most cost-effective route to maintaining disease freedom by reducing the number of tests on Jersey and Guernsey by 99.5% and 95.1%, respectively. However efforts should remain concentrated on ensuring the infection is never introduced, as well as retaining a sufficient surveillance safety-net to mitigate onward transmission, should introduction occur.

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Glossary

Breakdown	The discovery of one or more tuberculin reactor animals in a herd.
Sensitivity	True Positive Rate. The actual proportion of animals with the disease which test positive. It is a measure of the probability that a diseased individual will be correctly identified by the test.
Specificity	True Negative Rate. The actual proportion of animals without the disease which test negative. It is a measure of the probability that an individual without the disease will be correctly identified by the test.

1. Introduction

Bovine tuberculosis (bTB) is a chronic disease that inflicts a heavy economic burden on many countries where it is endemic in cattle. The causative agent of bTB is *Mycobacterium bovis*, which is part of the larger pathogenic *Mycobacterium tuberculosis* complex. It is predominately spread between cattle via aerosol droplets (Menzies and Neill 2000), though the possibility of infection from a contaminated environment cannot currently be excluded (Courtenay et al. 2006). The wide-spread pasteurisation of milk has largely eliminated most risk of zoonotic infection (Torgerson and Torgerson 2010), although areas where this is not commonly practised still see sporadic human cases of tuberculosis caused by *M. bovis* (Michel et al. 2010).

The Bailiwicks of Jersey and Guernsey are an archipelago of British Crown Dependencies (hereafter designated as CDs) off the coast of Normandy, France. Neither dependency is a member of the European Union, although there is free movement of agricultural goods and their derived products between the EU and the CDs, subject to compliance with governing legislation for movement controls. The cattle industries of the Channel Islands consist overwhelmingly of dairy herds and milk production, which represents a critical agricultural export for Jersey and source of pride for Guernsey. The island of Jersey is a completely closed system, while the Bailiwick of Guernsey will only import cattle from member islands within the Bailiwick (i.e. Guernsey, Sark, Herm and Alderney).

The concept of disease freedom does not necessitate a country (or herd) to be completely absent of infection. Official freedom from bovine tuberculosis (OTF) status requires that certain surveillance criteria be met, as well as a demonstration of disease prevalence below a mandated threshold (Cannon 2002). The European Union has set standards for intra-Community trade of cattle and in order for the Channel Islands to prove freedom from bovine tuberculosis, according to the European Union Council Directive 98/46/EC (amending Council Directive 64/432/EEC), a number of conditions must be met. The directive stipulates that a system for tracing cattle movements must be in place and all slaughtered cattle are subjected to post-mortem examination. Importantly, it also states that the percentage of bovine herds confirmed as infected with tuberculosis does not exceed 0.1% per year of all herds for six consecutive years and at least 99.9% of herds achieve tuberculosis-free status each year for six consecutive years. The World Organization for Animal Health (OIE) states that for a country to be free from bTB, at least 99.8% of herds and 99.9% of cattle must be demonstrably free from infection for three consecutive years. In order to establish whether or not Jersey and Guernsey meet these criteria, we utilised the information that neither Jersey nor Guernsey has shown signs of the disease in their herds in over 50 years. We also exploited databases of cattle movements and herd locations, allowing us to develop a simulation approach to determine the limits of current prevalence of bTB in both CDs.

Freedom from bTB has been displayed across a number of systems under an apparent absence of identifiable infection (Calvo-Artavia et al. 2013; Wahlstrom et al. 2010). These examples have relied on methods developed using stochastic scenario trees of herd prevalence and disease detection drawn from empirical evidence or expert opinion. The individual-based simulation model of bTB put forward here is an improvement over these aforementioned models largely because recorded animal movements can be taken into account, allowing the explicit spread of the pathogen to be observed at each time step. As a result, the current surveillance strategy could be tested retrospectively by seeding the disease and noting if, when, where it spreads and

how many animals and locations were infected as well as by the form of surveillance under which the infection is detected. Furthermore, adjustments to the testing schedules permitted a variety of surveillance scenarios to be tested for sensitivity were the disease to be introduced under a particular surveillance strategy.

M. bovis has a broad host range. Introduction of the pathogen, while very unlikely, could potentially enter the Channel Island systems via multiple routes:

Human and cattle: Although humans are capable of developing zoonotic tuberculosis caused by *M. bovis*, there is only anecdotal evidence of anthroponotic transmission from farm workers passing the disease on to cattle (Huitema 1969). Infection is known to predominantly have been by the respiratory route (Thompson et al. 1993), though there is some suggestion that infection could be spread by individuals with active genitourinary tuberculosis urinating in cowsheds (Schliesser 1974). Risky behaviour for contracting *M. bovis* from infected animals include consuming unpasteurised milk products, working with cattle in areas lacking ventilation and sleeping in cowsheds (Torres-Gonzalez et al. 2013). The main risk factors associated with spreading *M. bovis* infection between humans and cattle include prolonged close human/cattle contact, poor food hygiene practices and HIV/AIDS infection (Cosivi et al. 1998), all of which are low for countries whose citizens are likely to come into contact with Jersey or Guernsey Island cattle.

Before milk pasteurisation became routine, non-pulmonary tuberculosis in humans caused by *M. bovis* was relatively common. Risk of *M. bovis* infection is now considered negligible in the UK (0.7% of reported human tuberculosis cases were bTB in 2013 (Anon 2013)); by comparison, in 1944 *M. bovis* was the cause of an estimated 6.2% of human tuberculosis deaths (Wilson 1943). Presently 57% of all *M. bovis* infection cases in the UK are in people over 65 years old, 79% of whom were born in the UK, a majority of which are reactivations of latent infection (Anon 2014a) and these are unlikely to be a source of exposure to cattle in the Channel Islands. Other countries show higher prevalences, with zoonotic bTB estimated to contribute around 1.4% of human TB cases worldwide with an incidence rate of less than 1/100,000 in Europe. However, only an estimated 4% of the population of Jersey (Anon 2012) and 2.5% of the population of Guernsey (Anon 2001) are born outside Europe, making the risk of these infected individuals immigrating very unlikely.

Domestic animals and cattle: The closed nature of the cattle systems greatly reduces the risk of disease introduction via cattle-to-cattle transmission (Johnston et al. 2011). *M. bovis* has a wide range of spill-over hosts, however passive surveillance in the UK from 2004-2010 reports only very small numbers of cases in a variety of species: 7 dogs, 35 goats, 24 sheep, 83 pigs, 2 farmed wild boar, 34 llamas, 133 Alpacas and 116 domestic cats with bTB (Broughan et al. 2013). While owners are required to have an import licence and veterinary approval before moving both pet and farmed non-bovid livestock onto the CDs, dogs, cats and ferrets are allowed to travel freely with their owners to the Channel Islands from the UK and from the rest of the world with an officially approved pet passport (Anon 2014b; Anon 2014c). There is no evidence that either dogs or cats act as maintenance host species for bTB and the only evidence for ferrets transmitting bTB comes from New Zealand (Nugent 2011). While there has not been a systematic approach to surveillance for bTB in pets in the UK, evidence from the passive surveillance above suggests that it can be assumed to pose a negligible risk.

Wildlife and cattle: The main species implicated as bTB reservoirs include the Eurasian badger in the UK and Ireland, and feral pigs and deer in mainland Europe, however these species are not found on the Channel Islands. In a review of the status of *M. bovis* infection in a field survey of mammals in the UK, Delahay and others (2002) described the pathology and observed incidence rates of bTB. Among other animals, their findings included brown rats (5 of 412 sampled), present in both CDs, and moles (2 of 162 sampled), that are present on Jersey (Anon 2011). Of the species shown to harbour bTB in an extensive sampling of British farmland wildlife (Mathews et al. 2006), only the bank vole is present on the Channel Islands, although only one out of the 1,307 sampled in GB was infected. *M. bovis* is unlikely to persist in the wild on its own in groups of smaller mammals and these animals are thought to present a trivial risk to spreading the infection. Strict regulations on the introduction of non-endemic wildlife are in place in the CDs, and in its current state, wildlife is likely to be unimportant for the introduction of bTB to uninfected cattle.

2. Materials and Methods

2.1. Data

Only those farms with cattle present at the beginning and the end of the time period were considered, which excluded 16 and 20 farms from Jersey and Guernsey, respectively. As such, recorded births, deaths, animal movements between holdings and herd census data were used in this simulation relating to:

- 5,079 animals in 38 herds for Jersey (2003-2013)
- 2,820 animals in 25 herds for Guernsey (2001-2011)

The purpose of this analysis was to test the likelihood of detecting a hypothetically introduced infection at the beginning of the simulation period, where our intention was to examine the implications for future bTB infection risk and necessary surveillance.

2.2. Model description

The simulation models were constructed using a bespoke framework in which individual cattle were tracked throughout simulated lifetimes, where data on the explicit life histories of the individuals were known and could be incorporated directly in the simulation. Starting with a single infected animal on day one of the introduction (as qualitatively justified above), the progression of the system over time was simulated using a well known approach designed to efficiently simulate rare events (Gillespie's τ -leap method (Gillespie 1976)), here using a fixed time step of 14 days. Cattle births, deaths and movements between premises and to the abattoir were included as input data. While movements to abattoir were provided for Jersey, movements to abattoir were not available before 2011 for the Bailiwick of Guernsey. The proportions of deaths as movements to the abattoir were fitted using a beta distribution (Section 6.2 below) to infer likely movements to the abattoir. The resultant counts of simulated movements were confirmed to be a likely representation of actual movements by the States Veterinary Officer of Guernsey (personal communication, Chamberlain, 2014). Cattle were then infected by calculating the exposure of susceptible cattle to infectious cattle. Upon the detection of the infection, the simulation run terminated, printing the date, farm, number of animals present and number of reactors to an output file. The date of the simulated breakdown, defined as the discovery of one or more reactor animals in a herd, was tabulated for each island separately for

further analyses. Simulation outputs were also checked to count the number of times the infection went undetected by the surveillance measures or was removed passively through an animal death.

Following existing models (Conlan et al. 2012; O'Hare et al. 2014), the infection process was approximated by four distinct stages, with cattle being either susceptible, exposed, test sensitive (where the animal can test positive for bTB but is not yet infectious) and actively infectious (Figure 2.1). The exposed stage is a latent stage of the infection where the bacteria are present in the animal, but its immune system has not yet mounted a sufficient response so that the infection is detectable by the current Single Intra-dermal Comparative Cervical Tuberculin (SICCT) test. Cattle in the test sensitive and infectious stages are detectable by this test. Additionally, the surveillance of animals at the abattoir is parameterised to model the post-mortem detection of tuberculous granulomas in the lymph nodes. Both the intra-dermal skin test and abattoir surveillance are assumed to have 100% specificity, meaning that the possibility of a false positive was not considered. Susceptible cattle were considered to be mixed homogeneously and become exposed through contact with infectious individuals within the herd and through inward movements from infectious animals. Once an animal became infected, it remained so until at least one infected animal is detected or the simulation ran to completion, therefore cattle did not recover in the timeline of the simulation. Multiple simulations were run which allowed us to estimate the probability of detection, once disease was introduced.

Parameter estimates for the daily transmission rate (β), the daily rate of exposed cattle becoming test sensitive (σ), the daily rate of test sensitive cattle becoming infectious (γ), the probability that a test sensitive or infectious animal is detected by the SICCT (Ω_r) and the probability that a test sensitive or infectious animal is detected at the abattoir (Ω_s) were taken from the medians of the posterior kernel density estimates for the parameter distributions from low-incidence four-year testing areas of Great Britain (O'Hare et al. 2014). Parameter estimates for σ , γ , Ω_r and Ω_s were informed via Bayesian priors by previous field and experimental work (Downs et al. 2011; Bessell et al. 2012).

Table 2.1 Input parameters for the simulation model. Values were taken from parameter estimates bTB from modelling in low-incidence four-year testing areas of Great Britain (O'Hare et al. 2014).

Input		Value
Transmission rate	β	0.002
Exposed to test sensitive rate	σ	0.439
Test sensitive to infectious rate	γ	0.006
SICCT sensitivity	Ω_r	0.538
Abattoir test sensitivity	Ω_s	0.663

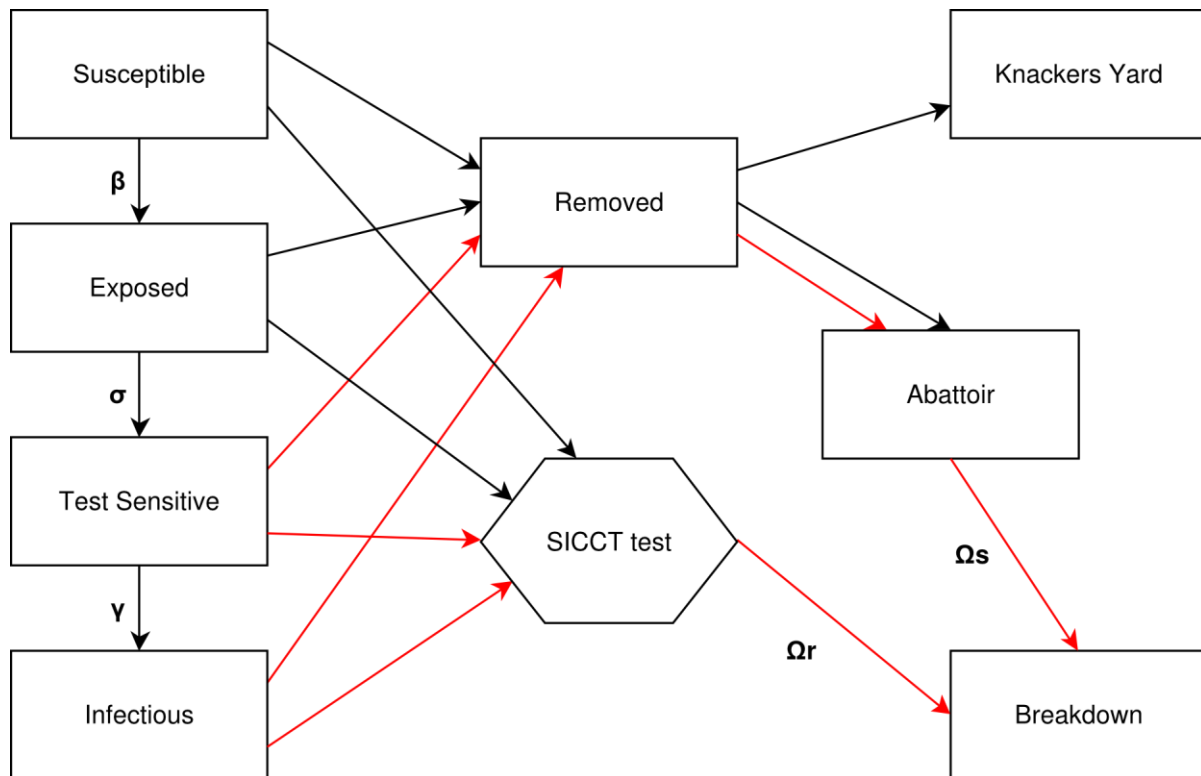


Figure 2.1 Simulation Model Schematic. Parameters correspond with those presented in Table 2.1. Red arrows indicate potential progression to a breakdown. The SICCT test is assumed to have a 100% specificity meaning that while Susceptible and Exposed animals can be administered the test, there is no possibility of a false positive.

An external force of infection representing any infection from other species was not included in the simulation models. As noted in the introduction, despite *M. bovis* having a wide host range, the Channel Islands do not have any wildlife reservoirs implicated in maintaining bTB infection. We also do not consider the possibility of spread between neighbouring farms as there are no data to parameterise such contacts in Jersey and Guernsey. While it is possible to explore these scenarios in a sensitivity analysis, as shown in the results, increased contact between farms (such as this additional risk of across-fence contact) only serves to increase the likelihood of detection. Additionally, in Guernsey, the presence of earthen mounds between fields also makes nose-to-nose contact between cattle unlikely, reducing the potential for spatial spread. Therefore, it is expected that any identified risk-based surveillance strategy will only be more effective under the circumstances already accounted for.

2.3. Amended surveillance strategies

Two alternative testing regimes to current practice were explored in order to evaluate the effect of differing surveillance strategies on the detection of bTB on both Jersey and Guernsey:

1. **Abattoir-only:** A strategy that relies entirely on abattoir surveillance
2. **Reduced:** A strategy that augments abattoir-only surveillance with additional testing for a restricted number of higher-risk herds.

2.3.1. Abattoir-only

The removal of ante-mortem skin testing and dependence on disease detection at abattoir represents the minimum level of disease surveillance that could be expected. Within the context of the model, the disease is only detectable after a recorded (Jersey) or simulated (Guernsey) movement to the abattoir and thus none of the 2,771 recorded skin tests on Jersey and 7,485 recorded skin tests on Guernsey would be undertaken.

2.3.2. Reduced

In principle, a wide range of scenarios could easily be considered by the simulation model and with the SICCT test costing an estimated average of £6.49 per animal per test (personal communication, Lowseck, 2014), there are opportunities for substantial savings should the number tested be reduced. Such approaches could range from a simple cut-off (e.g. only larger/smaller herds being tested), to more sophisticated approaches that consider targeting specific farms because of their number of movements, or because they are known to be at a higher risk of infection (e.g. by introduction of other bovids known to act as spill-over hosts, such as sheep or goats). The outcomes can be compared for likelihood of long-term infection, size of outbreak if it occurred and the likelihood of detection over time. Such scenarios must be informed by knowledge of the practicalities of the approach considered and therefore best informed by local representatives. As an example of the type of comparisons that can be made, we consider a simple approach based on the number of animals sent to the abattoir per annum. We consider in particular, whether retaining the current testing schedule for farms with fewer than seven movements to abattoir over the ten-year period and reliance on abattoir surveillance for the remaining holdings would result in similar disease surveillance but with reduced cost. This strategy saw a total of only 12 and 368 animals tested on Jersey and Guernsey, respectively (Table 2.2), to catch those few cattle that did not get sent to the abattoir.

Table 2.2 Number of animals tested as a result of the routine herd testing during current and reduced surveillance strategies over the 10-year study period. Jersey performed quarter herd tests rounded up to the nearest animal while Guernsey performed whole herd tests.

	Jersey	Guernsey
Current	*2,771	7,485
Reduced	12	368

* One quarter of 10,975 tests, rounded up to the nearest whole animal at each individual test

3. Current Practice Results

For each scenario as described above, 5,000 simulations were run. This number was deemed sufficient to obtain statistically robustly outcomes (see section 6.3 in the appendix). To facilitate meaningful comparison between the current surveillance and the amended surveillance schemes suggested earlier in this report, results from the current, abattoir-only and reduced surveillance schemes were plotted together. Descriptions of these suggested surveillance strategies appear in Section 2.3 above.

3.1. Cattle Movement Networks

Full details of the cattle-movement network analysis are given in appendix 6.4 below. In brief, our analyses suggested that the relatively few movements between herds in both CDs results in at most, a poorly connected network. However, what was also seen was that some pairs or groups of farms have so many reciprocal movements that they could be considered as single entities. In Jersey, there are also a few highly active farms which trade animals consistently with smaller farms however there appears to be little preferential trading in Guernsey. Therefore this suggested that trade restrictions or increased surveillance for more active farms is unlikely to be beneficial for disease prevention in the CDs.

3.2. Current surveillance

These simulations tested the effectiveness of ten years of disease surveillance, assuming a hypothetical disease introduction under the current strategy, presented in Table 3.1. The disease evaded detection in the Jersey simulations in 2.60% of the simulations run. In 0.04% of scenarios, at least one cow remained infected at the end of the simulation and was still undetected and in the remaining 2.56% of scenarios, disease went undetected by both tests but with all infected animals removed from the system, either through natural death or through slaughter. For Guernsey, the disease evaded detection in 2.47% of the simulations: in 1.64%, at least one cow remained infected and undetected while in 0.83% all infected animals were removed without detection. The percentage of simulations in which the disease was detected at abattoir was 98.87% and 64.20% for Jersey and Guernsey, respectively. The figure for Jersey suggests that an abattoir-only approach to surveillance may be sufficient, but that some additional testing in Guernsey above the abattoir surveillance is likely to be beneficial.

Table 3.1 Proportion (%) of simulations where the infection remained undetected under the surveillance schemes tested here.

	Jersey			Guernsey		
	Current	Abattoir-only	Reduced	Current	Abattoir-only	Reduced
Undetected	2.60	2.75	2.23	2.47	22.73	3.27
Spontaneous removal	2.56	2.63	2.19	0.20	6.49	0.31
Infection remaining	0.04	0.12	0.04	2.27	16.24	2.96

To determine the probability that disease is present but undetected in a given year (e.g. 2014), we consider two things:

- i. X , the probability that disease was introduced in any given year and
- ii. based on the simulation as in the preceding paragraph the probability P_Y that Y years after introduction, at least one hidden, infected cow remains (e.g. P_3 is the probability that after introduction of an infected cow in 2011, at least one undetected infected cow remains in 2014 and no disease was detected in the intervening years).

The per-introduction yearly probability of at least one infected cow remaining undetected is then P_Y times X . We assume that the rate of introduction is described by a random event (i.e. with a Poisson distribution). The approach of Alban and others (2008) uses a maximum rate of introduction of detected infection of $1/N$, where N is the number of years since the last time disease was identified (equal to 1/50 for Jersey and 1/74 for Guernsey). As the disease may have been introduced without detection on other occasions (i.e. it may have disappeared on its own), the actual rate of introduction is expected to be higher. However the differences in this context are negligible, as our simulations suggest that most disease introduction is in fact detected (see above). For our purposes, this rate was further modified by the observation that, both in Great Britain, Ireland and in continental Europe, current bTB prevalence in cattle is substantially lower than the last time an infected animal was detected. We assume that R , the reduction in prevalence of bTB in British cattle from circa 1950 to the current date, represents an appropriate estimate of the reduction in risk to the CDs. Then the overall probability is therefore $X=R/N$. In the UK an estimated 18% of all cattle were tuberculin reactors in 1945 (Ritchie 1945) and the provisional number of reactors of all cattle tested in Great Britain in 2013 was 0.378% (Defra 2014), making $R=0.021$ for the purpose of this exercise and the maximum rate of introduction per annum of 0.0004 and 0.0003 for Jersey and Guernsey, respectively. An alternative approach would be to consider instead for R to be the reduction of human TB caused by *M. bovis* in the same timeframe, however these estimates are at best uncertain because of the indistinguishable symptoms associated with human *M. bovis* and *M. tuberculosis* infections.

The overall probability of undetected infection can be estimated by assuming independent risks for every year prior to 2014. As the probabilities involved here are small, then a good approximation of the overall estimate of the maximum prevalence is simply the sum over all years, i.e. $X*(P_1+P_2+P_3+\dots+P_{20})$. Here we assume that the probability of undetected infection after twenty years is effectively zero (as the initial cohort of infected cows is likely to have disappeared) and between ten and twenty years, the probability of being undetected is constant (as we have only sufficient data to simulate for ten years). In practice, this probability will decline with each year as animals are removed from the system, so this is likely to be a conservative estimate.

Using the formula above with the simulated results, the estimated current probability of undetected infection for Jersey is 0.0001 and for Guernsey is 0.0005. If one were to assume a single test applied to all cattle, then the overall probability of detecting one test sensitive animal is 0.00005 and 0.0002, respectively. Both these results are well below the threshold of disease freedom stipulated by the OIE for animal level prevalence of 0.001.

In order to control for over-representation of infections persisting in holdings with very few animals, the average herd size was divided by the average system size for the entire period, to weight the probability of the detecting the infection. The unweighted and weighted probability that the infection was detected by the end of the 10 year simulation period is shown in Table 3.2 below.

Table 3.2 Unweighted and weighted probabilities of infection being detected after the 10-year simulation period using the Current, Abattoir-only and Reduced surveillance strategies presented in this report.

	Unweighted Probabilities		Weighted Probabilities	
	Jersey	Guernsey	Jersey	Guernsey
Current	0.9747	0.9754	0.9993	0.9988
Abattoir-only	0.9725	0.7866	0.9992	0.9515
Reduced	0.9781	0.9673	0.9993	0.9943

The annual cumulative probabilities are presented in Figure 3.1 for Jersey and Figure 3.2 for Guernsey. Both plots show a steep rise before levelling off after three and four years since the infection was introduced in Jersey and Guernsey, respectively. Jersey had a 80.65% chance of detecting the infection after the first year, while Guernsey had a 39.26% percent chance of detecting the infection. Weighting the farms as described above increased the chance of detecting the infection after the first year to 90.24% and 55.27% in Jersey and Guernsey, respectively. The discrepancy between the two CDs is largely due to the greater number of animals passing through the abattoir on Jersey.

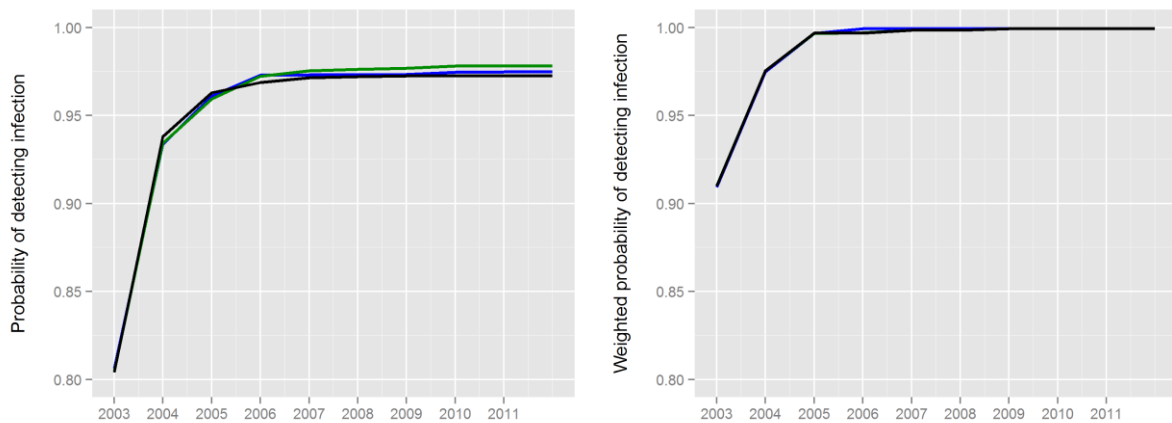


Figure 3.1 Jersey: Probability of detecting infection assuming a single introduction at the beginning of 2003. Blue lines represent the current surveillance, Black lines the Abattoir-only surveillance and Green lines the Reduced surveillance.

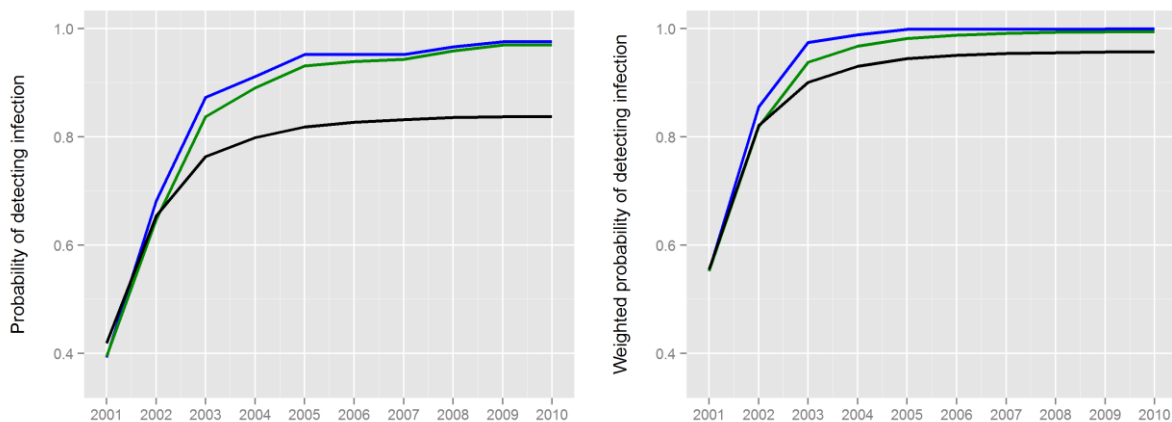


Figure 3.2 Guernsey: Probability of detecting infection assuming a single introduction at the beginning of 2001. Blue lines represent the current surveillance, Black lines the Abattoir-only surveillance and Green lines the Reduced surveillance.

An examination of the simulated epidemics over time can inform a number of key questions:

- If introduced, how long would it take for disease detection to occur?
- When detected, what proportion of herds and have been infected?
- How do these values change under altered surveillance strategies?

The epidemic size during the run of each simulation was plotted against time in order to gauge the spread and size of potential epidemics, where introduction has occurred. To illustrate the average outcome, the trend of the means was then smoothed, displayed in Figure 3.4 and Figure 3.6 with a 95% confidence interval indicated by the shaded regions. These figures show the likely characteristics of an outbreak if it was detected on a given date post introduction, (c.f. not how probable it was to occur on those dates. For the relative frequency of occurrence, see Figure 3.1 and Figure 3.2). Assuming an introduction in Jersey in 2003 (the beginning of our data range for Jersey) the majority of the disease was detected in the first half of the simulation period. The mean number of infected animals is bimodal, dipping around 2005. Overall, the mean number of infected animals at disease detection gradually increased through time until 2008 before gradually decaying, though very few infections were detected after this point. Mirroring the number of animals, the number of infected locations gradually rose until around 2008, after which point the number of locations gradually decreased. The mean number of infected locations never rose above four. Contrary to what one may expect, the relationship between outbreak size and time was not linear. The infections that evaded detection for longer were generally smaller with fewer animals over fewer locations. This suggests that any outbreak, should it occur under any of the surveillance scenarios, would not continue to spread throughout the cattle population, but would eventually disappear without additional effort being necessary to ensure this. Of those simulations in which the infection persisted, only a solitary farm with two animals ever harboured the infection.

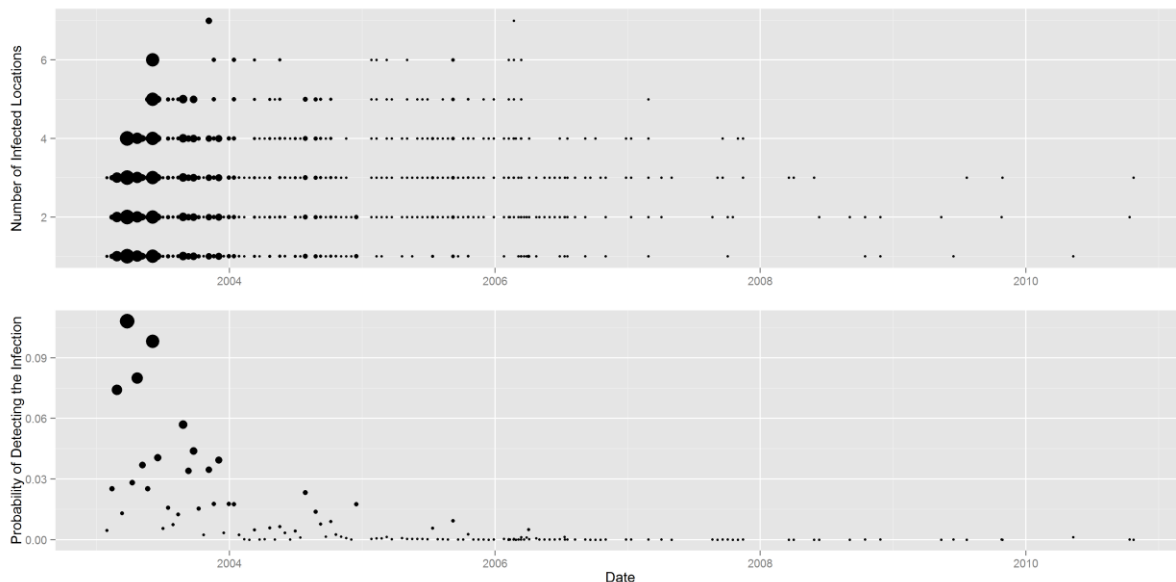


Figure 3.3 Jersey epidemic size at breakdown and probability of detecting the infection through time under current surveillance assuming a single introduction event at the beginning of 2003. The size of the points correspond to the relative number of breakdown events.

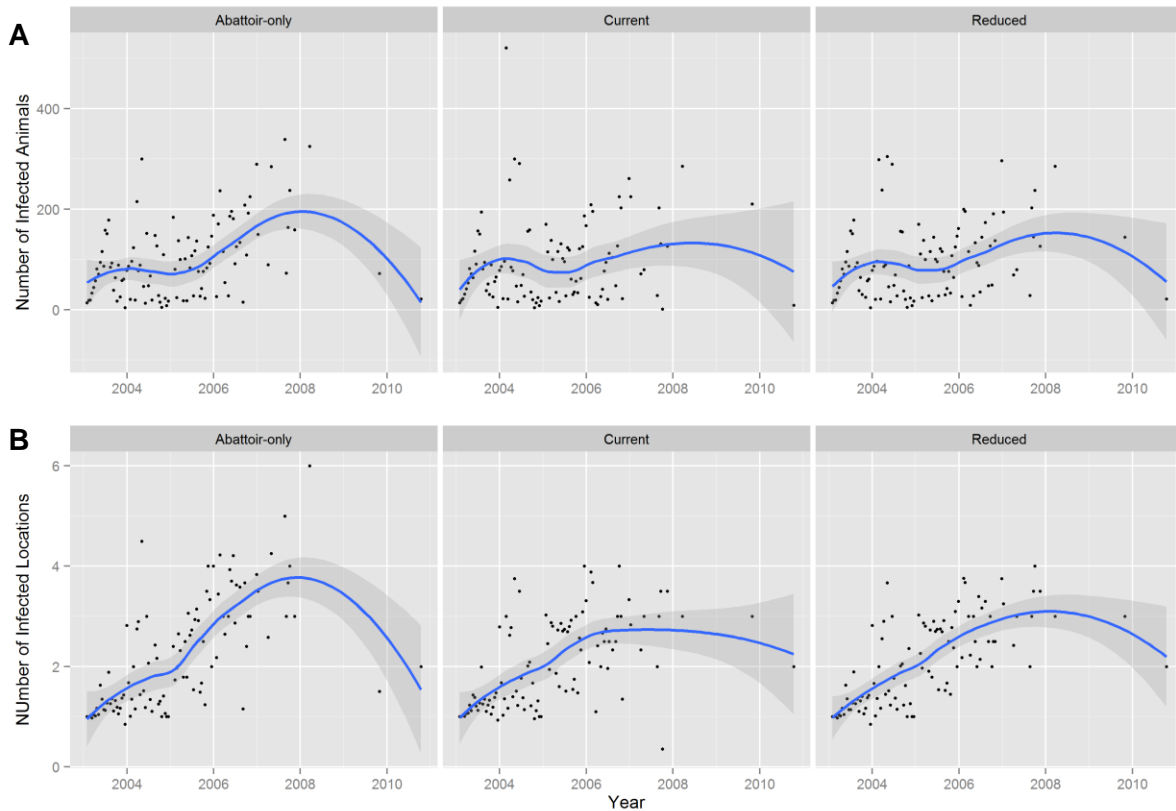


Figure 3.4 Jersey: Detected epidemic sizes through time of Abattoir-only, Current and Reduced surveillance assuming a single introduction event at the beginning of 2003. Points either indicate the mean number of infected animals (A) or mean number of locations (B) at each 14-day time step if a breakdown occurred. The number of infected locations may be 0 due to all infected animals being sent to the abattoir, resulting in a mean number of locations occasionally less than 1. The blue line indicates the smoothed mean of these points while the dark grey band is the 95% confidence interval of the line.

Similarly to Jersey, in Guernsey the majority of the disease was detected in the first six years of the simulation period, with a peak after the second year given an introduction in 2001 corresponding to eleven farms being tested on the same day (Figure 3.5), the first year of our data for Guernsey. The number of infected locations only rose until 2003, after which point the number of locations sharply decreased. The negative relationship between epidemic size and time was more striking on Guernsey than Jersey, with older outbreaks leading to very few infected animals (Figure 3.6). The only simulation runs in which the infection evaded detection were on small farms with a single animal, hence a mean of 1 infected animal was observed.

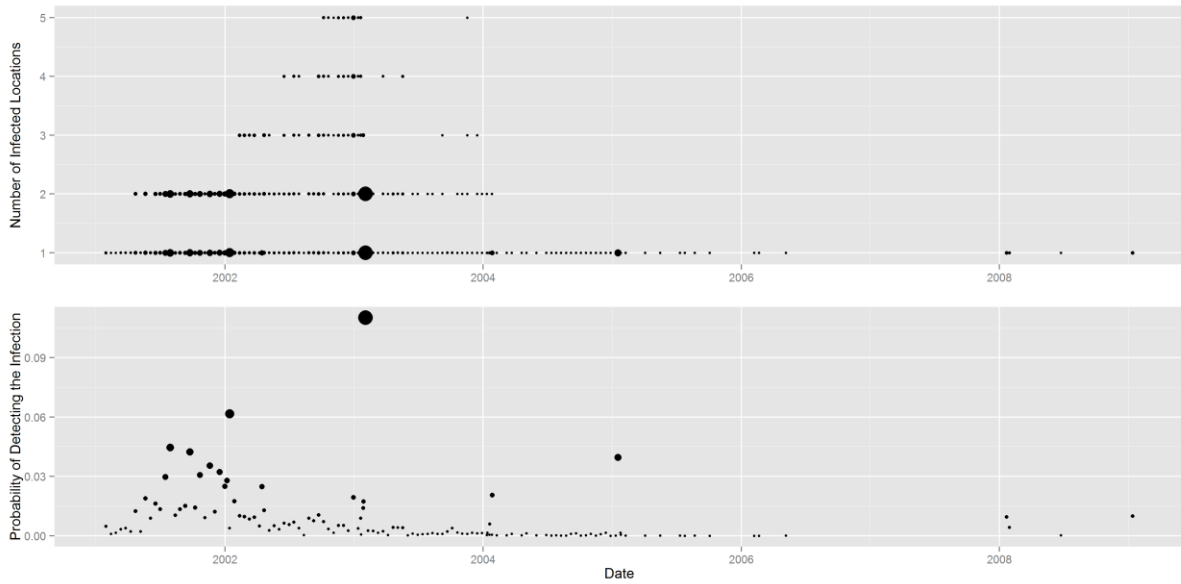


Figure 3.5 Guernsey epidemic size at breakdown and probability of detecting the infection through time under current surveillance assuming a single introduction event at the beginning of 2001. The size of the points correspond to the relative number of events.

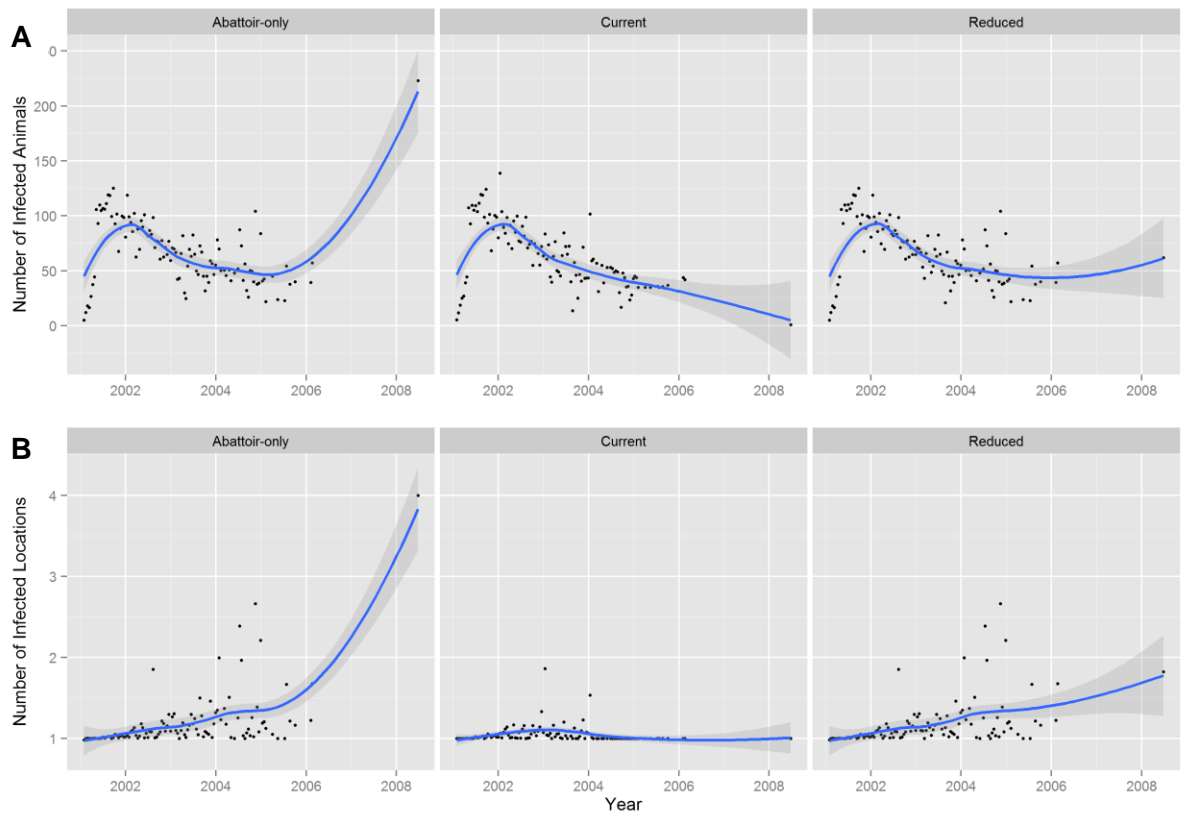


Figure 3.6 Guernsey: Detected epidemic sizes through time of Abattoir-only, Current and Reduced surveillance assuming a single introduction event at the beginning of 2001. Points either indicate the mean number of infected animals (A) or mean number of locations (B) at each 14-day time step if a breakdown occurred. The number of infected locations may be 0 in the data to all infected animals being sent to the abattoir, resulting in a mean number of locations occasionally less than 1. The blue line indicates the smoothed mean of these points while the dark grey band is the 95% confidence interval of the line.

Census data from the farms included in this study are presented as number of animals on a log scale in Figure 3.7 and Figure 3.8 for Jersey and Guernsey, respectively. The differing census categories in the figures reflect different national recording policies. The herds that had greater than 1% of simulations resulting in infection evading detection while remaining infected were categorised as "Infected". The boxplots show that, as expected, a majority of the herds on both islands were involved in milk production, with 'Female replacements over 24 months' on Jersey and 'Cows' on Guernsey making up the largest category. The boxplots also show that in both systems, in only the smallest holdings did infection evade detection with any frequency. While the infected farms on Jersey were a mixture of demographic types, the infected farms on Guernsey tended to be older animals. The number of infected farms evading detection was very small in both CDs (one and two for Jersey and Guernsey, respectively) so caution should be applied for interpretation of the results for higher-risk herd demography. However small, poorly connected farms, regardless of demographic makeup, are at a greater risk of the disease detection evasion.

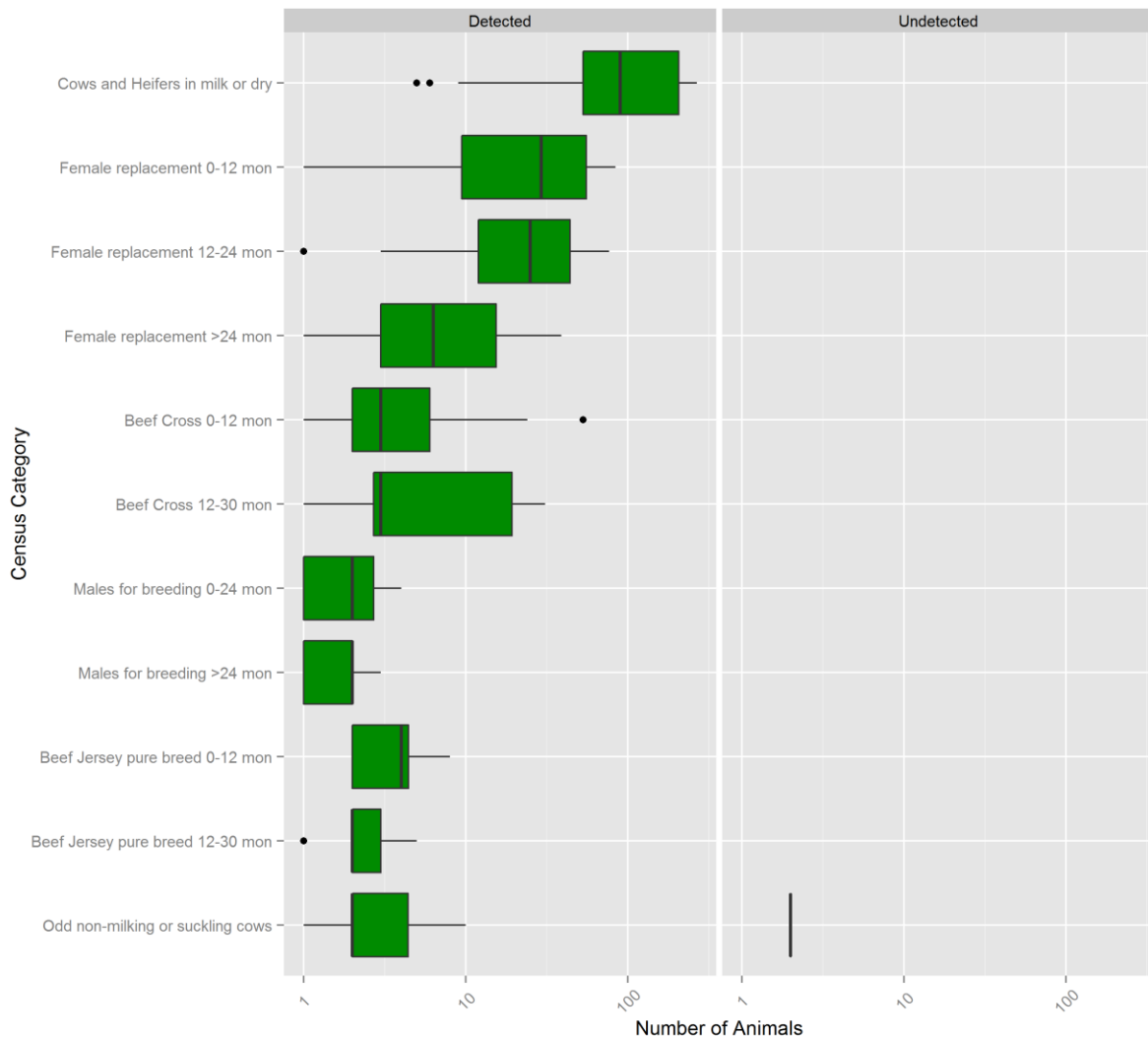


Figure 3.7 Demographic makeup of Jersey showing the number of animals present in each census category per farm, presented on a log scale. Boxes on the left indicate values from those farms in which the infection was detected in greater than 99% of the simulations while boxes on the right indicate farms where the infection was persistent and undetected in greater than 1% of the simulations.

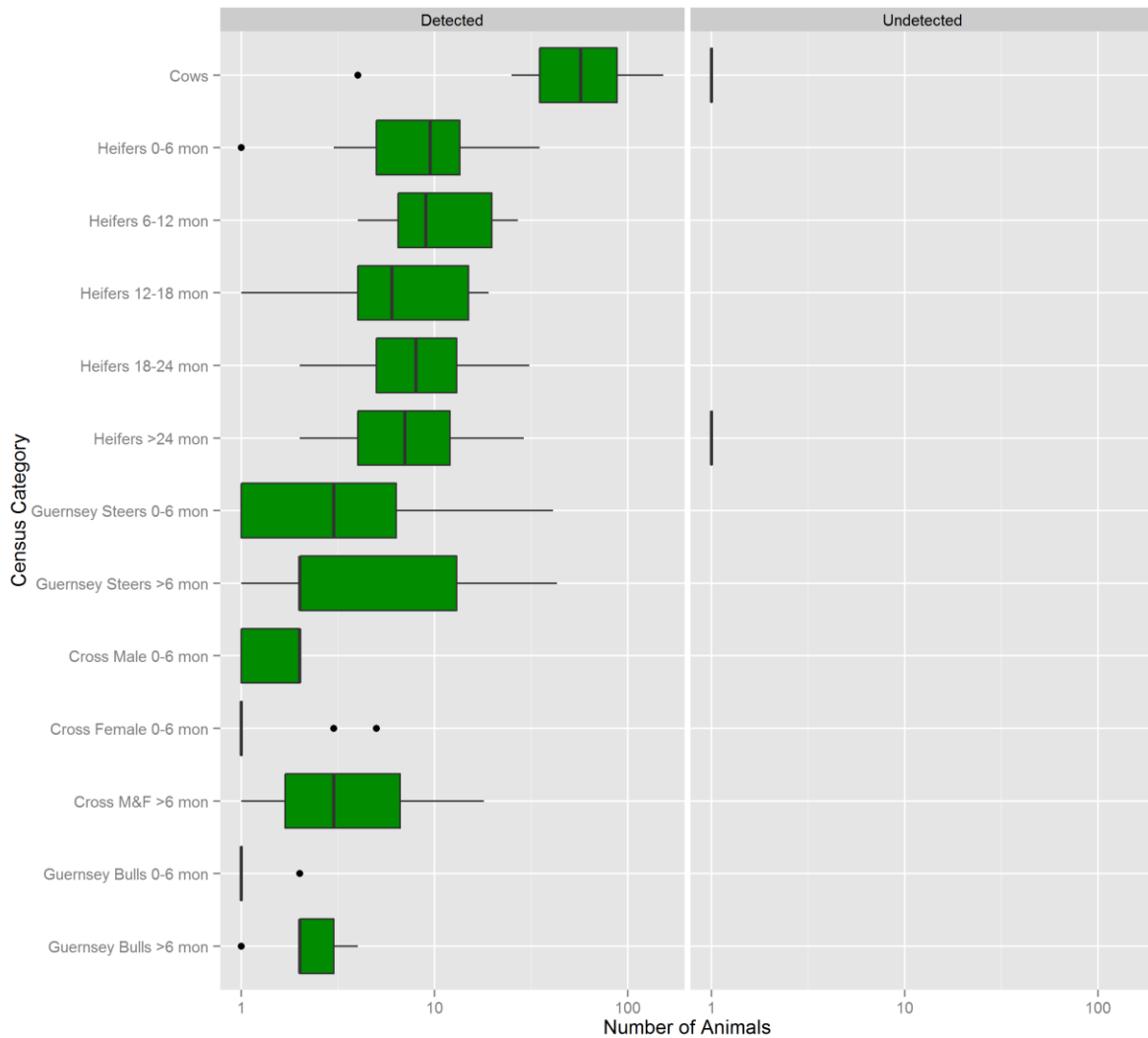


Figure 3.8 Demographic makeup of Guernsey showing the number of animals present in each census category per farm, presented on a log scale. Boxes on the left indicate values from those farms in which the infection was detected in greater than 99% of the simulations while boxes on the right indicate farms where the infection was persistent and undetected in greater than 1% of the simulations

4. Amended Surveillance Results

4.1. Abattoir-only

The effectiveness of the Abattoir-only surveillance was directly related to the number of movements to abattoir. Small-holdings did not often send their animals to the abattoir during the simulation periods, making any abattoir-based surveillance scheme ineffective for those particular holdings. Under the minimal (abattoir-only) surveillance strategy, the infection evaded detection in the Jersey simulations 2.75% of the time: 2.63% remained infected while 0.12% were spontaneously removed. Two farms located on the island of Sark do not have access to an abattoir, heavily influencing the results of the Guernsey system where the disease was undetected 22.73% of the time: 6.49% vanished and 16.24% remained infected. These values are presented in Table 3.1 for comparison.

The mean epidemic size of breakdowns in the Jersey simulation under abattoir-only surveillance was much larger than at the current level of surveillance (Figure 3.4). The majority of the disease was detected in the first half of the simulation period. The mean number of infected animals was slightly bimodal, dipping in around 2005 before reaching a peak at 2008 then decreasing sharply. Very few infections were detected after this point. Mirroring the number of animals, the number of infected locations rose until around 2008, after which point the number of locations sharply decreased. The mean number of locations rose to a maximum of six during the early part of 2008. The mean epidemic size when the infection evaded detection on Jersey was on a small farm with a pair of animals.

The epidemic size at each time step during the Guernsey simulation under the abattoir-only surveillance scenario was also plotted against time in order to gauge the spread and size of epidemic (Figure 3.6). While the majority of the simulated outbreaks were detected in the first six years of the simulation period, the number of infected animals peaked after the second year before gradually declining until 2006. The detection of a very large epidemic late in the simulation skewed the results, it should be stressed that this was a very unusual event. The number of infected locations only rose steadily until the large epidemic after 2008. The mean epidemic size when the infection was undetected ramped up from a mean of 20 for one farm to over 500 for seven farms.

4.2. Reduced

The reduced surveillance scheme represents a more cost-effective measure to establish disease freedom than the current practice. Under the current surveillance strategy, the State of Jersey performed 2,771 tests on the subject herds over the study period. The reduced surveillance strategy saw only 12 animals tested during the quarter herd tests. The percentage of the infection detected at abattoir rose slightly to 99.14%. The infection went undetected in 2.23% of the simulations: 2.19% saw the infection disappear spontaneously, while in 0.04%, the infection persisted. Under the current surveillance strategy, the Bailiwick of Guernsey performed 7,485 tests on the subject herds over the study period. The reduced surveillance strategy saw only 368 tests performed and consequently the percentage of disease detected at abattoir rose to 78.31%. Overall, the infection evaded detection in 3.27% of simulations: 0.31% disappeared spontaneously and 2.96% remained infected. To facilitate a comparison between the different surveillance strategies analysed here, these values are presented in Table 3.1 on page 9.

The mean epidemic size of breakdowns in the Jersey simulation under the reduced surveillance was larger than at the current level of surveillance, but smaller than the abattoir-only surveillance (Figure 3.4), as reflects the relative delays to detection resulting from decreasing levels of surveillance. The majority of the disease was detected in the first half of the simulation period. The mean number of infected animals was bimodal, dipping around 2005 before reaching a peak at 2008 before decreasing sharply. The number of infected locations rose until around 2008, after which point the number of locations sharply decreases. The mean number of infected locations never rose above four. Mirroring the current surveillance, the mean epidemic size when infection evaded detection on Jersey was on a small farm with a pair of animals.

The epidemic size at each time-step during the Guernsey simulation under the reduced surveillance saw a similar number of animals infected as the current surveillance scheme (Figure 3.6). The number of infected locations only rose gradually throughout, and despite the number of infected animals having a similar distribution with the current strategy, there were

many more farms infected at breakdown. The epidemic size when infection evaded detection was identical to the current surveillance scheme in which only single animals on single farms remained infected after the simulation period.

5. Discussion and Conclusion

The prediction of freedom from bTB in the Channel Islands was made by implementing the current surveillance strategies in bespoke simulation models to monitor the spread, point of detection and epidemic size in Jersey and Guernsey. The present study showed that both Jersey and Guernsey can be considered free from bTB, if we consider the maximum number of animals stipulated in the OIE requirements for freedom. Only the very small, poorly connected holdings could harbour the disease without detection for the entirety of the simulation period. Both cattle industries are small, and with respect to EU and OIE disease freedom, any detected introduction of disease could see the removal of OTF status simply because a single infected herd is a large proportion of all herds in the Channel Islands. Efforts should be concentrated on ensuring the infection is never introduced.

Importantly, the results of the simulation models for both CDs show that larger outbreaks tend to be detected very quickly. Under current surveillance schemes, the individual probability of detecting the infection both peaked within the first year and shortly after two years in Jersey and Guernsey, respectively. The annual cumulative probability of detecting a single introduced infection on both Jersey and Guernsey began to level off after three and four years, respectively. Assuming the more contemporary trading patterns are recognisably similar, it can be assumed with confidence that any introduction prior to 2010 would have been detected. A minimal surveillance scheme of abattoir-only surveillance and a reduced surveillance scheme based on the number of animals sent to slaughter was tested alongside the current recorded surveillance. Both amended schemes were able to detect a similar amount of infection when compared to current surveillance in Jersey. However, while the reduced surveillance scheme was able to detect infection close to the rates seen in the current surveillance scheme on Guernsey, farms that did not send animals to the abattoir hindered the effectiveness of the abattoir-only surveillance scheme.

Freedom from bTB has been demonstrated in a number of systems with very few recorded events. Sweden has been officially free from bTB since 1958. However a consignment of infected farmed deer was inadvertently introduced in 1991, and despite efforts to remove the offending animals, the disease may still be persisting at levels below detection. Wahlström and colleagues (2010) set out to demonstrate freedom from bTB infection in Swedish farmed deer using data from meat inspection, necropsies and tuberculin tests, concluding with confidence that the Swedish farmed deer population is free from *M. bovis*. Denmark is another country officially free from bTB, with their last confirmed case of bTB in 1988. In order to assess more resource-effective methods of surveillance, Calvo-Artavia and others (2013) concluded that as long as the probability of disease introduction was managed, any negative impact of moving to visual-only inspection was negligible.

In the simulations, the large proportion of breakdowns detected at the abattoir for Jersey may be due in part to the provided testing schedule. Although the simulation period began in 2003, routine herd testing during this period did not commence until 2006. The majority of herd

breakdowns occurred before 2006 (Figure 3.4), all of which were detected at the abattoir. Beginning the simulations during the period of routine herd testing would undoubtedly have resulted in detection of a greater number of breakdowns by the SICCT test, although this is beyond the scope of this exercise. The absence of recorded cattle movements to abattoir necessitated the creation of an estimated set of movements for Guernsey by drawing from a beta distribution, fitted from known data collected after the simulation period. The sensitivity of the model to abattoir surveillance highlights the usefulness of these records to better simulate the likelihood that the infection will be detected at the abattoir. We note, however, that while these historical patterns influence the relative contribution of abattoir surveillance to future disease detection, they do not change the fundamental result that even a small amount of testing would be sufficient, should official disease free status be achieved.

Both the intra-dermal skin test and abattoir surveillance are assumed to have perfect specificity, implying that the proportion of non-diseased (uninfected) animals that are correctly identified as negative by the diagnostic test is 100%. While the specificity for the SICCT test has been shown to be 99.99% in a sample of abattoir-confirmed disease-free cattle (Goodchild and Clifton-Hadley 2006). Any positive test result in either dependency would be subject to laboratory confirmation through culturing and testing of the suspect specimen.

With regards to the cattle industries themselves, the tenancy of land in both nations is very convoluted. Only a small proportion of farmers own the land they work and farmers often have multiple landlords. Coupled with that, short-term tenancy contracts result in farmers often grazing their cattle on fields not adjacent to the farm in addition to different fields every year. Epidemiologically, this pattern of land use would make disease tracking more difficult were an animal to become infected, although cattle movements do outperform environmental, topographical and anthropogenic factors in predicting the occurrence of bTB infection in England and Wales (Gilbert et al. 2005). If these factors in Jersey and Guernsey have a similar weight, the overall risk may be low, however it would require a more detailed comparative study to evaluate this risk properly.

Modifying the testing strategy schedule or changing the administered test may also reduce the overall cost of surveillance. Crucially, this would not likely impinge on the ability of either dependency to control the broader spread of the disease. The SICCT is used as a diagnostic test in the United Kingdom and Ireland to control for false positive reactors due to the presence of non-pathogenic *M. avium* spp. in the environment (Defra 2009). According to the Department for Environment, Food and Rural Affairs in the UK, cattle imported from the Channel Islands to the UK are only required to pass a single interdermal tuberculin test, and were the comparative test to be performed, only the reaction to the *M. bovis* tuberculin test would be considered (Defra 2013). A single interdermal tuberculin test is also consistent with the Council Directive 98/46/EC for proving freedom from infection. This test has much greater sensitivity (Downs et al. 2011) and shifting to a single tuberculin injection rather than the comparative test would be marginally more resource-efficient to not only for the cost of consumables, but also the time spent performing and reading the results of the test. In spite of the UK import directive, the presence of *M. avium* spp. on the CDs introduced by avian wildlife necessitates the use of the SICCT test.

In conclusion, the analysis presented here provides a quantitative estimate that the Bailiwicks of Jersey and Guernsey are currently free of bTB and that any previous introduction of the pathogen would have been detected by the surveillance strategies in place. The framework

presented here is highly customisable and could be easily adapted to new disease systems in a similar context where there is little or no evidence of the infection being present and quantitative confidence in the probability of freedom from disease is required. Future extrapolation of results is only possible, however, if the probability of introduction remains negligible.

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6. Appendix

6.1. Surveillance activities for bTB in the Channel Islands

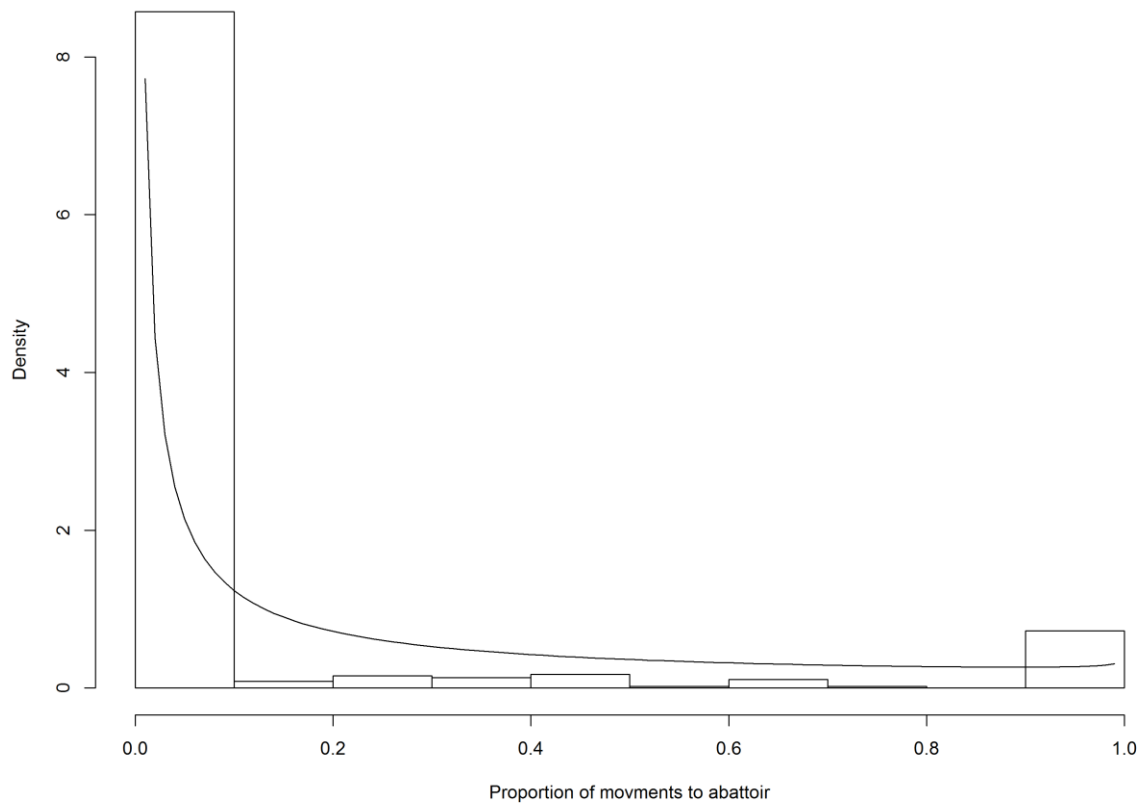
6.1.1. Abattoir monitoring

Every slaughtered animal intended for human consumption must undergo a series of quality checks to ensure that the meat is safe for the public. Post-mortem surveillance at the abattoir enables authorities to gauge the effectiveness of diagnostic testing. The sensitivity of these tests in identifying infected animals is heavily dependent on the progression of the disease. Enlarged and/or caseating lymph nodes may present themselves in animals having passed the ante-mortem skin tests, making abattoir surveillance pivotal in detecting the infection in areas with infrequent field-testing.

6.1.2. Routine herd testing

When bovine tuberculin is injected into the skin of an animal not sensitised to tuberculin antigens, there is no significant localised inflammation and the animal is deemed free from infection. Were an animal's immune system sensitised to the antigen by a current infection, the injection site should swell. However, the presence of non-pathogenic tuberculin antigens found in the environment can cause a false-positive reaction. As a result, a the SICCT is used to help discern the nature of the infection by simultaneously injecting the animal with antigens derived from *M. avium subsp. avium*, a pathogen more often found in birds, and *M. bovis*. This type of test is applied widely to cattle over six weeks of age in the UK and Ireland and in continental Europe for inconclusive test reactors. This test is also used in the Channel Islands.

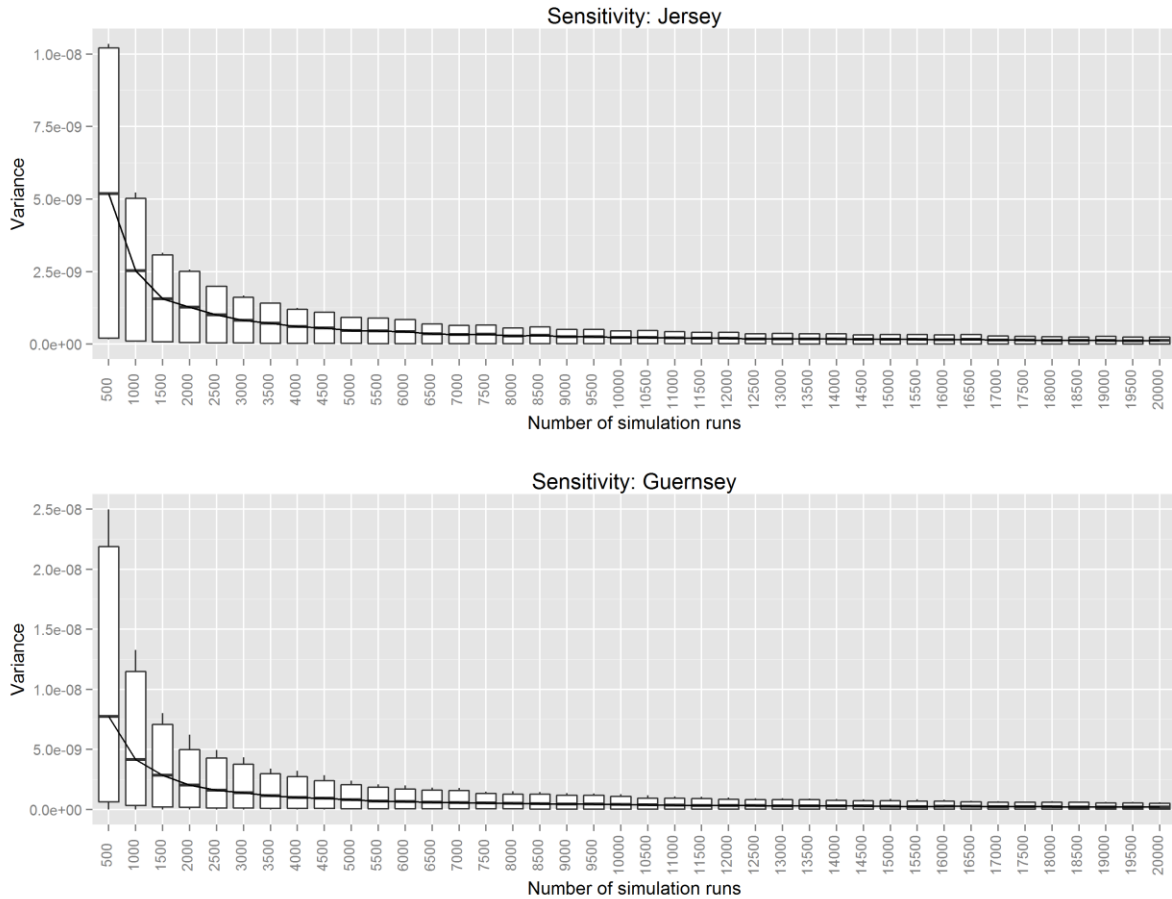
6.2. Simulated movements to abattoir in Guernsey



To simulate movements to the abattoir for Guernsey, a beta (0.02, 0.18) distribution was fit to the proportion of animal deaths sent to abattoir at each fourteen-day time step from 2011 to 2013 and applied to all recorded deaths during the simulation period. Randomly generated values above an assigned 0.5 threshold from said distribution were deemed movements to the abattoir. Two farms located on the island of Sark were excluded from the above calculations as they lack access to an abattoir.

6.3. Sensitivity

In order to validate the number of simulations chosen, one farm from each system was chosen at random for sensitivity analyses. The year and location of the breakdowns were tabulated on a sliding scale incremented by 100 and beginning from 100 to 20,000. The variance of these individual indices within the table were calculated over 1,000 replications.



Plotting the variances from the sensitivity analyses showed that after a steep decline, the difference in variance was negligible from around 5,000 onwards. Five thousand simulations were run for each seed farm to balance accuracy with the computation time.

6.4. Network results

In order to develop a better understanding of how likely herds were to be linked to each other via cattle movements, quantitative measurements of the cattle movement network were performed in igraph 0.7.0 (Csardi and Nepusz 2006) available in the open source statistical environment R. Four metrics were calculated to describe the overall structure of the cattle movement networks, summarized below in the Table 7.1.

- **Diameter:** The diameter of a network describes the maximum number of steps in the shortest path between two farms. Diameters were only calculated for the connected components (i.e. groups of farms that could be connected to each other by a series of movements of cattle). A low score (i.e. close to 1) for the diameter would indicate infection from any one farm has a good chance of 'reaching' other farms in a short period.
- **Reciprocity:** The reciprocity measures the proportion of trade links for which one in the opposite direction exists. A high reciprocity (i.e. near 1) indicates that, the ability of an introduced infection is less dependent on the particular farm that starts the outbreak, and therefore more likely to reach many farms.
- **Transitivity:** Transitivity measures the probability that any two farms connected to a third are connected themselves. High transitivity implies that, even if one farm has good biosecurity and farm level surveillance (and therefore is less likely to become infected), there remain other routes to transmit infection more broadly.
- **Degree Assortativity:** The degree assortativity coefficient measures the level of relationship between trade activity and network connectiveness. If the coefficient is high, this indicates that highly active farms tend to interact with other highly active farms. A high assortativity is an indicator that targeting highly active farms will be a productive approach to risk-based surveillance.

The cattle movement networks of both Jersey (Figure 6.1) and Guernsey (Figure 6.2) considered for these analyses are closed systems with 37 and 25 holdings, respectively. Jersey farms sent approximately 15.5 times the number of animals to the abattoir when compared to Guernsey, translated into a greater likelihood of detecting an infected animal on Jersey through abattoir surveillance. Concerning diameter, both Jersey (38) and Guernsey (41) were poorly connected networks. Values larger than the number of holdings indicate that the disease would require visiting at least one farm on multiple occasions to spread across the connected portion of the network. High reciprocity for Jersey (0.5974) and Guernsey (0.4118), however, indicates that return trade of animals was common and the source of the outbreak was not particularly important to the overall epidemic size. Transitivity values of 0.3250 and 0.3788 for Jersey and Guernsey, respectively, were indicative of relatively few connections between any two neighbours, indicating that there were few indirect routes for a farm to become infected. While the negative values of degree assortativity in Jersey indicated preferential trade with farms of with different levels of connectivity and informing the potential spread of the disease based on known infected locations, the assortativity of the Guernsey network near zero indicated no real trade preferences and suggested no farm is riskier for spreading the disease than any other.

Table 6.1 Network metrics describing the cattle movement networks of Jersey and Guernsey.

	Jersey	Guernsey
Farms	37	25
Animals*	5,079	2,820
Movements between holdings	1,301	754
Movements to the abattoir	5,632	362 [†]
Diameter	38	41
Reciprocity	0.5974	0.4118
Transitivity	0.325	0.3788
Degree Assortativity	-0.3362	-0.03

* at the end of the simulation period

[†] estimated

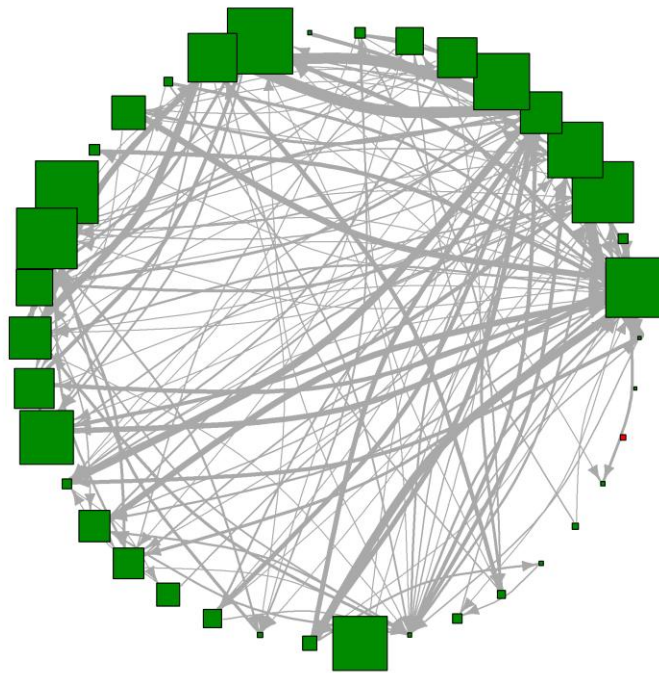


Figure 6.1 Jersey cattle movement network. Red boxes indicate those farms in which the infection was persistent and undetected in greater than 1% of the simulations while green boxes indicate the infection was detected in over 99% of simulations at some point during the simulation period. The size of the squares corresponds to the number of animals present on the farm at the end of the simulation period. Arrow widths correspond to the number of animals moved between premises over the simulation period.

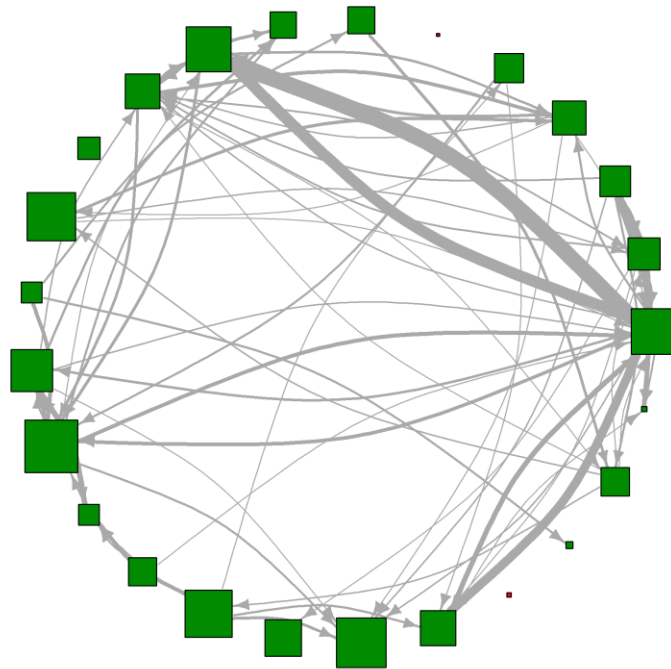


Figure 6.2 Guernsey cattle movement network. Red boxes indicate those farms in which the infection was persistent and undetected in greater than 1% of the simulations while green boxes indicate the infection was detected in over 99% of simulations at some point during the simulation period. The size of the squares corresponds number of animals moved between premises over the simulation period.