

The role of contact structure on disease spread between flocks

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Summary

The 2001 UK Foot and Mouth epidemic highlighted the role of movements in the spread of infectious diseases between farms. However, information on contact between farms via both sales and shows is sparse. To progress mathematical models for the between flock dynamics of infectious disease we therefore need to improve our understanding of the way in which flocks mix. In this paper we present a sub-set of data recording the attendance by breeders of pedigree sheep at agricultural shows. Preliminary analyses suggest that over half of all individuals attending shows enter at least two shows and that the majority of shows are indirectly connected via common entrants.

Introduction

The development of mathematical models to describe the dynamics of infectious diseases in farm animal populations provide a tool with which to test hypotheses on the routes of disease transmission and to compare the spread of infection with and without a variety of control strategies. The level of complexity incorporated into a model depends in part on the purpose for which the model is developed, the mechanisms for disease transmission and whether specific or generic conclusions are required. There is a fine balance between maintaining model tractability and ensuring all major influencing factors are represented in a model. Models that attempt to mimic the real world often suffer from a lack of information on parameter values, are computationally expensive and difficult to validate.

A major simplifying assumption used in many mathematical models for disease spread is that individuals within the population mix homogeneously thus all susceptible animals have an equal chance of becoming infected. This approximation is reasonable for within flock dynamics. However, there are clear problems with this assumption when considering the spread of disease between flocks. The standard mean-field model ignores a number of important properties of disease transmission between flocks, in particular, the finite number of contacts each farm has; the variation in number of contacts per farm; and the clustering of groups of farms due in part to spatial location of the farm and to the species and breed farmed. These factors affect the rate that a disease can spread between farms, the maximum epidemic size and the spatial distribution of disease (Read & Keeling, 2003).

Recently a number of pair-wise models have been proposed which bridge the gap between full simulation models and mean-field models (Eames & Keeling, 2002; Keeling, 1999). These models incorporate pairs of connected nodes as variables rather than treating each node independently and as a result give a much closer match to predictions on disease spread derived from simulations based on full network structure than mean-field models. Thus by collating information on true network structure we

can improve our estimates of disease spread whilst maintaining a relatively parsimonious approach.

The overall aim of our project is to develop a generic model for the structure of the British sheep population based on available data. Here we consider the relation “co-occurrence at show X” focussing on the structure of the network for one breed of pedigree sheep.

Materials and Methods

A questionnaire consisting of ten short answer questions was sent out in November 2000 to all show society secretaries listed in The Showman’s Directory (Lance and Lance, 1999) and in the Farmers Guardian Year Book and Desk Diary (Anon, 2000) (Webb & Sauter-Louis, 2002). In addition, respondents were asked to provide a copy of the show schedule. For each breed category, within each show, the entrants surnames, initials, addresses and postcodes were extracted from the show booklets and recorded in a database.

Results

Of the 141 respondents who answered “YES” to “Are sheep shown/ present at the show”, 110 provided show booklets or schedules, of these 70 detailed names and addresses of entrants and a further 12 contained only the names of entrants. The majority of shows divide competition classes by breed with rare breeds frequently grouped together in one category. Results are presented below for one breed of sheep.

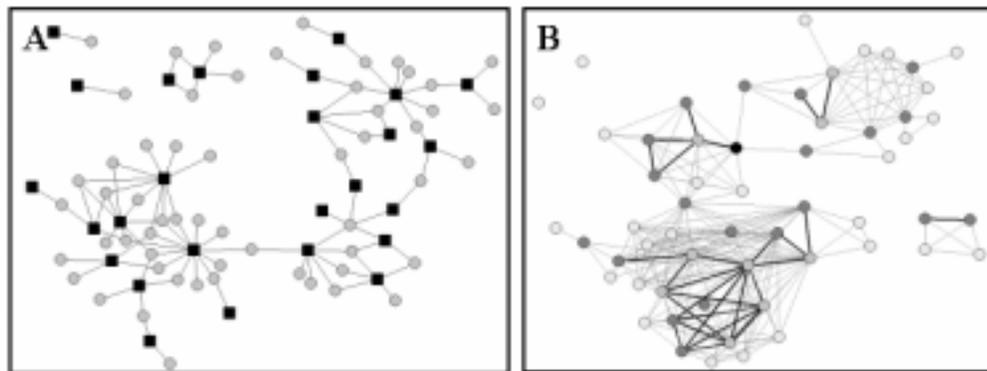


Figure 1: A: Graph of the two-mode network between breeders (circles) and shows (squares); B: Graph of the co-occurrence matrix for breeders. A line between two breeders indicates that they attended at least one common show. Thicker lines indicate that two breeders attended at least two common shows. Breeders are shaded according to the number of shows that they attended from light grey (one show) through to black (five shows).

For the breed considered, details of 26 shows were obtained. Just over half the entrants competed at two or more shows. The maximum number of shows attended by an individual competitor was five. The maximum number of competitors per show, for this breed, was 13 (Fig 1A). Twenty-two of the shows were linked into one large connected component via one or more common competitors (Fig 1A). The co-occurrence network for competitors at shows highlights the role of two of the competitors who act as bridges between three highly connected sub-components

within the largest connected component (Fig 1B). The first of these individuals attended five shows out of those recorded in the database however the second only attends two shows (Fig1A, Fig 1B).

Discussion

There are a number of different approaches to collating data on contacts between farms. In this study we used an indirect approach relying on information on who attended shows. This enabled us to consider a much larger population than would be feasible by questioning farmers individually. However, missing show booklets mean that it is possible that there are more individuals who compete at multiple shows and a higher proportion of breeders taking part in shows.

Previously we have developed a model for the contact structure of the relation “co-occurrence at show X” whereby the probability of attending a given show was based on geographical distance from shows (Webb& Sauter-Louis, 2002). The proportion of competitors attending two or more shows was much lower than obtained here. This suggests that a generic model for the network structure of the relation “co-occurrence at show X” needs to incorporate bias towards attendance at shows for certain breeders. Future work on the attendance at show relation will focus on methods to model this bias

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