

Quantitative Risk Assessment

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Quantitative risk assessment

Risk management is concerned with making unwanted events less likely to happen and applies for example to technological risks as well as financial risks. Risks are defined through hazards, which represent situations and events causing loss or damage. Hazards are characterised quantitatively through the magnitude of loss, damage or cost incurred by the hazard and the probability that these events occur (Nash and Nash 1995). Risk is reduced by changing one or both of these two parameters. Risk assessment or analysis involves comparing between alternative approaches to manipulating or controlling the hazard and ultimately requires decisions to be made as to the most appropriate strategy. In the framework for risk management suggested by the Presidential-Congressional commission on risk assessment and risk management (Anon 1997a), it is used during the phase where different options for addressing risks are compared (see Figure 1). Modelling techniques can be used very effectively to simulate the consequences of different decisions or actions. The principles are quite simple, in that the analyst develops a model or a number of models representing the quantitative relationships between different actions and their consequences. This *quantitative risk assessment* or *risk analysis* (QRA) can be based on a *deterministic* or *stochastic* modelling approach (Law and Kelton 1991). The difference between both approaches has to do with two issues, namely *risks* and *uncertainties*. *Risks* are quantitative estimates of the perceived probability of particular events happening. The fact that they are called probabilities implies that their outcome in any given situation is subject to *uncertainty* or *randomness*. In *deterministic modelling* this uncertainty is being ignored whereas in *stochastic modelling* it is in fact taken account of. This also means that a *deterministic model* will generate only a single value for the outcome parameter and the *stochastic* a probability distribution of possible outcomes.

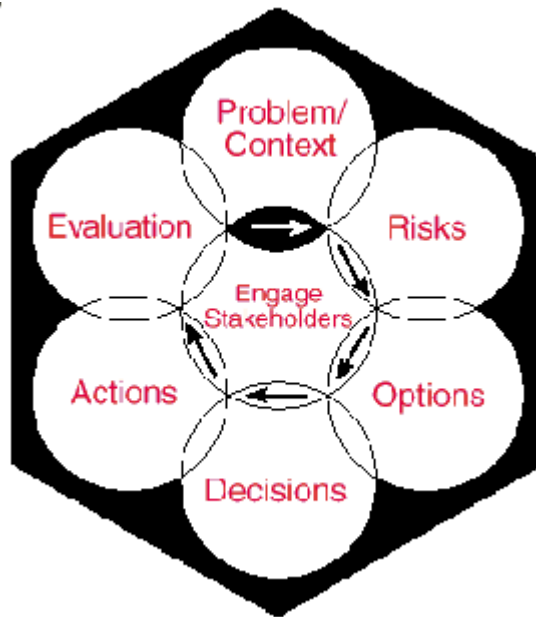


Figure 1: Framework for risk management (from Anon 1997a)

Development of simulation models for QRA

A QRA model can be designed using the following development phases: Development of conceptual model, development of deterministic model, development of stochastic model, model verification, validation and credibility

Development of conceptual model

As a first step the development of a QRA model requires that the structure of the problem be decided. This can be done through a systems analysis, where the main components of the system are identified. The relationship between sets of *input* and *output variables* have to be defined. *Parameters* are used to represent the quantitative aspects of these relationships. The *variables* can be observed in the real system, whereas *parameters* cannot be observed directly (Zeigler 1976). During the systems analysis the objective should be to disaggregate the problem into its component variables. The smaller the components the easier it may be to define them and to identify the ones with well known and the ones with uncertain or unknown parameter settings. After having defined the components of the model, the relationships between them have to be defined. These relationships then need quantitative estimates of the associated parameter values, which are typically probabilities. The estimates can be derived from *expert opinion* or *data*. The aforementioned tasks can all be accomplished using drawing or flow-charting software or simply on the back of a piece of paper. Decisions about components, relationships and parameter settings should probably be based on discussions with a number of different experts in the area the model is attempting to represent. It is important to use graphical tools during the design phase, as this

will facilitate discussion and modification of model structure in the presence of less computer literate experts. Without agreement on and acceptance of the conceptual model it will be very difficult to convince decision makers or stakeholders to accept the conclusions from the modelling exercise. Figure 2 presents the different phases leading to the development of a conceptual model.

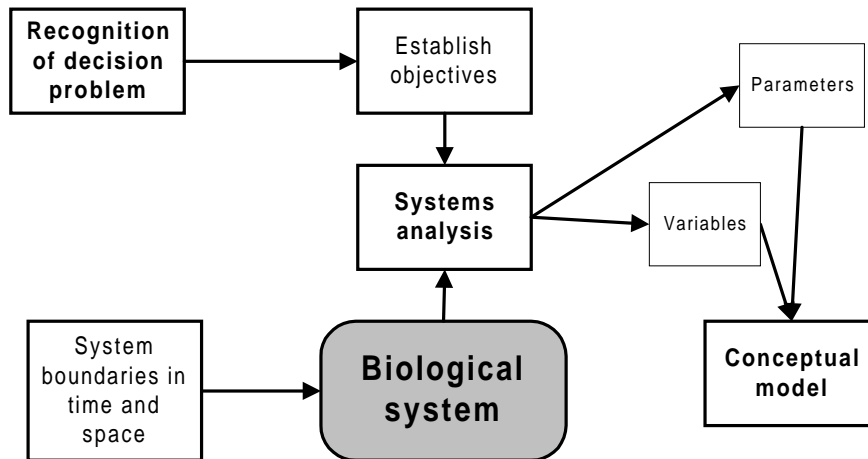


Figure 2: Development of conceptual model

Development of deterministic model

As a next step, manual calculations could now be performed. But it would be cumbersome to go through “what if” scenarios multiple times, specifically for complex models. At this stage the model should be implemented using computerised spreadsheet software. This means that the model basically has to be converted into a set of linked equations, where spreadsheet cells represent different model *input* and *output variables* as well as their quantitative relationships with other variables of the model through the associated *parameters*. At this stage, the parameter settings for this model will be single values such as average population size, disease prevalence or diagnostic test sensitivity, as defined by expert opinion or other data. This means that the *output parameters* will be *determined*, which is why the model is called *deterministic*. This type of model can be used to perform “what if” analyses, where the effect of changing selected input parameters on the outcome variable is assessed. But the analyst has to remember that a deterministic model assumes that the *input variables* are known and the *parameters* are not uncertain. In reality this rarely will be the case.

Development of stochastic model

This phase of the model development mainly requires replacing single parameter values with probability distributions where considered appropriate by the analyst. These can be either derived from data or from expert opinion. Likely data sources include for example experimental or field

studies or published literature. In this case it is very important to assess the validity and representativeness of the information, before using it in the model. If direct access to the data is possible, the statistical properties of the required parameters can be estimated and an empirical or theoretical probability distribution can be fitted. In the case of expert opinion, specific parametric and nonparametric distributions can be fitted based on information provided by experts. Both approaches are described in Vose (1996).

Model verification / validation / credibility

During the *verification* stage the analyst essentially has to review the model structure in order to ensure that the model performs as intended. This means that the translation from the conceptual model to the spreadsheet QRA model has to be checked. This is followed by model *validation*, where the analyst determines if the model is an accurate representation of the risk analysis problem. This is usually done by comparing model output given particular input parameters with real data. Figure 3 presents the iterative process required during these phases of QRA model development. If the stakeholders can accept the model, its results and are prepared to use it as an aid for decision making, then the model can be called *credible*. This last step is essential and can be the most challenging, as it ultimately decides if the model will be used for decision making.

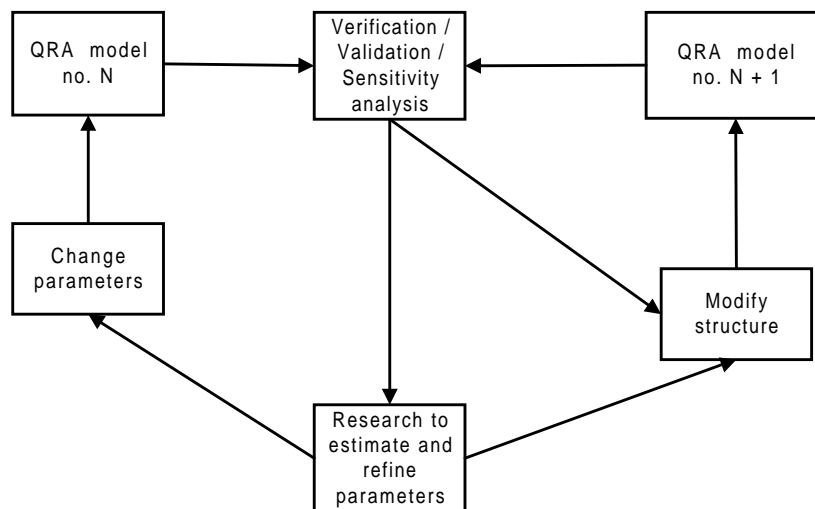


Figure 3: Model verification / validation process

Development of a QRA model for the risk of introduction of Newcastle disease into a country

The objective is to develop a QRA model for the expected number of introductions of Newcastle disease (ND) into a target country through purchase of flocks of layer hens from a particular source country. The consequences of changing the diagnostic testing scheme from two to a single test will be assessed. The assumptions for this exercise include that the flocks considered for

importation will be tested for ND virus infection using the haemagglutination inhibition test during two separate quarantine periods. As soon as a single hen in a flock has been diagnosed positive, the flock cannot be imported into the target country. **This is a hypothetical example and should not be used as the basis for real-life decision making!**

Modelling approach

Step number 1 – Development of conceptual QRA model

The first step involves disaggregation of the problem into quantifiable components. With this particular problem, the following variables are likely to be important:

- Number of poultry herds in source country
- Prevalence of infected flocks in source country
- Size of poultry herds
- Seroprevalence of ND virus infection within infected flocks
- Number of imported flocks per year
- Size of imported flocks
- Probability of not detecting infection during quarantine influenced by
 - Number of animals sampled
 - Sensitivity of diagnostic test method
 - Number of samplings
- Probability of transmission in target herd
- Probability of spread from target herd to other herds

Figure 4 presents a diagram of these different processes, which influence the risk of introducing ND into a target country.

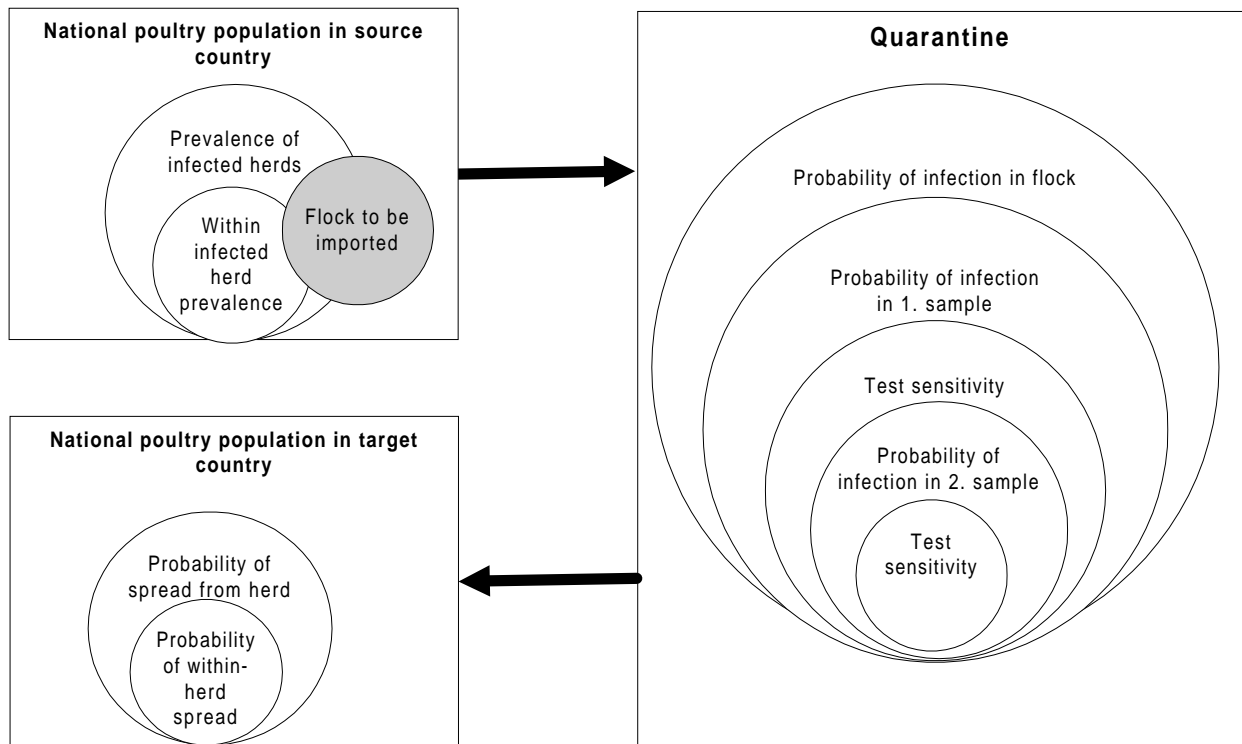


Figure 4: Diagram of probability processes influencing the risk of ND introduction into a target country as a consequence of importing layer hens

Assuming that the above list has been accepted by stakeholders and decision makers as including all relevant components or variables influencing risk of ND introduction, parameter values have to be estimated for each of these variables. This should be done in consultation with experts who have experience with the disease in the field and / or laboratory. For the purposes of this exercise, a set of hypothetical estimates will be used, some of which have been derived from a more detailed QRA model developed by Audigé and Vicari (personal communication) for the same disease. In addition the following assumptions were made about the epidemiology of infection process. The risk of infection does not vary between different age groups of poultry. There is no difference in probability of purchase between infected and uninfected flocks. No transmission occurs within flocks occurs during quarantine.

Table 1: Variables and estimated parameter values for risk of ND introduction QRA model

<i>Variable</i>	<i>Parameter estimate</i>
• Number of herds in source country	6000
• Prevalence of infected flocks in source country	0.10
• Size of herds	16000
• Seroprevalence of ND virus infection within infected flocks	0.10
• Number of imported flocks per year	20
• Size of imported flock	450
• Probability of not detecting infection during quarantine	
• Number of animals sampled on each occasion	10
• Sensitivity of diagnostic test method	0.76
• Number of samplings	2
• Probability of transmission in target herd	0.10
• Probability of spread from target herd to other herds	0.10

Step number 2 – Development of a deterministic QRA model

With this information available a deterministic model can be developed which represents the relationships between the different variables in a quantitative way. This will be done using the spreadsheet software Microsoft Excel 97 (Microsoft Corporation, Redmond, WA).

As a first calculation the expected number of infected flocks coming into quarantine has to be calculated. Figure 5 presents the data and the formulas to perform these calculations. On average 2 infected flocks are expected to come into quarantine.

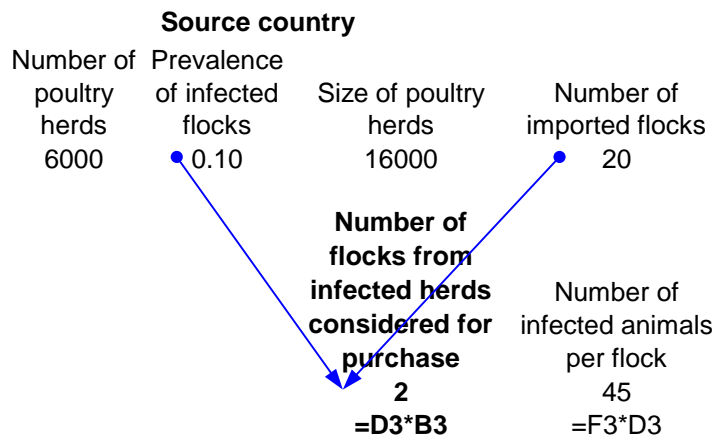


Figure 5: Spreadsheet calculations for number of infected flocks coming into quarantine

This information can be used to quantify the number of infected flocks escaping detection during quarantine after random samples of 10 hens have been tested serologically for presence of ND infection (see Figure 6). It is expected that about every 2.1 years an infected flock will remain undetected using a single test procedure. With 2 independent serological tests the interval increases 8.7 years.

	D	E	F	G	H	I
1	Quarantine					
2	Number of imported flocks	Within-infected flock sero	Size of purchased	Sample size	Test sensitivity	No. samplings
3	20	0.10	450	10	0.76	2
4						
5	Number of infected animals per flock	Number of infected animals included in sample	Probability of failing to detect any infected animals in sample 1	Number of false negative flocks coming through quarantine with single test	Probability of failing to detect any infected animals during sample 2	Number of false negative flocks coming through quarantine with two tests
6	45	1	0.24	0.48	0.24	0.1152
7	=F3*D3	=G3*E3	=(1-H3)^E6	=C6*F6	=(1-H3)^E6	=C6*F6*H6
8	Average number of years between events					
9				2.1		8.7

Figure 6: Spreadsheet calculations for the number of infected flocks which are able to pass through quarantine

The final step of this model relates to the likely effect that these imported infected flocks will have on the target poultry population (see Figure 7). The results indicate that over the period of a year on average every 87 years an outbreak in importing herds will occur, if flocks are being tested twice. With only a single test, there will be an outbreak on average every 21 years. As a result of outbreaks in importing herds, spread of infection to other herds can be expected every 868 and 208 years with two tests and a single test respectively.

	G	H	I	J	K	L	M
1	Quarantine			Target country			
2	Sample size	Test sensitivity	No. samplings	Risk of transmission	Risk of spread		
3	10	0.76	2	0.1	0.1		
4							
5	Number of false negative flocks coming through quarantine with single test	Probability of failing to detect any infected animals during sample 2	Number of false negative flocks coming through quarantine with two tests	Number of outbreaks in importing herds with both tests	No. outbreaks through between herd spread with both tests	No. outbreaks in importing herds without single test	No. outbreaks through between herd spread without single test
6	0.48	0.24	0.1152	0.01152	0.001152	0.048	0.0048
7	=C6*F6	=(1-H3)^E6	=C6*F6*H6	=I6*J3	=J6*K3	=G6*J3	=L*K3
8	Average number of years between events						
9	2.1		8.7	86.8	868.1	20.8	208.3

Figure 7: Calculations required to obtain the expected number of outbreaks caused by introduction of infected flocks into the target country over the period of a year

In summary, the results suggest that outbreaks as a consequence of introducing infected flocks are reasonably unlikely, mainly due the low risk of transmission once infected flocks have been introduced into their target herds. But seems quite clear that changing to a single test would increase the risk of outbreaks in the target country substantially.

Step number 3 – Development of a stochastic QRA model

The deterministic model has the major disadvantage that it only reports average expected outcome values. It does not provide any information about the likely spread of outcome values, in this case, the number of expected outbreaks. In addition, for many of the parameters used for the development of this model the true estimates are not known. Therefore, these parameters are uncertain and it would be more appropriate to represent them through probability distributions. At this stage of model development, assuming that the model structure is considered to adequately represent the underlying problem, single value estimates of the model input parameters will be replaced with probability distributions. The spreadsheet add-in software @Risk (Palisade Corporation, FAX: 607-277-8001, <http://www.palisade.com>) in conjunction with software RISKview Pro from the same company will be used to perform this task in the spreadsheet software Microsoft Excel 97.

Replacing single values with distributions requires estimates of spread as well as most likely values. The software @Risk provides the two non-parametric distribution types Triangular and BetaPERT for this purpose. Other potential candidates include the binomial and beta distribution, as well as the hypergeometric distribution.

With stochastic or Monte Carlo simulation modelling it is possible to develop a model which is closer to reality, in that events of interest can be modelled directly. In this particular case every individual flock considered for importation during a year will be simulated separately. But as a first step input distributions for the model parameters have to be specified.

The type of probability distribution and the required parameters can be defined interactively using the RISKview software. Once the shape of the distribution appears acceptable, the required formula can be pasted directly into the Excel spreadsheet. Figure 8 shows an example of the use of this software for defining the input distribution of within-herd infection prevalence. Table 2 presents the selected distributions for the input parameters. Most of the probability distributions used for this model are triangular distributions. They could be replaced by the BetaPERT distribution which generates a similar shape, but its mean is less dependent on the specified minimum and maximum values (see Figure 18). In the case of a triangular distribution, a single expert suggesting unrealistically high values as input parameters could have a disproportionately strong influence on the shape of the distribution used in the simulation.

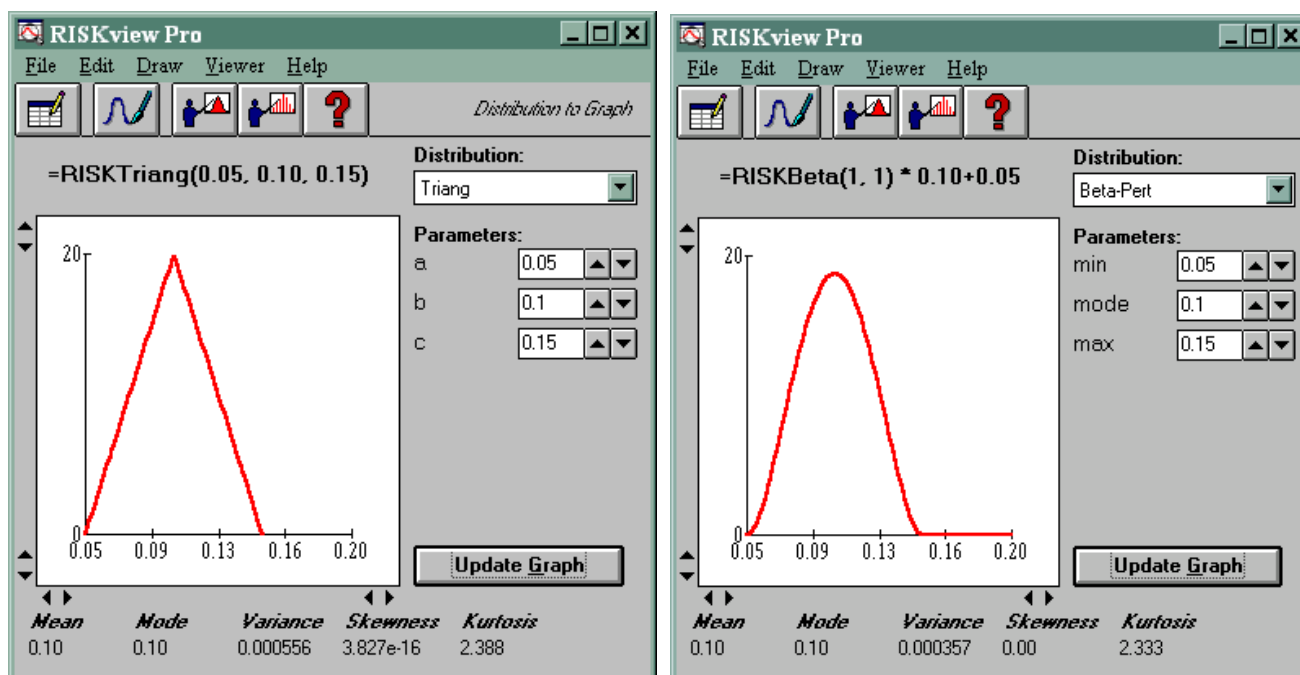


Figure 8: Example of the use of RISKview PRO for defining the input distribution for within-herd infection sero-prevalence (comparing triangular with BetaPERT distribution)

Table 2: Variables and the associated input probability distributions for risk of ND introduction
QRA model

Variable	Type of distribution	Parameters
• Number of herds in source country	Single value	6000
• Prevalence of infected flocks in source country	Triangular	RiskTriang(0.05,0.1,0.15)
• Size of herds	Triangular	RiskTriang(10000,16000,20000)
• Seroprevalence of ND virus infection within infected flocks	Triangular	RiskTriang(0.05,0.1,0.15)
• Number of imported flocks per year	Triangular	RiskTriang(15,20,30)
• Size of imported flock	Triangular	RiskTriang(350,450,500)
• Probability of not detecting infection during quarantine		
• Number of animals sampled on each occasion	Single value	10
• Sensitivity of diagnostic test method	Triangular	RiskTriang(0.7,0.76,0.8)
• Number of samplings	Single value	10
• Probability of transmission in target herd	Triangular	RiskTriang(0.05,0.1,0.3)
• Probability of spread from target herd to other herds	Triangular	RiskTriang(0.05,0.1,0.2)

In the case of the triangular distributions the values in brackets following the function specification RiskTriang represent minimum, most likely and maximum values. For variables which can only take on discrete values, the value generated by the triangular distribution function was converted into an integer using the appropriate Excel function.

Using this input data the stochastic processes influencing individual flocks being considered for importation have to be represented. Each flock will be represented as a separate row in the spreadsheet. The first event of relevance is whether the herd of origin is infected or not. This

depends on the prevalence of infected herds in the source country. It can be modelled by combining an IF clause with a uniform random number distribution function covering a range from 0 to 1. The IF clause compares the generated random number with prevalence and returns a value of 1 if it is less or equal than prevalence, otherwise the value in this cell becomes zero (see Figure 9).

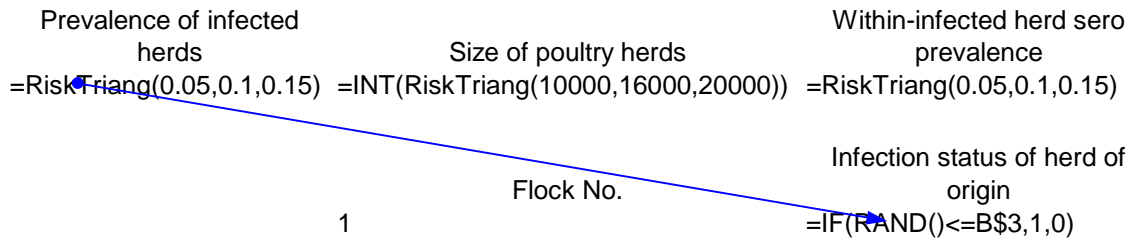


Figure 9: Spreadsheet formulas for simulation of flock infection status

The number of infected animals within the flock considered for importation was estimated using the binomial distribution, but conditional on the herd of origin being infected (using an IF clause, see Figure 10). Then, the hypergeometric distribution was used to generate the number of infected animals in the sample for diagnostic testing. An IF clause was used again, as this calculation was only relevant if the flock did in fact include infected animals (see Figure 11).

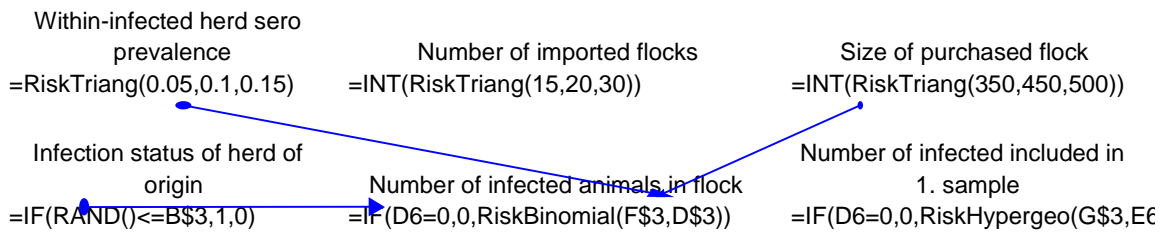


Figure 10 : Calculation of number of infected animals in flock from infected herd coming into quarantine

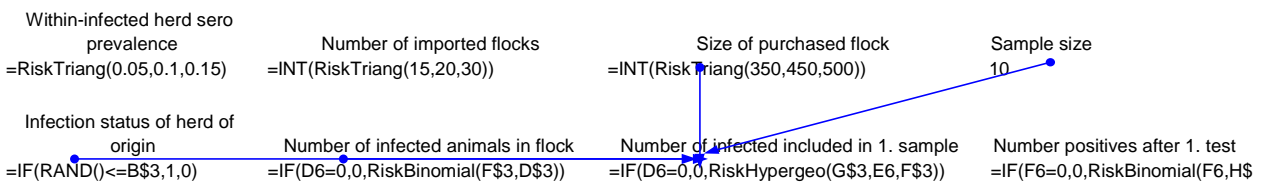


Figure 11 : Calculation of number of infected animals included in first sample for diagnostic testing

The next calculation involves estimation of number of infected animals which will show up positive during the first diagnostic testing. This can be simulated using the known number of infected animals and the test sensitivity as the input parameters for a binomial distribution (see Figure 12). The IF clause is used to exclude flocks without infected animals in the sample for diagnostic testing. Diagnostic infection status of the flock after the first test is assessed on the

basis of combining a nested IF clause with a logical AND statement (see Figure 13). For the second diagnostic test the calculations are similar as discussed above (see Figure 14).

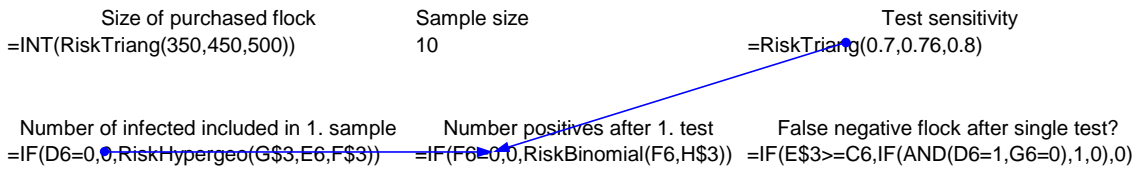


Figure 12: Estimation of number of infected animals detected by diagnostic test

$$\text{False negative flock after single test?} \\ =\text{IF}(\text{E\$3} \geq \text{C6}, \text{IF}(\text{AND}(\text{D6}=1, \text{G6}=0), 1, 0), 0)$$

Figure 13 : Calculation to assess if flock is diagnosed as false negative after first test

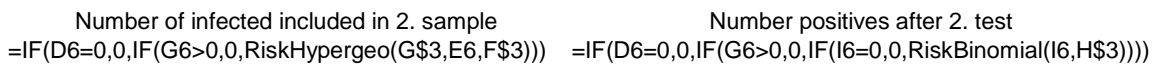


Figure 14 : Calculations for sampling for and result of second diagnostic test

The subsequent interpretation of the combined test results as to the false negative status of the flock is presented in Figure 15 using methods described above.

$$\text{False negative flock after two tests} \\ =\text{IF}(\text{E\$3} \geq \text{C6}, \text{IF}(\text{AND}(\text{D6}=1, \text{G6}=0, \text{I6}=0), 1, 0), 0)$$

Figure 15: Calculations to assess if flock is diagnosed as false-negative based on combined test results

The uniform random number generator in combination with nested IF clauses is used to estimate if an introduced flock will cause an outbreak within the target herd (see Figure 16). Similar calculations were performed to simulate the effect of the introduction on the infection status of herds other than the target herd (Figure 17).

$$\text{Infection of target herd with two tests} \\ =\text{IF}(\text{E\$3} \geq \text{C6}, \text{IF}(\text{K6}=1, \text{IF}(\text{RAND}() \leq \text{J\$3}, 1, 0), 0), 0)$$

Figure 16: Calculation for occurrence of outbreaks in target herd on the basis of introduced infected flocks

Spread of infection to other herds with two tests
 =IF(E\$3>=C6,IF(L6=0,0,IF(RAND()<=K\$3,1,0)),0)

Figure 17: Calculations to estimate the occurrence of outbreaks in herds other than the target herd as a consequence of the importation

The above described calculations were copied into as many spreadsheet rows as there were likely to be flocks considered for importation. The simplifying assumptions made here, is that all flocks during a single iteration will have the same flock size, number of infected animals and test sensitivity. This could be easily changed if considered important, by using the associated distributions directly at the flock level. But there will be varying numbers of infected flocks included in each iterations. The output variable of interest for this model is the total number of false negative flocks, the number of expected outbreaks and secondary outbreaks for single and double diagnostic testing scenarios. To take account of the variation in flock numbers for importation, each of the above output variables was adjusted for this by using an additional IF clause as presented at the beginning of the formulas presented in Figures 12, 15 to 17. The condition is repeated at the beginning of each of these formulas.

Performing simulations

The model has now reached a stage where it can be used for simulations for model verification and validation. It contains 188 input and 6 output distributions. Simulation runs consist of iterations, which basically represents the number of times the computer draws random numbers for the simulation model. For the purpose of this exercise 1000 iterations will be used. In @Risk the number of iterations is controlled in the simulation settings menu. This will take less than a minute with this model on a Pentium 166 Mhz computer with 48MB RAM. If the simulations take too long the number of iterations can be reduced to about 200 to 300. If the analysis of the simulation output takes too long due to a large number of input distributions, it is possible to prevent @Risk from collecting data on all distributions under the *Simulation settings* menu on the *Sampling* tab dialog box. It is also possible to specify particular distributions for which @Risk should collect simulation data, by adding the statement RiskCollect()+ to the beginning of the respective spreadsheet formulas (note that the *Collect distribution samples* option in the *Simulation setup* has be selected)

The software @Risk provides some very useful functions which can be used to analyse and present the simulation model output. This can be done on the basis of numerical or graphical data. The latter provides a particularly effective method for conveying the results to others.

Histograms or relative frequency plots can be used to show the spread and shape of the output data. The graphs are based on dividing the data into a given number of classes and calculating the probability that the output variable can take on a value within a particular category. The number and width of the intervals covered by individual classes has a dramatic influence on the shape of the histogram. The analyst may want to begin with inspecting some of the input distributions to confirm that their spread and shape is as intended (see Figure 18). Figure 19 uses histograms to show the simulation output for the number of false negative flocks imported into the target country over the period of a year. With a single test, 40% of iterations did not have any false negative flocks coming into the target country, whereas the remainder had at least one false negative importation. If two tests were used, about 70% of iterations did not have any false negatives coming through. The cumulative ascending frequency plots presented in Figure 20 allow the reader to very quickly obtain the probability of the outcome variable being less than a particular value. It conveys the same information as a table of percentiles for a particular distribution. The conclusion from both sets of graphs is that the use of two tests does reduce the risk of introducing infected flocks into target herds considerably. Table 3 presents a numerical of the simulation statistics.

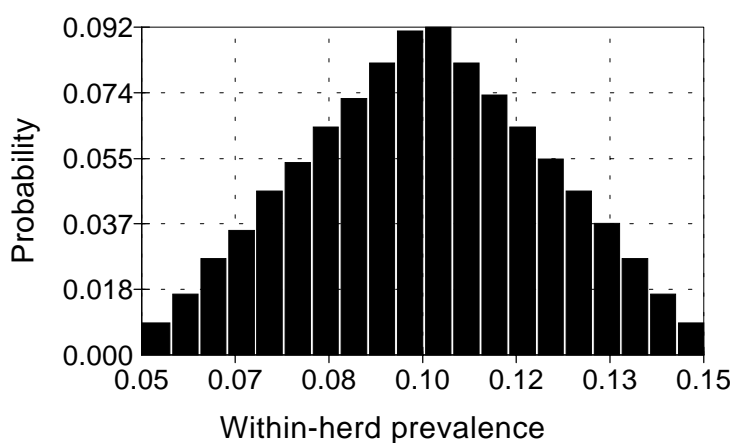


Figure 18: Input distribution for within-herd seroprevalence

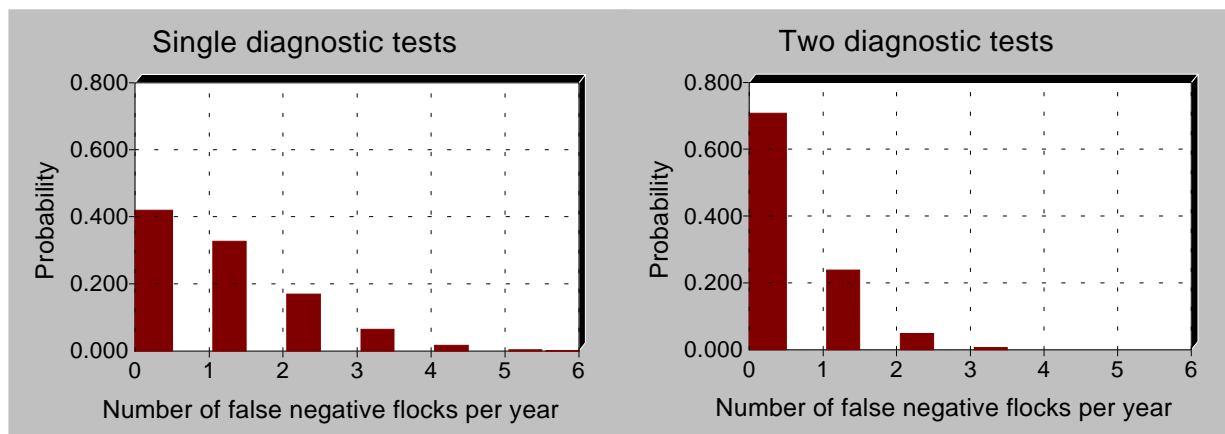


Figure 19: Probability distributions for number of false negative flocks imported into the target country over the period of a year for both diagnostic testing strategies

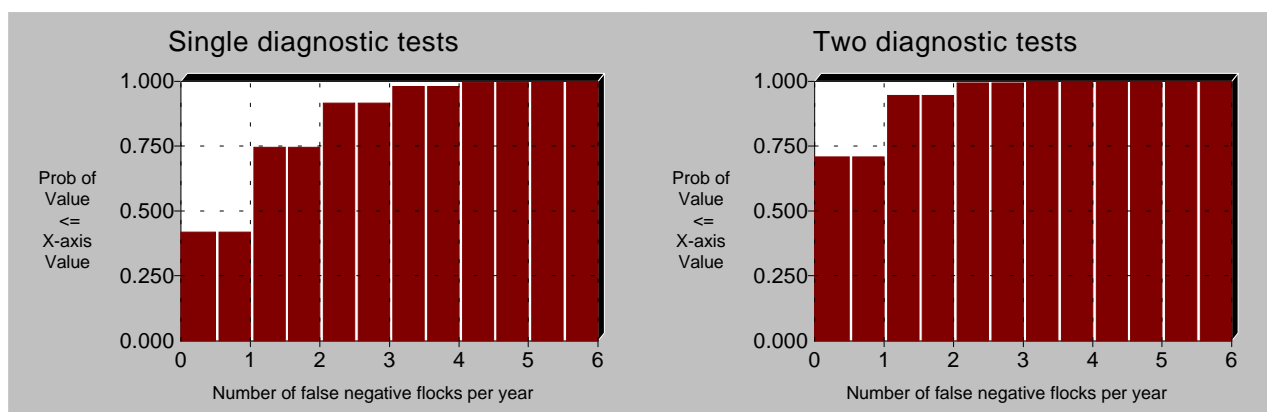


Figure 20: Cumulative ascending probability distributions for number of infected flocks remaining undetected during quarantine over the period of a year for both diagnostic testing strategies

Table 3: Summary statistics for selected input and output distributions

Name	Minimum	Mean	Maximum
Outbreaks with single test	0	0.09	2
Total number of false negative flocks using single test	0	0.97	6
Total number of false negative flocks using two tests	0	0.38	4
Spread with single test	0	0.01	1
Outbreaks with two tests	0	0.05	1
Spread with two tests	0	0.004	1
(Input) Prevalence of infected herds	0.05	0.1	0.15
(Input) Size of poultry herds	10127	15334	19854
(Input) Within-infected herd sero prevalence	0.05	0.10	0.15
(Input) Number of imported flocks	15	22	30
(Input) Size of purchased flock	352	433	497
(Input) Test sensitivity	0.70	0.75	0.79
(Input) Risk of transmission	0.05	0.1	0.15
(Input) Risk of spread	0.05	0.12	0.19

A comparison between output variables can be performed by showing them side-by-side or by generating three-dimensional histograms such as presented in Figure 21. This particular graph illustrates the fact that due to with-herd risk of transmission being set relatively low the risk of transmission from infected imported flocks to the target herd is rather low. These types of graphs cannot be generated in @Risk, but can be easily produced by transferring the simulation output data to a spreadsheet or statistical analysis software. The risk of the occurrence of at least one of the different types of events is summarised in Figure 22. This particular graph provides a quick overview of the main results from this simulation run.

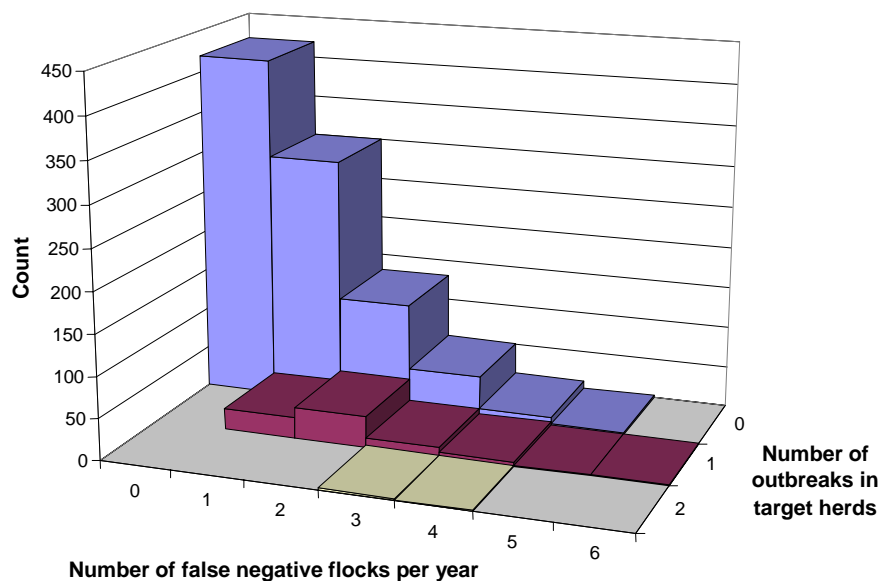


Figure 21: Three-dimensional histogram of the relationship between simulation output distributions of number of false negative flocks imported per year and number of outbreaks in target herds

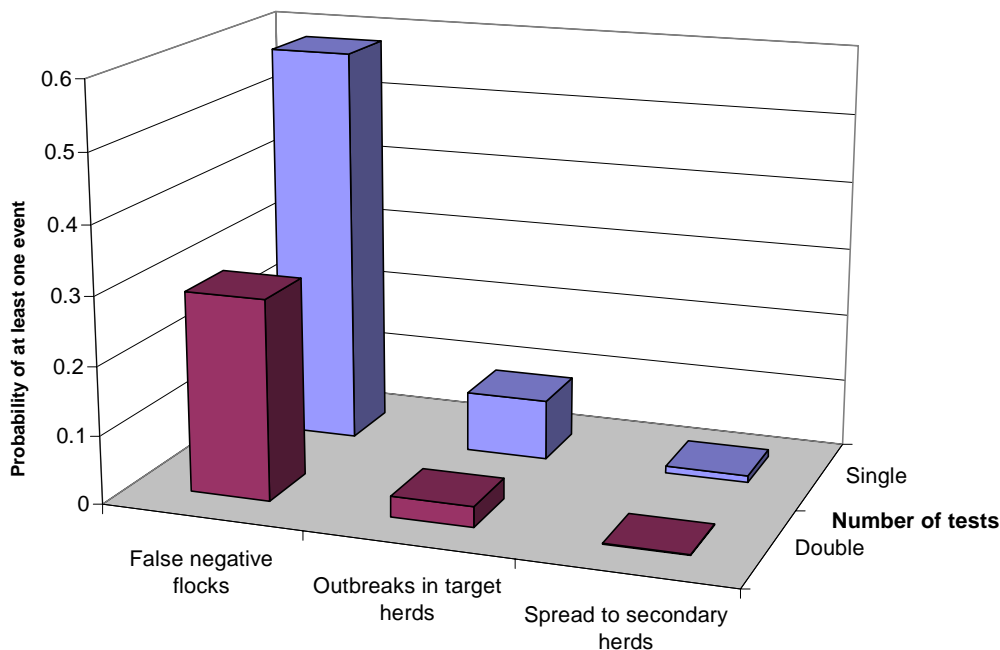


Figure 22: Three-dimensional histogram for the probability of occurrence of the each of three types of outcome events and testing strategies

Once the first simulations have been conducted, and it appears that the model output is sensible, more detailed investigations into the relationships between different input parameter settings should be conducted. This particular step is also called sensitivity analysis and can be seen as a component of the model verification / validation as well as of the application / analysis phase. The basic principle of sensitivity analysis is to vary any input parameters, or in the case of a stochastic simulation model input distributions. With the ND QRA model, it may be useful to assess the sensitivity of model output to changing the prevalence within infected herds, or more importantly to vary for example transmission probability within target herds. The @Risk software performs sensitivity analyses by testing the statistical relationship between different input distributions and a particular output distribution through assessment of their correlation. The results can be presented as a Tornado chart which presents the relationship between an output variables uncertainty and the uncertainty in any input variables. The length of the bar representing a particular input distribution indicates the strength of the relationship. Figure 23 shows a Tornado graph for the outcome variable number of false negative flocks imported into the target country. The strongest positive correlation exists with the prevalence of infected herds, followed by the number of imported flocks. A negative correlation exists between number of infected flocks remaining undetected during quarantine and within-herd prevalence. The latter reflects the increased probability of detecting infection within the flock during quarantine if prevalence in the

herd is higher. The sensitivity analysis will suggest the variables which need more accurate estimates as the ones which do have a strong influence on the outcome variable. On the other hand parameters which do have a negligible influence could be considered for removal from the model. The analyst should strive to keep the model structure as simple as possible and therefore avoid or remove any variables which only contribute unnecessary complexity.

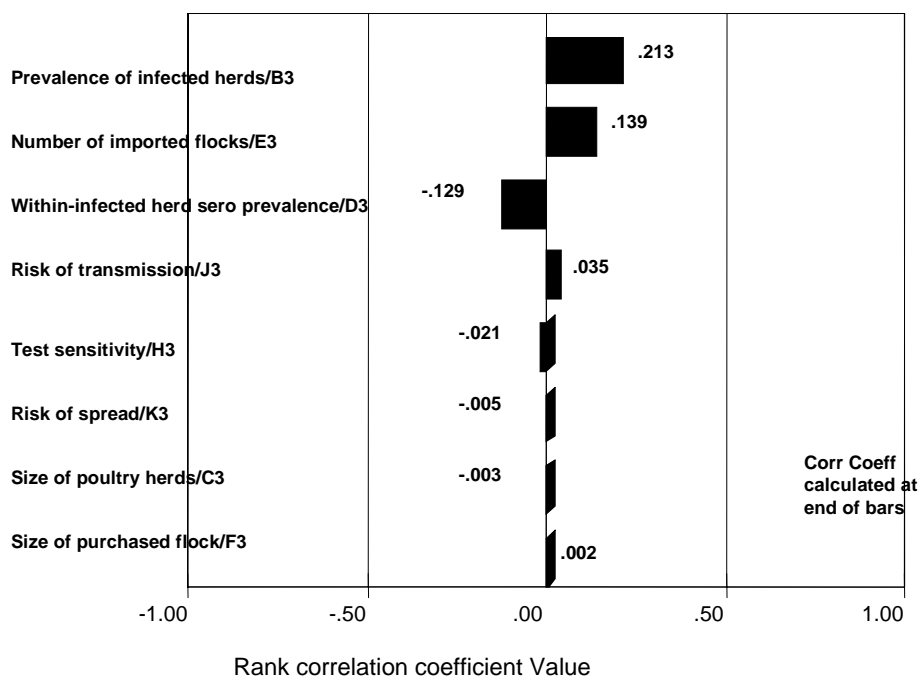


Figure 23: Tornado graph displaying Spearman rank correlation coefficients of relationship between number of false negative flock importations and various input probability distributions

The analyst may now want to refine the model by taking account of the dependency between the risk of outbreaks within target herds and the prevalence of infection in the false-negative imported flocks. This could be done by using variable arguments when defining the distribution functions or through use of a specific @Risk function which introduces a defined correlation between two sampling distributions (see @Risk documentation for examples). The analyst may also decide that is required to model the processes leading to a flock or herd being infected should be modelled at more detail.

Specific comparisons between strategies can be conducted using standard epidemiological analysis techniques. The relationships could be quantified using measures of strength (odds ratio) and measures of potential impact (attributable risk and fraction). In the case of the ND model, the public domain software WinEpiscope 1.0 (de Blas,I., Ortega,C., Frankena,K. and Noordhuizen,J. 1996;) was used for these calculations after the simulation output was summarised into a tabular

format using the Pivot table function in Microsoft Excel. Figure 24 presents the results screen after running the analysis for the ND output data. The results indicate that with a single test strategy the risk importing infected flocks is almost twice as high as in the case of a double testing strategy. The confidence limits for the relative risk do not include unity, indicating that it is different from unity at the 95% confidence level. In terms of the impact of not using a second test the attributable risk suggests that this represents an increase in risk of 0.3. This figure is particularly important as it can be used for quantifying the potential economic effects of a change in strategy. The attributable proportion indicates that 50% of the infected flocks being imported can be attributed to not having been tested twice.

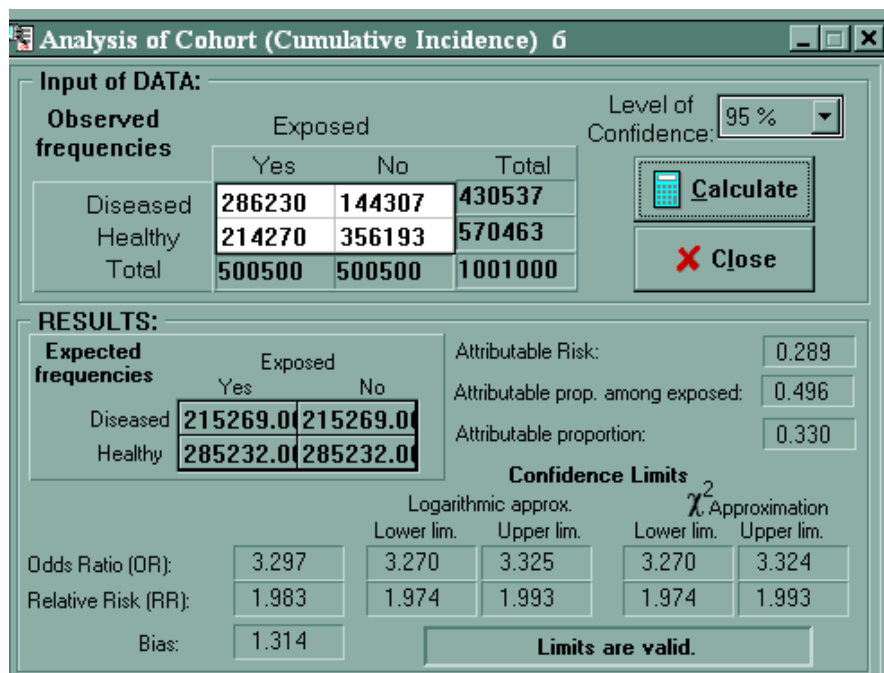


Figure 24: Comparison of risk of false negative flocks between single and two diagnostic test strategies using WinEpiscope software

The Report

At the end of the analysis should be a report and / or presentation to the decision makers or stakeholders. As mentioned above without the target group accepting the model used, they are unlikely to make use of the conclusions produced from this risk analysis. The report should make use of graphical presentation where possible. Vose (1996) writes that the main objective of the report will be to answer the questions that the analyst had intended to answer. He continues that often reports rely too much on statistical data, the key questions are not answered, graphs and tables present data with too many decimal places, too many meaningless graphs and statistics are included. Vose emphasises that the assumptions behind the model have to be presented to the reader.

Final words

Methods for stochastic modelling in risk management and risk characterisation have become very popular of the last few years. This is mainly attributed to the availability of fast computer hardware and simulation tools such as @Risk. These methods are likely to better accommodate the inherent uncertainty associated with most of the processes to be modelled. Particularly with deterministic models the decision makers, risk managers or stakeholders will very easily forget that many of the underlying parameter values were in fact unknown and estimates had to be used during the modelling process. The analyst should always remember that qualitative information can be very valuable. The Presidential-Congressional commission on risk assessment and risk management suggested in its report (Anon 1997b) that measures of uncertainty should be used very cautiously when communicating risks to risk managers and stakeholders. Very often this information is being misunderstood. Often target groups unfamiliar with distributions will interpret them as implying that all the values in the range may be equally plausible. The commission also writes in the report that when confronted with a range of possible outcomes decision makers tend to focus on a particular portion of the range, thereby ignoring the shape of the distribution as such.

On the other hand, a quantitative risk analysis could have possibly prevented the explosion of the space shuttle *Challenger*. Dalal *et al* (1989) estimated a median risk of 0.14 (90% CI 0.02-0.37) for the occurrence of an explosion given an outside air temperature of about 0°C. The authors used a logistic regression model to come up with this prediction. In this case, an analysis of the sensitivity of the risk of damage to O-ring seals to outside temperature would have indicated that changes had to be made. Both graphs presented in Figure 25 are based on the same data, which is the number of O-ring failures over a range of temperatures. The qualitative approach which lead to the graph on the right was used to assess risks, but failed to show the increasing uncertainty associated with decreased temperature. The graph on the left, which is based on the predictions produced by a logistic regression model very clearly, shows the increase in uncertainty when temperatures reach below 60°F. If this rather simple quantitative model would have been available at the time, more experiments into the behaviour of the O-rings under low temperature conditions would have been conducted and thereby the explosion could have been prevented.

It is not very difficult to develop quantitative models. It is much more challenging to develop a working communication link between analysts, risk managers and stakeholders.

Without effective risk communication quantitative models will remain ignored and be seen as purely theoretical constructs without a relationship to reality.

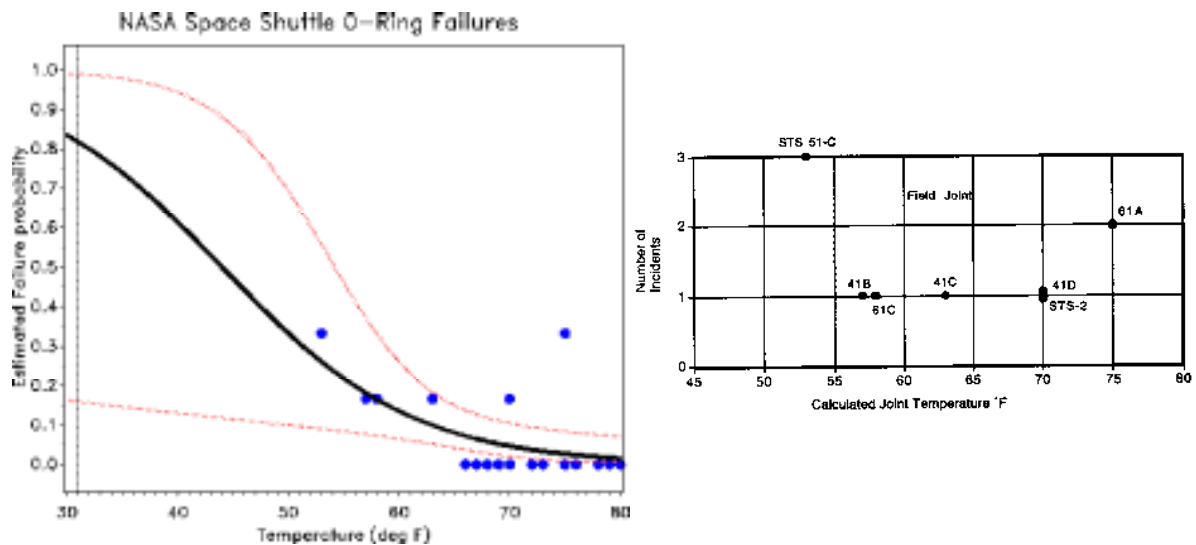


Figure 25: Appropriate and inappropriate methods for risk characterisation: Probabilistic prediction on the basis of a logistic regression model (image on left) and a tabulation of events over a limited range of different temperatures (image on right)

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