

DISEASE MANAGEMENT BENEFITS FROM CLUSTERED POSITIONS OF FARMS

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ABSTRACT

With respect to the distance dependent livestock disease spread the distance between locations of farms determines the probability of infection. If farms are clustered, certain farms may serve as stepping stones between clusters of farms. These foothold farms facilitate a global spread of a disease. Foothold farms are risk farms. If surveillance were targeted to these risk farms, a global spread could be avoided at low costs by their exclusion from the epidemic cycle. The implementation of an algorithm for identification of foothold farms is the objective of this work.

MOTIVATION & TASK

- Distances between farm locations are proportional to the probability of distance dependent infection.
- Some farms a stepping stones (footholds) for the disease to spread. These farms are risk farms.
- If risk farms are identified and protected from infection, a mayor outbreak can be avoided at low costs.

Task

The identification of foothold farms.

METHODS

- Measure of connectivity (Keitt et.al., 1997)
- Infection pathways connect farms

$$C = \frac{\sum_{j=1}^K n_j R_j}{\sum_{j=1}^K (n_j)} \quad R_j = \frac{1}{n_j} \sum_{i=1}^{n_j} [(x_i - \bar{x})^2 + (y_i - \bar{y})^2]^{1/2}$$

j : disease cluster $j = \dots K$

R_j : radius of gyration for cluster j

n_j : number of farms in cluster j

x_i, y_i : location of farm i in cluster j

\bar{x}, \bar{y} : cluster center (mean of x, y locations)

- Work bench (Simulation experiment)
- Random generation of farm locations (Diggle et.al., 1976)
- Implementation of a spatio-temporal stochastic SiR model with distance dependent infection
- Calculation of C
- Exclusion of single farms from the infection cycle and calculation of the probability of an avoidance of a major outbreak.

$$\text{logit}(\Pr(Mo = 0)) = \alpha + \beta_i x_i \quad i = 1 \dots N$$

$$Mo = \begin{cases} 1 & \text{if } C > C^* \\ 0 & \text{if } C \leq C^* \end{cases}$$

α = setoff

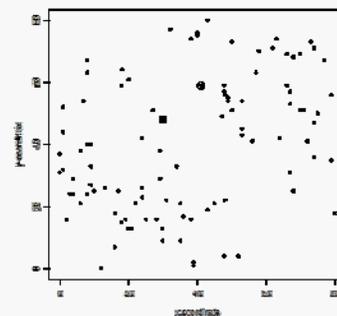
β_i = parameter estimate

x_i = farm removed

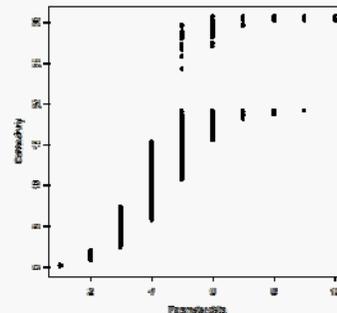
Calculation of $ORI = \exp(\beta_i)$ and 95% CL
(Corner point estimation used with SAS Proc GenMod)

RESULTS

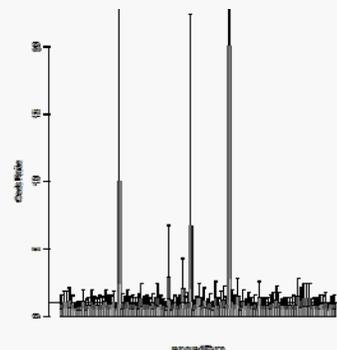
a) Positions of farm clusters and identified foothold farms



a) Dependency of (c) on the infectivity of the disease



a) Odds ratios of farms protected from infection



SUMMARY AND DISCUSSION

The algorithm presented in this study is capable of identifying foothold farms facilitating a global spread of a livestock disease. If these farms were excluded from the epidemic cycle, a far reaching spread of the disease agent could be significantly avoided. For now, only distance dependent spread is considered. This restriction can be lifted if heavy tail distributions were used as a model for the spatial spread of a disease (Jansen et.al., 1999)

References:

- P.J. Diggle, J. Besag and Gleaves J.T. Statistical analysis of spatial point patterns by means of distance methods. *Biometrics*, 32:659-667, 1976
H.K. Janssen, K. Oerding, F. van Wijland and H.J. Hillhorst. Levy-flight spreading of epidemic processes leading to percolating clusters. *The European Physical Journal B*, 7:137-145, 1999.
T.H. Keitt, D.L. Urban and B.T. Milne. Detecting critical scales in fragmented landscapes. *Conservation Ecology*, 1(1):4, 1997