Appendix S1: Pseudo-code for livestock as sentinels for wildlife disease

I. Set the distribution parameters from which to draw random variates of model parameters for each iteration of the model

   A. Number of iterations (*iter*)

   B. Sampling period (e.g. annual from 2000 – 2014)

      1. Calculate number of periods (*nPeriods*)

   C. Beta parameters (*a, b*) for the prior of the probability of no disease in wildlife (eq. 9 and 10)

   D. Beta parameters (*c, d*) for the annual probability of new incursion into the area

   E. Spatial resolution of grid cell system for analysis (*resol*; e.g. 100 m)

   F. The design prevalence (P^*; eq. 6 and 8)

   G. The rate of increase of the design prevalence

   H. Mean and variance parameters for σ^2 (μ, ε^2; eq. 2)

   I. Beta parameters (*e, f*) for the disease diagnostic tests

   J. Beta parameters (*g, h*) for the I_{max} parameter (eq. 1 and 2)

II. Import the data

   A. Spatial data delimiting the area over which disease eradication will be declared (e.g. shapefile or raster)

      1. Mask out un-suitable habitat that will not contain homerange centers of possums

   B. Herd surveillance data (e.g. *.csv file)

   C. Spatial data on farm boundaries for all farms (e.g. shapefile or raster)

      1. Mask out areas where livestock cannot move (e.g. fenced off areas or very dense vegetation)

   D. Spatial data on the relative risk of disease infection (e.g. raster; eq. 8)

III. Pre-process the spatial data

   A. Loop through each farm

      1. For each farm, create an empty raster the size of the full extent

2. Loop through grid cells

a) Identify grid cells within and adjacent to the farm where possums could live but livestock cannot access

b) Apply the distance decay function $exp\left(-\frac{d_{jk}^2}{2\sigma^2}\right)$ for each grid cell (eq. 2)

c) Populate the farm-specific raster with the results of distance decay function

B. Make a design prevalence array

1. Make an empty array with the length of the number of sampling periods (e.g. number of years)

2. Populate the first position with the design prevalence (I.F. above)

3. Subsequent entries are a function of the rate of increase (I.G. above)

C. Calculate the *EPIAve* for year sampling period (eq. 7)

1. Use the relative risk map (II.D. above; eq. 8)

2. Use the herd testing data (II.B. above) to identify grid cells that will be searched

IV. Process the data

A. Loop through the iterations (I.A. above)

1. Make an empty raster of dimensions of the full extent in which to store the SeU_j values.

2. Draw random variates for all model parameters from distributions specified in I. (except *iter, resol,* P^*, and rate of increase of P^*, which are constant for all iterations).

3. Loop through the *nPeriods* (I.B.)

a) Loop through the grid cells in (all columns and rows)

(1) If a grid cell is in the extent of interest, loop through all farms, and calculate the SeU_{jk} (eq. 1-4)

(2) Calculate SeU_j (eq. 5)

b) Calculate the *SeUAve* and *SSe* (eq. 6 or 7)

(1) Record the *SSe* in a 2-dimensional storage array [*iter, nPeriods*]

c) Calculate the $P(free|S^-)_t$ (eq. 10 or 11)

(1) Record the $P(free|S^{-})_t$ in a 2-dimensional storage array [*iter, nPeriods*]

B. Make table of results

1. Calculate the mean and 95% CI of SSe for each sampling period

2. Calculate the mean and 95% CI of $P(free|S^{-})_t$ for each sampling period