

Modelling Transmission of Scrapie in Cellular Automata

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1. Introduction

- Transmission of scrapie between flocks is by sheep movements.
- Cellular automata (CA) are often used for modelling similar spatial dynamics in ecology.
- CA are relatively rare in veterinary epidemiology. Perhaps because they considered abstract.
- Here a cartogram transformation links a CA model to the actual distribution of sheep farms in the UK.

Figure 1:
Simulation example and actual scrapie notifications 2000 on cartogram of Great Britain.

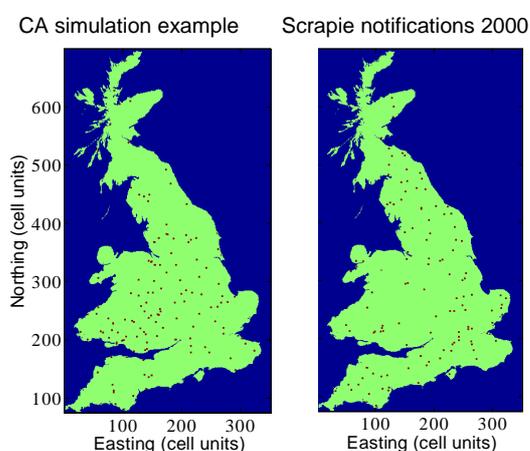
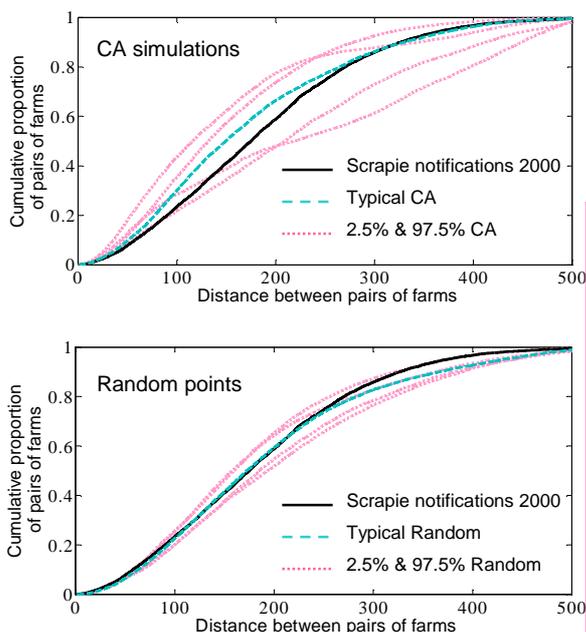


Figure 2:
Cumulative distribution function for distances between all pairs of scrapie notifications 2000 vs. 1000 replicates of CA simulation and of 132 random points.



2. Objectives

- Develop a CA based on observed sheep movements.
- Compare it with recorded scrapie cases.
- Question here: **Could an outbreak (Woolhouse et al. 2001; Bradley 2001) generate the scrapie distribution we observe in Great Britain?**

3. Methods

- Movement data = fallen stock records 2002-2005: collection = death holding, ear tag = birth holding.
- >85% sheep died at birth holding, but c. 1200 distinct movements from c. 1000 birth holdings.
- A cartogram transformation of Great Britain, using CartogramCreator in ArcGIS™ 9.1 (www.esri.com) (Wolf 2005), generated a grid with c. 80,000 land cells, each representing 1 sheep farm based on the 2004 agricultural census.
- Distances (cell diameters (c.u.)) from birth to death holdings were measured after mapping to the grid.
- Cellular automata (CA) ran in Matlab 7.1 (www.mathworks.com) and parameterized from movement data. Risk factors were treated as uniform.
- CA started at a random farm and was scaled to generate one new infected farm / infected farm / time step. A farm remained infected with probability 0.8.
- CA stopped when >300 farms infected. 132 farms randomly selected (underreporting) for comparison with 132 farms with notified scrapie cases in 2000.

4. Results

- Simulated scrapie distribution widespread and sparse with local clusters, like observed cases (Figure 1).
- Distribution of distances between simulated scrapie cases mostly consistent with notifications (Figure 2).
- Distribution of distances between notified cases also like random points (Figure 2).
- The empirical cumulative distribution function at short distances indicates that local clustering of notified cases is less than expected from CA simulation and greater than from random points (Figure 2).

5. Conclusions

- Cartogram transformation facilitates comparison of CA simulation with observations and analysis.
- The widespread, sparse distribution of scrapie does not contradict the outbreak hypothesis.
- However, the distribution is also consistent with random spacing (representing endemic disease).
- Initial analysis suggests that local clustering of scrapie cases is present, but low relative to that expected from sheep movements.

References:

- Bradley, R. 2001, Will scrapie in sheep in Great Britain disappear? Trends in Microbiology 9, 260-261.
 Wolf, EB. 2005. Creating contiguous cartograms in ArcGIS 9. In: 25th Ann. ESRI Int. Users Conf., 25-29 July 2005.
 Woolhouse, MEJ., Coen, P, Matthews, L, et al., 2001, A centuries-long epidemic of scrapie in British sheep? Trends Microbiol. 9, 67-70.