marlon

monitoring the safety of animal feed

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The use of Syndromic Surveillance in Monitoring of feed-related Risks

Part 2 – Model Construction and Framework

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The MARLON Project

Monitoring of Animals for Feed-related Risks in the Long Term

The Marlon project aims to create an inventory of which epidemiological and monitoring initiatives exist, both inside and outside the EU, providing useful data for to monitor the health impacts of animal feeds, in particular those containing GM ingredients, on livestock animals. It will also collate, in a systematized manner, information on the factors that have to be considered when developing an epidemiological model specifically geared towards this purpose.

Model Construction & Framework

Step 1

- Put data from expert opinion or survey generation in the Inputs page;
- The syndromes have multiple clinical signs and diseases, which can be edited as required.

Reproductive

Consider the different proportions of Baseline Cases on the farms which you frequently visit - What proportion of cows calving in the last 12 months would normally experience the following?: (minimum = the lowest estimate on the farm with the least 'normal' baseline cases, and maximum = the highest estimate on the farm with the largest frequency of baseline cases.)

Type of Dairy	Risk Strata	Question	Min	Most Likely	Max	Confidence (1-5)
Cows	Mild	Premature Calving (Calves born live under 270 days post AI/Bulling)	2	3	5	4
		Endo-metritis	2	7.5	15	4
		Retained Placentae	2	4	10	4
		Overlong Calving Interval (365d +)	2	5	10	4
		Returns after first AI.	30	40	60	4
	Severe	Non-Septic Abortion	0	1	3	4
		Septic Abortion	0	1	3	4
		Foetal Malformations	0	0.25	0.5	4
		Stillbirths	0	1	2	4

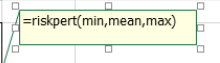
Model Construction & Framework

Step 2

- Use the Pert Distribution in @Risk to generate a value for the opinion sampled from the distribution
- Data given by Experts was provided in Percentage form, so this step also includes a conversion to a probability.
- If your data is in the form of a probability you will need to adjust this.

Reproductive

Type of Dairy	Risk Strata	Question	Q1	Q2	Q3	Q4	Q5
Cows	Mild	Premature Calving (Calves born live under 270 days post AI/Bulling)	0.0342	0.0645449	0.53361	0.52903607	0.114965965
		Endo-metritis	0.0745	0.1125879	0.47504	0.2520054	0.030790842
		Retained Placentae	0.0364	0.092052	0.6042	0.24268024	0.089639915
		Overlong Calving Interval (365d +)	0.0419	0.1422161	0.40306	0.02422751	0.027326724
		Returns after first AI.	0.3824	0.6130736	0.49653	0.93427266	0.280584305
	Severe	Non-Septic Abortion	0.0093	0.0205027	0.53829	0.71573096	0.546667069
		Septic Abortion	0.0086	0.0202607	0.81655	0.78648083	0.471253567
		Foetal Malformations	0.0025	0.0027093	0.28831	0.21280013	0.394072798
		Stillbirths	0.0151	0.0201744	0.22656	0.08254706	0.235171546



Model Construction & Framework

Step 3

- Duplicate the population considered to represent both an affected group and a ‘baseline’ group.

Step 4

- Integrate the Effect of the GM (or other feed) into the model. This is simulated as a change in prevalence of the syndrome of interest multiplied by the proportion of farms exposed to the GM feed. For the purposes of the model, there is an assumption that either farms are fed GM feed or not as such - this is considered as a binary variable. If data for feed consumption becomes available later, this could be incorporated at this step
- This is replicated for the comparison group with an alternative exposure of farms to GM feed;
- This is because is it nearly impossible to evaluate farms which are GM (or any other feedstuff free) so a comparison between the two populations with the same level of risk is required.

Model Construction & Framework

Step 5

- Calculate the Probability of an animal producing a positive detection for each clinical sign, or condition for both ‘baseline’ and ‘exposed’ groups.
- This is simply expressed as:
  - **Endemic conditions / clinical signs:**
    - P(1) = P(clinical signs) x P(farmer detection) x P(Veterinary consultation) x P(Samples taken) x P(disease confirmed)
  - **Emerging or Unknown Conditions**:.
    - P(1a) = [P(clinical signs) x P(farmer detection) x P(Veterinary consultation) x P(Samples taken) x P(disease not confirmed)] +[p(clinical signs) x P(farmer detection) x P(Veterinary Consultation)]

Model Construction & Framework

Step 6

- Sensitivity of detection for the farm for each condition for both baseline and exposed groups.

  - **Sens = P(1/1a)*Proportion of animals on the farm.**

- This is particularly important for groups of animals with different risk strata.
- It gives the probability that one animal on the farm will be detected as abnormal.
- Data input is at farm level all the way through so there is no conversion from animal to farm level as this is not applicable here.

Model Construction & Framework

Step 7

- Component (Syndromic) sensitivity of detection.
  - **P(Syndrome) = 1- [1 – P(condition)]* 1 – P(condition)]….**

Step 8

- Combine all component output values into one sheet for further analysis for both the base line and exposed groups.

Model Construction & Framework

Step 9

- Simulate the number of farms detected in the country of interest using @risk function *riskbinomial*.
  - This gives the number of farms which would be able to detect a change away from the baseline should it occur.

		Baseline		Exposed					
Proportion of Exposed Farms.		0		1					
		Component Probabilities.				Number of farms Identifyed with the syndrome of interest.			
		Baseline		Exposed		Baseline		Exposed	
		Endemic	Unknown	Endemic	Unknown	Endemic	Unknown	Endemic	Unknown
Reproductive	Mild	0.000126942	0.011169608	0.000152294	0.013391505	4	239	2	268
	Severe	0.026277634	0.002154624	0.014355897	0.142719744	563	43	266	2832
Eyes, Ears and Integument	Mild	0.013980835	0.060154064	0.016772799	0.103675608	244	1178	354	2041
	Severe	3.33759E-08	0.000157995	4.00418E-08	0.000832109	0	7	0	15
Musculo-Skeletal System	Mild	0.012399893	0.009289616	0.014876084	0.011129464	266	194	299	227
	Severe	0.000215809	0.055467053	0.000258911	0.059881185	1	1113	6	1181

Farms Simulated for the population of interest using
= riskbinomial (Pdetection, number of farms in the country).

Model Construction & Framework

Step 10

- Calculate the probability that there will be a difference in the levels of detection between the exposed and the baseline.
  - This is achieved by asking Excel to count 1 for every time there is a greater than 5% increase in the number of farms detected.
  - (The 5% threshold can easily be changed, this is the 'confidence' which is at the top of the page.

➢ **= IF (PExposed>=PBaseline+PBaseline*(1-Confidence)),1,0)**

Step 11

- Simulate the probability of detection over multiple iterations.
  - This is achieved in @risk simply by using the riskmean function, i.e. the total number of 1's and 0's added together divided by the number of iterations.

Model Construction & Framework

Step 12 (1)

- Use the RiskSimtable function to run the simulation multiple times for varying levels of the change in prevalence. These formulae are in the cell at the top of the page which is called “Change in prevalence due to Feed related Risk”

		Baseline		Exposed					
Proportion of Exposed Farms.		0		1					
		Component Probabilities.				Number of farms Identifyed with the syndrome of interest.			
		Baseline		Exposed		Baseline		Exposed	
		Endemic	Unknown	Endemic	Unknown	Endemic	Unknown	Endemic	Unknown
Reproductive	Mild	0.000126942	0.011169608	0.000152294	0.013391505	4	239	2	268
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Farms Simulated for the population of interest using
= riskbinomial (Pdetection, number of farms in the country).

Model Construction & Framework

Step 12 (2)

- @risk will run the simulation a number of times (you need to tell it how many). The numbers on the top are the number of simulations, in this case 9. Each simulation will be run with a different level of risk associated with the feed. In this example, it varies from 0% to 20% effect on clinical signs.

  - **= Risksimtable (Range of cells for the value to be varied amongst).**

- This simulates the magnitude of change, which would need to be caused by a feed related risk, and how this risk affects the detectable difference

Model Construction & Framework

Step 13

- Ask @risk to save the mean values for the probability of the farms being reported for each of the difference levels of risk.

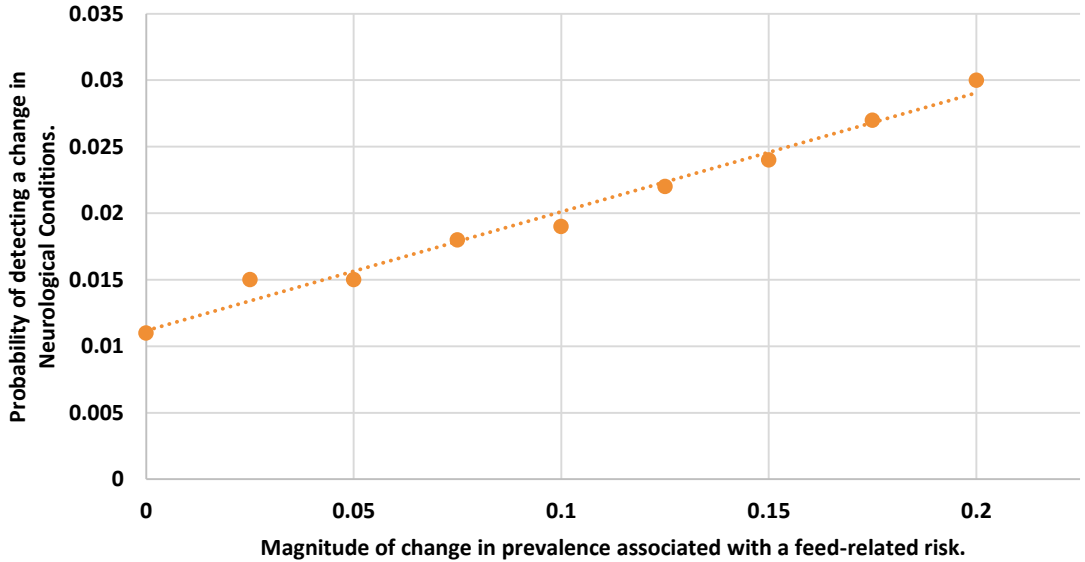
➢ **= riskmean (variable of interest, number of simulation)**

Step 14

- Plot the magnitude of change against the probability of detection to show at which level of change the current surveillance system would be able to detect a change in endemic or unknown conditions.

Model Construction & Framework

Representation of the change in the probability of detection in risk associated with feed with 95% confidence using data from the UK passive surveillance system.



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