

## A simulation model for studying the role of pre-slaughter factors on the exposure of beef carcasses to human microbial hazards

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### Abstract

A Monte Carlo simulation model was constructed for assessing the quantity of microbial hazards deposited on cattle carcasses under different pre-slaughter management regimens. The model permits comparison of industry-wide and abattoir-based mitigation strategies and is suitable for studying pathogens such as *Escherichia coli* O157:H7 and *Salmonella* spp. Simulations are based on a hierarchical model structure that mimics important aspects of the cattle population prior to slaughter. Stochastic inputs were included so that uncertainty about important input assumptions (such as prevalence of a human pathogen in the live cattle-population) would be reflected in model output. Control options were built into the model to assess the benefit of having prior knowledge of animal or herd-of-origin pathogen status (obtained from the use of a diagnostic test). Similarly, a facility was included for assessing the benefit of re-ordering the slaughter sequence based on the extent of external faecal contamination. Model outputs were designed to evaluate the performance of an abattoir in a 1-day period and included outcomes such as the proportion of carcasses contaminated with a pathogen, the daily mean and selected percentiles of pathogen counts per carcass, and the position of the first infected animal in the slaughter run. A measure of the time rate of introduction of pathogen into the abattoir was provided by assessing the median, 5th percentile, and 95th percentile cumulative pathogen counts at 10 equidistant points within the slaughter run.

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Outputs can be graphically displayed as frequency distributions, probability densities, cumulative distributions or  $x$ - $y$  plots. The model shows promise as an inexpensive method for evaluating pathogen control strategies such as those forming part of a Hazard Analysis and Critical Control Point (HACCP) system. © 1999 Elsevier Science B.V. All rights reserved.

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## 1. Introduction

Contamination of beef products with bacterial pathogens has emerged as a prominent public health issue. *Escherichia coli* O157:H7 and other enterohaemorrhagic *E. coli* (EHEC) are perhaps the most-important pathogens at present due to their propensity to cause outbreaks of severe illness (Griffin and Tauxe, 1991; Dorn, 1993; Bettelheim, 1996). *Salmonella* spp., *Campylobacter* spp. and *Listeria monocytogenes* are other microbial hazards also known to occur in raw and improperly prepared beef products (Menning, 1988; Jay, 1992). It is clear that for many meat-borne pathogens, the gastrointestinal tract of clinically normal cattle is an important reservoir of infection (Roberts, 1982). These organisms find ready access to the food chain at processing due to the inevitable transfer of bovine faecal flora onto carcasses. New opportunities are being sought to improve the microbial safety of beef products by applying interventions in both the 'pre-harvest' and 'post-harvest' periods. Pre-harvest control measures are those that can be implemented while cattle are on the farm, during marketing and transport, and while waiting at abattoirs. Such measures have the appeal of not placing total reliance on the hygienic practices of processors, food handlers and consumers. They are also consistent with the belief that, where possible, control should be exercised at all possible points within the food chain.

The search for better control measures has focused on a new philosophy based on the vertically integrated nature of meat production. This approach includes Hazard Analysis and Critical Control Point (HACCP) systems (National Advisory Committee on Microbiological Criteria for Foods, 1992) a strategy widely promulgated in the food processing and animal slaughter industries (Buchanan, 1995; Notermans et al., 1995). Implementation of control systems such as HACCP requires knowledge of the relative merits of mitigation strategies that could be implemented in the pre-slaughter period. However, the process of converting live cattle into beef product is long and complicated. Consequently, it is very difficult to specify an optimal combination of interventions using an experimental or observational study approach. A proposed solution has been to use risk assessment to specify the criteria for improving the microbial safety of meat (Berends et al., 1993; Baird-Parker, 1994). The first step in this process is to develop a quantitative method for assessing how the quantity of microbial hazards found on beef carcasses varies according to pre-slaughter influences.

A computer simulation model was constructed in which the major outcomes of interest were the probability distributions of carcasses being contaminated with various quantities of pathogen, and the number of pathogen shedding animals entering the abattoir. A Monte Carlo approach was adopted so that uncertainty in input assumptions could be propagated

through the model and be reflected in uncertainty in outcomes. The objective was to develop a means of assessing the relative importance of several candidate mitigation strategies for controlling carcass contamination in the pre-slaughter period. A requirement was that the model should be able to adapt to a range of meat production systems and bacterial pathogens yet be conceptually simple enough to be accepted as a decision support tool in the red meat industry. The model was also constructed with a view to prioritizing which aspects of the pre-slaughter management of cattle should be targeted for future research. This paper reports on the methods used to construct the model and describes some general scenarios that the model can be used to study.

## 2. Description of the model

### 2.1. Development and presentation of the model

The simulation model was developed using an object-oriented visual programming language (Borland<sup>®</sup> Delphi<sup>™</sup> version 2, Scott's Valley, California). This environment provides the computational speed and freedom necessary to implement a model containing four levels of hierarchy in combination with Monte Carlo sampling methods. It also permitted sorting routines (which are required for executing control strategies) to be called from within each iteration of the simulation. Spreadsheet-based simulation tools (although convenient for some modelling scenarios) are poorly suited to this level of programming complexity. Because the model has application as a decision support tool, it was developed as a stand-alone application for use under 32-bit Microsoft<sup>®</sup> Windows<sup>®</sup> operating systems. Wherever possible, input assumptions are validated against system-defined 'legal' values at the time they are entered into the model. Entry of 'illegal' parameters for a probability distribution causes an error message to be generated. Each output variable is summarised by calculating minimum, maximum, mean, skewness, kurtosis, and percentiles at 5% intervals. A graphical system for viewing output as either frequency distributions, probability densities, probability mass functions (for discrete outcomes), cumulative distribution functions or  $x$ - $y$  plots was provided. Any continuous outcome can also be plotted as a kernel density estimate which provides a smoothed version of the underlying histogram with unwanted random noise removed (Silverman, 1986). Statistical and graphical output can be printed directly from the program or saved to file. Raw data from simulations can be extracted as a text file for further analysis.

### 2.2. Model structure

A hierarchical model structure was developed to provide an intuitive representation of animal movement from farm to slaughter (Fig. 1). This structure mimics how individual animals from a herd are aggregated into a sale-lot, and how sale-lots are aggregated into truck-loads. The animals killed at an abattoir on any one day are derived from an integer number of truck-loads. Individual animals, sale-lots and truck-loads are tracked in the model until the completion of each iteration. The usual practice of keeping together the

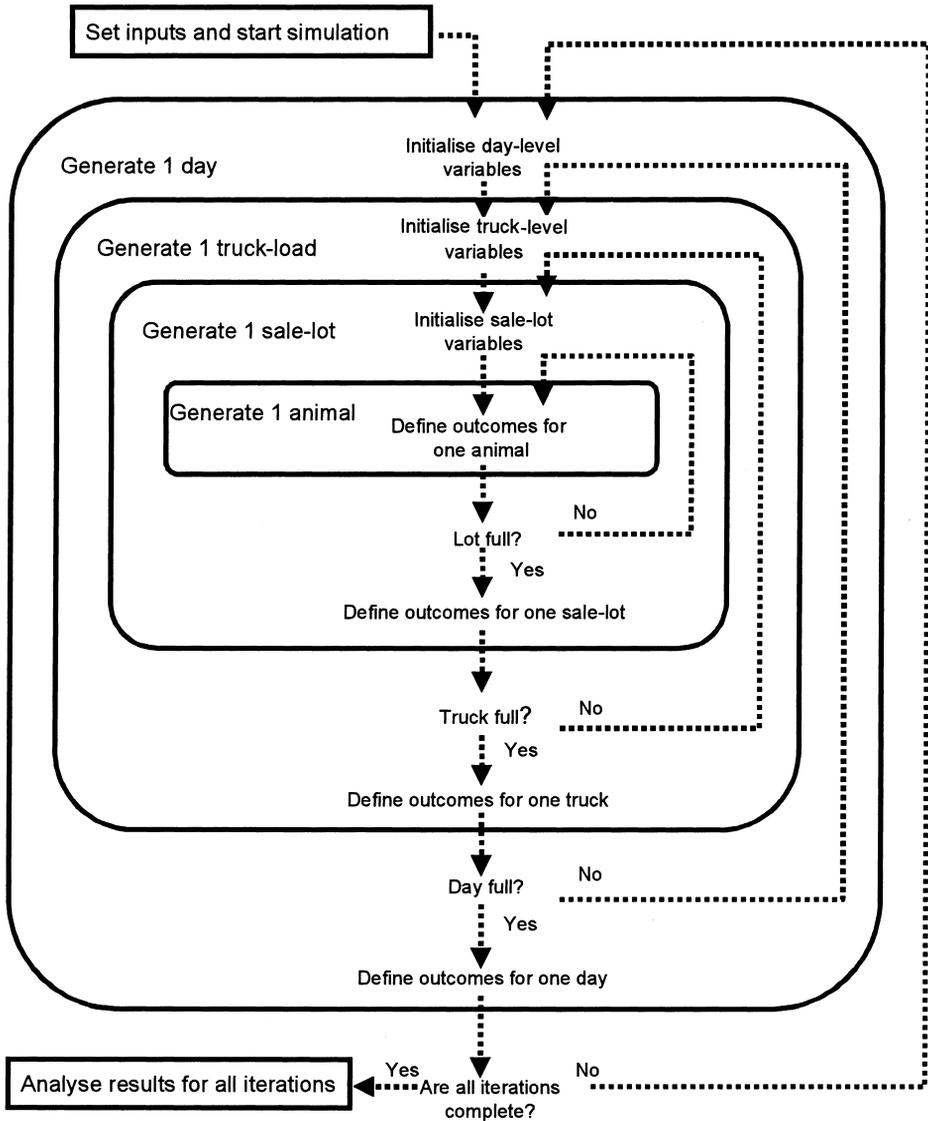


Fig. 1. Diagrammatic representation of the hierarchical model structure showing the flow of information between day, truck-load, sale-lot, and animal sub-models.

animals belonging to each sale-lot during marketing, transport and slaughter is reflected in the logic of the model. After a sale-lot is formed, it is described using variables determined by the attributes of each constituent animal. Similarly, truck-loads of animals are described by their constituent lots and constituent animals, and a 1-day slaughter run is described by its constituent truck-loads, sale-lots and animals. In this way the effects at the individual-animal level are allowed to percolate through the system altering the status

Table 1

Data fields belonging to animal objects and their purpose within the model for studying pre-slaughter factors influencing the contamination of beef carcasses with microbial hazards

Animal data field	Purpose
BIF	concentration of bacterial pathogen in faeces (CFU/gram)
BOC	count of bacterial pathogens deposited on the carcass (CFU)
CowTS	tag score of the animal
CowInf	Infection status of the animal
CowNumb	numerical position of the animal in the slaughter queue
CowTest	test status of the animal
LotNumb	number of the lot to which the animal belongs
TruckNumb	number of the truck to which the animal belongs

of each sale-lot, truck-load and day. Data structures used by cow, lot, truck, and day objects are defined in Tables 1–4.

Using the classification method of Hurd and Kaneene (1993), this model can be described as having a causal perspective based on knowledge of an underlying process, as dealing with chance using stochastic sampling, and as having a structural application perspective (the model portrays the underlying mechanisms of pathogen movement throughout the system). The model is also of a discrete entity type since each animal, sale-lot, and truck-load is dealt with as a single item. It can be broadly described as a systems simulation model. Each iteration of the model represents one day at the abattoir and outputs from the model are measures of the hygienic quality of carcasses produced on that day. Days within a simulation are therefore not regarded as consecutive days over a long period of time. Rather, they are each an independent prediction of possible outcomes for any one day if the input variables were to correspond with a true life scenario.

Table 2

Data fields belonging to lot objects and their purpose within the model for studying pre-slaughter factors influencing the contamination of beef carcasses with microbial hazards

Lot data field	Purpose
CowList	a list of all the animal objects belonging to the lot
CowRisk	the probability that an animal in this lot is infected
CowSens	individual-level test sensitivity applying to animals in this lot
CowSpec	individual-level test specificity applying to animals in this lot
Fastingtime	fasting time experienced by this lot
FirstInf	position of the first infected animal in the lot
HerdInf	infection status of the herd of origin
HerdTest	herd test status of the herd of origin
LotTS	the lot tag score derived as the mean of individual tag scores
LotInf	infection status of the lot
LotNumb	numerical position of the lot in the slaughter queue
LotReactors	number of test positive individuals in the lot
LotSize	number of animals in the lot
LotTest	the test status of the lot
Source	the source of herds from which the lot originates
Trucknumb	truck to which this lot belongs

Table 3

Data fields belonging to truck objects and their purpose within the model for studying pre-slaughter factors influencing the contamination of beef carcasses with microbial hazards

Truck data field	Purpose
FirstInfInTruck	position of the first infected animal in the truck
FirstInfLotInTruck	position of the first infected lot in the truck
LotList	a list of all the lot objects belonging to the truck
NumfromInherd	number of animals on the truck from an infected herd
NumfromInflots	number of animals on the truck from an infected lot
TruckHerdTest	number of lots from herds testing positive for the pathogen
TruckLotTest	number of test positive lots in the truck
TruckNumb	numerical position of the truck in the slaughter queue
TruckNumInf	number of infected animals on the truck
TruckNumInfLots	number of infected lots on the truck
TruckNumLots	number of lots on the truck
TruckSize	number of cattle on the truck
TruckSource	the source of lots for this truck

### 2.3. Input assumptions

Fixed and uncertain (stochastic) input variables are shown in Table 5. Uncertain input variables are specified by selecting a probability distribution and appropriate parameters. An infected animal is defined as one whose faeces contains the pathogen of interest (Table 5). Infected lots, trucks and herds each contain at least one infected animal. Inputs describing the concentration of pathogen refer to the number of colony-forming units per gram of contaminant (CFU/g) but can also be supplied as  $\log_{10}$ CFU/g. Tag scores refer to a subjectively assessed nine-point scale that grades the extent to which the hides of cattle are contaminated with faecal matter and soil. Such rating systems are currently in use in the North American slaughter industry and have been evaluated for inter-rater reliability (Jordan et al., 1999). Herd-level sensitivity and specificity are the counterparts of individual-level sensitivity and specificity. For example, herd sensitivity is defined as the probability of classifying a truly infected herd as infected when an imperfect test (of known individual-level sensitivity and specificity) is applied to a given sample size of animals drawn randomly from the herd (Martin et al., 1992). Customized dependencies can be specified by defining up to five different sources of lots. Each source can be distinguished by a unique combination of input variables as indicated in Table 5. The choice of which source of lots will be sampled is determined by a user-specified discrete probability distribution.

Some fixed model inputs contribute to a stochastic effect within the model. For example, during a simulation the actual number of animals per truck-load is a random quantity. This is achieved by continuously requesting a sale-lot of animals from the lot sub-model until the truck has met or exceeded the minimum load size. When the maximum load size is exceeded, then the most recently included lot is truncated so that the load size is equal to the maximum load size. Similarly, the actual number of animals slaughtered in a day is a random quantity because the day submodel requests new truck-

Table 4

Data fields belonging to day objects and their purpose within the model for studying pre-slaughter factors influencing the contamination of beef carcasses with microbial hazards

Day data field	Purpose
AllCowsList	a list of all the animal objects belonging to all lot objects belonging to all the truck objects in the day
AllLotsList	a list of all the lot objects belonging to all truck objects in the day
AllTruckList	a list of all the truck objects belonging to the day
ASFinfCow <sup>a</sup>	position of the first infected animal after sorting of lots or trucks
ASFinfLot <sup>a</sup>	position of the first infected lot after lot or truck sorting
ASFinfTruck <sup>a</sup>	position of the first infected truck after truck sorting
AvgBugsInFaeces <sup>a</sup>	mean pathogen count in 1 g of faeces from each animal
AvgBugsOnAll <sup>a</sup>	mean count of pathogens deposited on all carcasses
Buildup <sup>a</sup>	array for storing data on cumulative carcass contamination collected at 10 equal spaced points within the slaughter run
Carcassquantile <sup>a</sup>	selected quantile of the count of pathogens on each carcass
ConstantFt	constant term in equation describing grams of tag transferred to the carcass
CowRiskArray	holds values for cow risk of infection for each source
FaecalQuantile <sup>a</sup>	selected quantile of the per animal concentration of pathogen in faeces
FirstInfCow <sup>a</sup>	position of the first infected animal in the slaughter run
FirstInfLot <sup>a</sup>	position of the first infected lot in the slaughter run
FirstInfTruck <sup>a</sup>	position of the first infected truck load of animals in the slaughter run
HerdRiskArray	holds values for herd risk of infection for each source
LinearFastArray	holds values of the linear fasting effect for each source
LinearTag	linear term in equation describing grams of tag transferred to the carcass
NumContact <sup>a</sup>	number of animals in contact with infected herds, trucks or lots
NumCows <sup>a</sup>	number of animals within the day
NumFromInfHerd <sup>a</sup>	number of animals from infected herds
NumFromInfLot <sup>a</sup>	number of animals from infected lots
NumFromInfTruck <sup>a</sup>	number of animals from infected trucks
NumInfCows <sup>a</sup>	number of infected animals in the slaughter run
NumInfLots <sup>a</sup>	number of infected lots in the slaughter run
NumInfTrucks <sup>a</sup>	number of infected trucks in the slaughter run
NumLots <sup>a</sup>	number of lots within the day
NumTrucks <sup>a</sup>	number of trucks within the day
SumBugsOnAll <sup>a</sup>	total count of pathogens deposited on all carcasses in one day
AllTruckList <sup>a</sup>	a list of all the truck objects belonging to the day

<sup>a</sup> Denotes a model output available for density estimation and analysis.

loads of cattle from the truck submodel until the target number of animals to be slaughtered has been exceeded.

#### 2.4. Dependencies

Other than the above customized dependencies included for performing experiments by simulation, several other important relationships were defined within the model. A linear function was used to describe the effect of the duration of fasting (hours) on the increase in the logarithm of concentration of pathogen in fresh faeces. The concentration of pathogen at time  $t$  was made equal to the initial concentration (on the log scale) plus

Table 5

Uncertain and fixed input variables, whether or not they can be used to distinguish different sources of lots, the sub-model location in which sampling occurs (uncertain variables) and the sub-model site of action for each variable

Variable description	Sampling mode	Can be used to distinguish sources of lots	Sub-model in which sampled	Sub-model site of action
Choice of random-number generator	fixed	no	na	entire model
Concentration of pathogen in faeces at the farm	uncertain	yes	animal	animal
Constant amount of tag transferred (g)	uncertain	no	day	animal
Control options	fixed	no	na	lot, truck, day
Fasting effect – linear	uncertain	yes	day	animal
Fasting time (h)	uncertain	yes	truck	animal
Linear amount of tag transferred (g)	uncertain	no	day	animal
Maximum truck capacity	fixed	no	na	truck
Mean lot tag score	uncertain	yes	lot	animal
Method of modelling concentration of pathogen in tag	fixed	no	na	lot
Minimum fasting time	fixed	no	lot	animal
Minimum truck capacity	fixed	no	na	truck
Number of iterations per simulation	fixed	no	na	day
Number of positive animal tests defining a positive lot	fixed	no	na	lot
Probability that a herd is infected	uncertain	yes	day	lot
Probability that an animal within an infected herd is infected	uncertain	yes	day	animal
Random number seed	fixed	no	na	entire model
Sensitivity of herd test	uncertain	no	lot	lot
Specificity of herd test	uncertain	no	lot	lot
Target number of animals slaughtered in one day	fixed	no	na	day
Sensitivity of individual test	uncertain	no	animal	animal
Specificity of individual test	uncertain	no	animal	animal
Weighting of sources of lots	fixed	yes	truck	lot, animal
Within lot variance in tag score	fixed	yes	na	animal

the product of the linear coefficient multiplied by the duration of fasting. Because composition of ration affected the value of the linear coefficient when *E. coli* biotype 1 was studied (Jordan and McEwen, 1998), the coefficient can be made dependent on the source of lots. The duration of fasting is itself a stochastic input and is used to represent the total amount of time animals are off feed prior to slaughter. It is possible to apply a minimum duration of fasting to all lots to comply with recommendations facilitating hygienic removal of the viscera at slaughter (Gracey, 1986).

In this model, the relationship between tag score and the weight (in grams) of tag transferred to carcasses was designed to take account of the similarity (clustering) of tag scores within sale-lots. This is achieved using a standard linear model approach by deriving an individual-animal's tag score as the sum of the mean tag score for the lot of origin plus a variance component describing the variability of tag scores within a lot. This

method was chosen because values of the mean lot tag score and variance within sale-lots can be obtained from a regression analysis of tag scores obtained at processing plants.

A third dependency is the relationship between tag score and the amount of faeces transferred from hide to carcass. Although the results of studies semi-quantifying this relationship are somewhat in disagreement (Dixon et al., 1991; Ridell and Korkeala, 1993; Van Donkersgoed et al., 1997), the notion that greater hide contamination causes greater carcass contamination has a very strong intuitive appeal and is a broadly reflected sentiment found in the literature. In the model, once each animal is allocated a tag score, the amount of tag (grams) transferred to the carcass is described as a constant plus a linear function of tag score (where both the constant and linear coefficients are stochastic). The amount of fresh faeces transferred to carcasses (i.e., from the rectum) is not dependent on tag score and is described only by a probability distribution. Unfortunately, there currently exists little objective basis for estimating the coefficients for the transfer equation and for the amount of fresh faeces transferred thus these were determined subjectively.

The total count of pathogen deposited on a carcass is the sum of that derived from fresh faeces and that derived from tag. Both are arrived at by multiplying the concentration of pathogen in fresh faeces or tag for that animal by the amount of fresh faeces or tag transferred to the carcass of that animal. The concentration of pathogen in faeces is determined by a stochastic starting value plus the effect of fasting as described above. A choice is provided for determining how the concentration of pathogen in tag is modelled. The simplest option is to set the concentration in tag equal to the concentration in the faeces of that animal. A more appealing alternative (because it accounts for the fact that tag is comprised of faeces from animals shedding the pathogen and those not shedding the pathogen) is to set the concentration of pathogen in tag equal to an estimate of the concentration expected in well-mixed faecal waste at the feedlot. This is achieved using a 'diluted-pool model' whereby the concentration in tag is a function of the mean concentration in the faeces of infected animals weighted by the proportion of animals infected. The advantages of the diluted-pool approach are that the faeces from non-infected animals dilutes the pathogen contributed by infected animals to the tag pool, and that the amount of dilution is dependent on the prevalence of infection in the herd.

## 2.5. Control modes

The model permits users to evaluate 10 different control modes based upon several general strategies. These strategies are intended to represent measures that currently could be adopted and those which might be implemented in the future should there be technical advances in diagnostic testing, improvements in animal handling facilities, and/or changes in industry-management practices. The first general strategy involves the testing of all individuals prior to slaughter with a test of given sensitivity and specificity, followed by classification of lots based on the number of test-positive animals, then placement of test-positive lots at the rear of the slaughter queue. A second strategy is based on testing of each sale-lot of cattle on farm followed by total exclusion of test-positive lots from consignment to the processing plants. A third strategy (similar to that described by Ridell and Korkeala, 1993) is to assign faecal contamination scores to cattle

when they arrive at the abattoir, then classify each lot as clean or contaminated based on a function of these scores. Contaminated lots are then placed at the rear of the slaughter queue. A fourth strategy relies on information about the test status of the herd of origin. Lots from test-positive herds or truck-loads containing at least one lot from a test-positive herd are moved to the rear of the slaughter queue. A variant of this fourth strategy is to consign to slaughter only those sale-lots which originate from herds with a negative test status. Combinations of the above strategies also can be implemented and in total this provides the ten different modes of simulation (in addition to the standard mode) for evaluation of these novel control measures. Within the inner workings of the model, the quicksort algorithm (Flanders, 1996) is the mechanism by which lots and truck-loads of cattle are sorted within the slaughter queue.

### *2.6. Propagation of uncertainty*

The Monte Carlo approach allows an appraisal of the effect of uncertainty in input variables (Morgan and Henrion, 1990). In this regard, the total uncertainty is comprised of variability due to inherent randomness in a quantity and any doubt or ignorance that might exist about the way this variability is described (Hoffman and Hammonds, 1994). Such uncertainty is propagated through this model as follows: Each simulation consists of a user determined number of iterations. At every iteration, a value is randomly sampled from each of the specified input distributions and is fed into the model to produce a single output value. At the end of the simulation, each output value from each iteration is collected and summarised statistically (as moments and percentiles) and graphically. Therefore, each simulation defines a distribution for the output variable based on a large number of combinations of different levels of each input variable.

A flexible system was built into the model for specifying probability distributions for uncertain input variables. For each uncertain input one of the following parametric probability distributions was made available for selection: Bernoulli, binomial, beta, exponential, gamma, geometric, log-normal, negative binomial, Normal, Poisson, transformed beta, triangular, uniform and Weibull. Background information and definitions for these distributions have been reviewed (Evans et al., 1993). Provision of these distributions permits the definition of uncertainty based on a theoretical understanding of a variable's behaviour and the estimation of parameters from data using the method of the moments or the method of maximum likelihood (Freund, 1992). In addition, probabilities may be defined by discrete (including fixed value), empirical grouped (histogram) or empirical ungrouped distributions (Law and Kelton, 1991). These latter options permit probability densities to be derived from actual observations, expert opinion, or curves derived by non-parametric methods such as piece-wise polynomials or Bezier curves (Chan, 1993).

### *2.7. Random variates*

An issue central to the integrity of a Monte Carlo risk model is the quality of random variates used to generate uncertain input variables (Burmester and Anderson, 1994). Generation of random variates from any of the available input distributions is a two-step

process. The first step is to generate uniform random variates on the 0–1 interval. It is critical that the random generator chosen for this task produces uniformly distributed random variates having a long period of recurrence and without serial correlation (Barry, 1996). The RAN2 (Press et al., 1989) and Marse and Roberts (Law and Kelton, 1991) linear congruential generators were both coded into this model because published algorithms are available and their performance has been favourably reviewed (Barry, 1996). Once uniform random variates have been generated, the second step is to pass them through an algorithm to obtain a random variate from a particular probability distribution. Algorithms used for this task are those described by Law and Kelton (1991) and Kachitvichyanukul and Schmeiser (1988) and are mostly based on the inverse transform method.

Mistakes made during the conversion of published algorithms into computer code are potentially a serious source of error. To verify the correctness of algorithms for generating random numbers, a test program (also written in the Delphi programming language) was developed using code identical to that employed for generating random numbers in the main model. The test program was used to produce sequences of 10 000 random variates from each distribution with parameters specified by arbitrary values. Each sequence of random variates was then charted as a probability density and compared to a graphical representation of the parent probability distribution using the BestFit software package (Palisade Corporation, Newfield, NY). Test distributions were also assessed on the basis of their compliance with theoretical minimum and maximum values, mode, and (where necessary) mean and moments about the mean.

## 2.8. Simulation outcomes

A range of outcomes was chosen to represent the daily performance of abattoirs with respect to pre-slaughter control measures. Between iterations, each outcome is independent since there is no carryover effect from one iteration to the next. Outcomes included the number of infected animals, the number of infected lots, and the number of infected trucks. The time of initial entry of pathogens into the abattoir is of relevance because once pathogens are introduced, they may cross-contaminate carcasses later in the queue. Hence, the model also included outputs recording the position of the first infected animal, position of the first infected lot and position of the first infected truck in the slaughter queue. Two outcome variables that expand on this concept are the cumulative total of carcass contamination and the cumulative total of pathogen counts in 1 g of faeces from each animal. These respectively measure the total amount of pathogen on all carcasses, or in 1 g of faeces obtained from each animal up to and including a particular point in the slaughter queue. Thus, an impression of the build up of contamination on carcasses for each day is obtained by recording this information at 10 equidistant points (number of animals) from the beginning of the slaughter queue to the end. To summarise this information over all days within a simulation, the median of these cumulative totals is plotted against position in the slaughter run. Variation around the median is shown by 5th and 95th percentile plots. The concentration of pathogens in faecal matter and the count of pathogens deposited per carcass are evaluated using the mean and a selected percentile for each day. The number of animals from an infected lot, the number of animals from an

infected truck and the number of animals from an infected herd are provided as a surrogate measure of the degree of cross-contamination of the hides of animals with faeces containing pathogen. The number of animals in contact with infected animals, infected lots and infected trucks are also provided. Total number of animals, lots and truck are outcomes provided for verifying model logic. Outcomes are listed in the description of data fields belonging to day objects in Table 4.

### 2.9. Analysis of output

All outputs from the model are described by finding minimum and maximum values, mean, skewness, kurtosis, and percentiles in 5% steps. While these statistics precisely characterise the output in numerical terms, they are usually less informative for decision making purposes than a graphical representation of the data. Consequently, output from this model can be portrayed as a probability mass function (suited for outcomes with a discrete distribution), frequency histogram, probability density function (suited for outputs that are best represented as a continuous distribution), or as a distribution function (cumulative probability distribution). In general, probability densities provide the most easily understood representation of the data (Fox, 1990). However, depiction of densities as simple histograms can often misrepresent the true nature of the underlying distribution (Venables and Ripley, 1997). For this reason, output can be subjected to distribution-estimation techniques in which the potential biases of histogram representations are minimised by a procedure known as ‘kernel-smoothing’. An adaptive kernel-smoothing technique using an Epanechnikov kernel was implemented for estimating probability densities (Silverman, 1986), and when the data have a theoretical lower bound of zero, the reflection technique described by Silverman (1986) was employed to ensure  $f(x)$  is zero for negative  $x$ .

## 3. Discussion

While a risk-assessment approach to microbial food safety seems promising, there are some difficulties with its application (Anon, 1995). First, existing frameworks have evolved largely from the study of abnormalities in humans following exposure to chemicals in the environment. These frameworks have been touted as adaptable to the field of microbial food safety, although there are some major differences between the way microbial and chemical agents contaminate product and induce disorders in humans. Secondly, there are large gaps in our understanding of the dynamics of pathogens at all stages of meat production. While some quantitative risk-assessment approaches can deal with this by describing the uncertainty in input assumptions, methods for dealing with uncertainty in the structure of risk models are lacking (Morgan and Henrion, 1990). The solution proffered in this paper was to divide the production process into discrete units and to develop conceptually simple and intuitively appealing models for each unit. Completed units can then be linked together to provide a larger model that addresses a significant component of the beef production process. Although the models are conceptually simple, their implementation as computer code required rather sophisticated

programming techniques. However, by using a programming approach, it is likely that the model described here can be linked to other models (such as that of Cassin et al., 1998) which addresses post-slaughter processing and the response of humans to various doses of pathogen.

The foremost advantage of a simulation approach for specifying criteria for improving the microbial safety of meat is the avoidance of the difficulties and expense associated with quantifying abattoir outcomes by conventional methods. Although microbiological sampling of carcasses is often practised, methods are not standard with respect to number of carcasses sampled, sites of sampling, techniques for removal of bacteria from the surface of carcasses, storage of specimens, and laboratory processing (Anderson et al., 1987; Hudson et al., 1987; Gill et al., 1996; Karr et al., 1996). Furthermore, most of the testing procedures — especially those necessary for enumerating bacterial pathogens are inefficient (Johnson et al., 1994). Therefore, they cannot be applied to a large enough sample of carcass sites and animals to provide a meaningful comparison of the benefits of even a modest number of pre-slaughter interventions (Hathaway et al., 1988). Nevertheless, the studies that have been completed to date are very valuable in that they form a basis for understanding the contamination of meat carcasses. It is this knowledge that permits the meat production system to be studied through simulation in an attempt to identify optimal control strategies.

The model developed in this paper is capable of evaluating a number of control mechanisms applicable to the pre-slaughter period. These mechanisms can be grouped according to which input variables and control options are manipulated to represent the intervention(s) of interest. Simulation then follows and shows the effect these changes have on traits measuring the hygienic quality of carcasses produced in an abattoir in a 1-day period. One mechanism is based on reducing the prevalence of infected herds or reducing the prevalence of infected animals within infected herds, or both. For example, the benefit of a campaign encouraging livestock producers to administer a hypothetical vaccine to animals can be evaluated. To do so, the following assumptions are made: animals from source A are assumed to be from herds where vaccination has not been adopted and those from source B are from vaccinated herds. Compared to source B, source A is given both a higher prevalence of infected herds and a higher prevalence of infection within infected herds. These differences in herd and individual prevalence between sources A and B reflect an assumption about the effect of the hypothetical vaccine on reducing the pathogen's ability to colonise the animal host. Other assumptions can be made about the effect of the vaccine in reducing the concentration of pathogen in the gut contents of infected animals. The probability of herds being derived from source A reflects the proportion of managers who adopt correct vaccine use. Therefore, the model can estimate the benefit of a program where cattle owners are not 100% compliant with recommendations on the use of the vaccine (there is a dependency between source of cattle and prevalence of infection).

A second mechanism is based on reducing the opportunity for cross-contamination of animals and carcasses by acting on knowledge of the pathogen status of animals, lots, trucks or herds. This could, for example, involve the use of a hypothetical but imperfect rapid test applied to all animals upon arrival at the abattoir. Imperfection in test performance is described by values for individual-animal sensitivity and specificity, and

the model translates this information into lot-level test accuracy based on the number of test-positive results deemed to designate an infected lot. In this scenario, for example, it is assumed that sale-lots classified as positive are moved to the rear of the slaughter queue. Alternatively, it is possible to exclude test-positive lots or herds from the abattoir, or to sort sale-lots or truck-loads of cattle based on the test status of the herd of origin. The outcomes of interest under this mechanism of control are: the position of the first infected animal in the final slaughter queue; a plot showing the time rate of increase in the cumulative pathogen count summed over all carcasses; and a plot showing the time rate of increase in the cumulative total of pathogen counts from 1 g of faecal material from each slaughtered animal. Similar test-and-sort options are available at the truck and herd levels.

A third group of scenarios is based on controlling the transfer of faeces onto carcasses by reducing the extent of faecal contamination present on the hide of animals prior to slaughter. For example, one might examine the effectiveness of an industry-wide campaign that encourages beef producers to market their cattle with less faecal contamination of hides. This entails providing the model with assumptions about the distribution of tag scores in the cattle from herds where the preventive practice is adopted and in herds where it is not adopted. A variant of this third mechanism (which is related to the mechanism of reducing the opportunity for cross-contamination) is to change the slaughter order based on severity of tag score. This forces the model to move lots with high mean tag score towards the rear of the slaughter queue. In both cases within the third group, one would be interested in viewing how this affects the time rate of increase in the cumulative total of pathogen counts on all carcasses. Ideally, the greatest amount of carcass contamination occurs at the rear of the slaughter queue. Under these conditions, a larger proportion of animals will pass through the slaughter chain with a reduced risk of cross-contamination during processing.

A fourth mechanism is based on reducing the number of pathogens per gram of faeces. In practice, this mechanism is invoked by exploiting knowledge about a risk factor that contributes to changes in the concentration of the pathogen in faeces. The duration of fasting prior to slaughter is one such hypothesised risk factor. Similar effects might be realised through modification of rations (Jordan and McEwen, 1998), use of a chemotherapeutic agent that discourages growth of the pathogen in the gastrointestinal tract of host animals, or inoculation of cattle with probiotic bacteria (Zhao et al., 1998). In the model, simulation of this mechanism entails dividing the population of herds into two sources and in one source reducing the assumed quantity of pathogen (CFU/g) shed in the faeces of infected animals. The adoption rate of the practice concerned is reflected by adjusting the proportion of lots being derived from a source where the control is practised.

When the model is used to simulate each of the above mechanisms, uncertainty in the output is obtained by sampling from the input probability distributions. Latin-hypercube sampling (LHS) is often regarded as a superior method of generating random variates compared to the simple random sampling (SRS) which was used in this study (McKay et al., 1979). LHS is a form of stratified sampling with the number of strata being equal to the number of times each distribution will be sampled from during a simulation (Vose, 1996). When LHS is used, the sampling algorithm must use information on the stratum

intervals to create all the random variates to be used in a simulation, and all this must be done before the first iteration. Because of this model's hierarchical structure, the number of animals generated within the day, truck and lot submodels vary with each iteration and so it is not possible to determine the stratum intervals for LHS prior to simulation. Thus, LHS cannot be implemented in this model. However, LHS places less emphasis than SRS on sampling from the tails of input distributions (Vose, 1996), and this will provide a less accurate depiction of the tails of outputs which is often the focus of a quantitative risk assessment. Therefore, the inability to implement LHS in this model is a small disadvantage which is largely outweighed by the intuitive appeal of the hierarchical model structure.

Simulation studies can have shortcomings. Perhaps foremost is the fact that the relationships encompassed in a model are constrained by the extent of knowledge about the system under study. Simulation models therefore do not replace a conventional experimental or observational approach to research. Instead, they build on existing knowledge about the system and attempt to unite this information into a cohesive structure. Limitations in the structure and capabilities of a model are indicators of gaps in scientific knowledge and locating these gaps is a useful outcome of the modelling exercise. Nevertheless, when the model is used for predictive purposes, an appreciation of its limitations is necessary for the correct interpretation of the model and use of the output.

Transmission of pathogens between animals during marketing, transport and waiting prior to slaughter is a possibility that is not allowed for in this model. Brownlie and Grau (1967) working with cattle, and Grau et al. (1969) working with sheep, found evidence suggesting that transmission of *E. coli* and *Salmonella* spp. among animals during marketing and transport can occur especially if the time from farm to slaughter is prolonged. As well, in vitro studies suggest that cattle that are fasted prior to slaughter are more susceptible to colonisation with *E. coli* O157:H7 (Rasmussen et al., 1993). However, the data published in the aforementioned studies are too sparse to generate a quantitative estimate of the probability of transmission. Nor are the data adequate to quantify the likelihood that pathogens will be shed in faeces at the time of slaughter as a result of infection at a given prior point in time. To compensate for this, the model provides estimates of the number of animals in contact with an infected herd, truck or lot. This 'number of animals in contact' outcome is a relevant outcome to consider in circumstances where there is a need to make qualitative judgments about the importance of cross contamination between animals before slaughter.

A possible limitation of this model is the absence of a mechanism that fully accounts for all the conceivable pathways that pathogen-laden faeces can contaminate a carcass. Faeces that contaminate an animal's carcass may be derived directly from the gastrointestinal tract of the same animal at the time of carcass dressing. Alternatively, it may be derived from the animal's hooves or hide. In the latter case, the faecal material may originate from the animal itself, or from direct transfer from another animal, or from contact with the environment. Currently, the model assumes that the animal's own faeces and tag (derived from a pool of faeces) are the only sources of contamination and the concentration in tag on hide is either the same as that in fresh faeces or is determined by the diluted-pool model. Research is required to elaborate the relative importance of the other pathways and to indicate the concentration of pathogen in contamination from other

sources. The architecture of the model described here is flexible enough to incorporate this information should it become available.

Validation is a traditional method used to study how the limitations of a model may impact on the usefulness of model output. It involves a comparison of observations from the actual system under study with model output (Martin et al., 1987). The input variables used to generate model output are set in accordance with the state of the actual system at the time data were collected. Validation is therefore a test to see how well the model reflects reality. Notwithstanding its merits, validation is a technique that is difficult to apply to quantitative risk-assessment models. The difficulty arises because such models have evolved as an alternative to conventional research techniques which cannot be implemented for cost or practical reasons – and yet it is these same research techniques that would necessarily be used to generate the data for validation. In the case of pathogens on carcasses, it is difficult to quantify both the model inputs and outputs using conventional research methodology. The disadvantage of being unable to validate a model is somewhat offset by use of a Monte Carlo approach that estimates uncertainty in outcomes – something which conventional research methodology cannot easily achieve.

Above all, the limitations of the model need to be placed into the perspective of the original objectives. The principal purpose of risk assessment modelling is to generate a tool that helps to make better decisions (Hathaway, 1991). Although it is ideal that the resulting model is a comprehensive and accurate representation of the real system, this is not an absolute requirement. What is necessary is that the model represents the best synthesis of information about the problem that is currently available. Models that are found to be deficient in the future can be modified. In this sense, they act as a springboard for developing further understanding of a system.

The combination of a hierarchical model structure, Monte Carlo sampling and accommodation of dependencies is an approach that could be used in other areas of animal-health decision-making. For example, import–export risk assessments may also be aimed at providing probabilistic estimates of the likelihood of introduction of a contagion into animal, human or plant populations. Often a hierarchical model design will best describe the pathways of entry of the pathogen because this structure best resembles many of the systems used for the marketing and distribution of agricultural produce. The model described here could be modified and used for this purpose.

In conclusion, the model described in this paper permits inexpensive and rapid investigation of the impact of pre-slaughter factors on the hygienic quality of beef carcasses. Models such as this make it possible to evaluate control strategies that could not be investigated by an alternative approach due to the prohibitive cost or excessive level of intervention required. In a follow-on publication, carcass contamination with *E. coli* O157:H7 is modelled, and pre-slaughter mitigation strategies that could alleviate this problem are explored.

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