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# Using social network analysis to inform disease control interventions

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ABSTRACT

Contact patterns between individuals are an important determinant for the spread of infectious diseases in populations. Social network analysis (SNA) describes contact patterns and thus indicates how infectious pathogens may be transmitted. Here we explore network characteristics that may inform the development of disease control programes.

This study applies SNA methods to describe a livestock movement network of 180 farms in New Zealand from 2006 to 2010. We found that the number of contacts was overall consistent from year to year, while the choice of trading partners tended to vary. This livestock movement network illustrated how a small number of farms central to the network could play a potentially dominant role for the spread of infection in this population. However, fragmentation of the network could easily be achieved by "removing" a small proportion of farms serving as bridges between otherwise isolated clusters, thus decreasing the probability of large epidemics.

This is the first example of a comprehensive analysis of pastoral livestock movements in New Zealand. We conclude that, for our system, recording and exploiting livestock movements can contribute towards risk-based control strategies to prevent and monitor the introduction and the spread of infectious diseases in animal populations.

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## 1. Introduction

Movement of livestock between farms or markets is a strong determinant of the spread of transmissible pathogens in animal populations (Keeling and Eames 2005; House and Keeling, 2011). Detailed knowledge about movement of livestock can thus be a useful tool to inform control strategies. A classic example is provided by the foot-and-mouth disease (FMD) epidemics of 2001 in the UK. A few long-range movements, mostly via markets and dealers, spread the infection widely at an early stage (Kao 2002; Kao et al., 2006; Shirley and Rushton, 2005). Consequently, more stringent and accurate livestock tracing systems, in addition to mandatory movement restrictions, were implemented in the UK (Vernon, 2011). Analysis of animal movement can also provide a useful framework to study the spread of endemic diseases and has been extensively used for tuberculosis, both in cattle populations (Gilbert et al., 2005; Woolhouse et al., 2005) and wildlife (Corner et al., 2003; Drewe et al., 2011; Porphyre et al., 2008).

Landcorp farming limited (LC) is a state-owned enterprise, comprised of 122 farms[1] located throughout New Zealand, representing the regional variety of farm types of the country's pastoral livestock industry. New Zealand farming is characterized by all-year pastoral farming in which pasture availability drives the annual production cycle and different livestock species are often co-grazed on the same pasture. LC farms are typical of this farming system and most LC farms host multiple livestock species (cattle, sheep and/or deer—mostly red deer). LC keeps detailed records of the shipments of livestock off and onto their farms. Most movements occur between LC farms with a small proportion of movements to non-LC farming enterprises. The movement records of LC were unique in New Zealand, in that they provided a complete set of movement events over several years within a corporate group of farms representing a relatively closed population. We propose that this information could provide some insight into factors potentially influential in disease spread. A better understanding of these

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[1] 122 farms as per 2012, this number is subject to annual changes and increased to 137 in 2014. The number of different LC properties involved in the network analysis is 112.

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factors is a necessary first step in developing rational interventions to limit disease spread.

In this study we analysed the contact pattern arising from movements of sheep, cattle and deer to and from LC farms from 2006 to 2010. Our aim was to use social network analysis (SNA) to describe the trading pattern of LC farms and to understand how contact through trading might influence the spread of infectious diseases. A preliminary step was to assess the consistency of network characteristics over time, and a sequel was to discuss the effect of targeted control measures with respect to various aspects of disease spread in this particular network. This analysis will help to prioritize the allocation of resources to enhance biosecurity in this network of farms.

## 2. Material and methods

Definitions of the technical terms related to SNA used in this paper are provided in Table 1.

### 2.1. Movement data

The data available for analysis included all livestock movement records to and from the properties of LC for the period 1 July 2006–30 June 2010 (inclusive). LC farms primarily exchange livestock within the company, but some movements also involved properties outside LC. Livestock species involved in the movements were dairy cattle, beef cattle, sheep and deer. Two types of movements were recorded. A transfer was defined as the *permanent movement* of livestock from one property to another (equivalent to a sale). The format for a transfer was an annual summary record: for every pair of farms between which livestock transfers occurred in a given year, there was one summary record for each species moved corresponding to the sum of all the annual transfers for this species. Agistments were defined as *temporary movements* of livestock (equivalent to a lease). These occurred when animals were sent from one LC property to another – or to a property outside LC – for a limited period for grazing management, followed by another agistment movement record back to the property of origin. Detailed data for agistments were available, thus each agistment corresponded to an actual shipment of animals including the date on which the movement event occurred.

The LC movement database contained: the source and destination property; the type of movement (transfer or agistment); the date (year for transfers, calendar date for agistments); the species involved: sheep, beef, dairy or deer; and the total number of animals of each species moved in one year for transfers, or the actual batch size for agistment events.

Using these data, we constructed yearly networks consisting of all recorded livestock movements within the LC enterprise from the 01st July to the 30th of June and we described the contact pattern in terms of consistency over time, size, centrality measures and cohesion (see Table 1). We finally analyzed the characteristics of this contact pattern that were believed to be key for disease transmission.

### 2.2. Data analysis

The consistency of farm movement events was evaluated across successive years. All subsequent analyses were carried out using data for the year 2009–2010 only, as movement records were most complete for this year. The recorded data represented a census of the movements to/from the LC farms. However, some non-LC farms traded with LC farms, thus acting as satellites of this network. For these commercial farms, only the movements to/from LC farms were known while movements to/from other commercial farms were not included in the data. To avoid biases, all the movements were used to calculate farm-level network properties (such as degree or betweenness) but only measures for the LC farms were reported. Similarly, network-level statistics (degree distribution, standard deviation and average degree, degree correlations and effect of targeted control) were calculated using only the LC farms. Since the non-LC farms contributed to the overall connectivity, they were kept to calculate measures of network cohesion. The analyses were performed using the software package Pajek for SNA (Batagelj and Mrvar, 2008), and the *igraph* package (Csárdi and Nepusz, 2006) within R (R Development Core Team, 2014). Networks were plotted using Gephi (Bastian et al., 2009).

**Table 1**
Definitions of social network terms used in this study.

| Parameter | Definition |
|---|---|
| General terms | |
| Directed path | The pathway between nodes (farms) accounting for the direction of the contacts (i.e. livestock movements). A movement from nodes A to B or a movement from nodes B to A thus defines two different pathways. |
| Undirected path | The pathway between nodes (farms) ignoring the direction of the contacts. A movement from nodes A to B or a movement from nodes B to A thus defines the same pathway. |
| Measures of centrality | |
| In-, out-degree | The number of contacts to or from a node (farm), respectively, during a defined period. In-degree is potentially positively correlated with the probability of introduction of infectious agents. Out-degree is potentially positively correlated with the probability of spreading infection. |
| Weighted in-, out-degree | The weighted in- and out-degree were defined as the total number of animals (as opposed to the total number of contacts) received or sent by a farm, respectively, during a defined period. |
| Betweenness | The frequency by which a node falls between pairs of other nodes on the shortest path connecting them (Freeman, 1978). Betweenness is a measure of centrality used to quantify a node's potential to 'control' the flow, or curtail paths within a network. |
| Measures of cohesion: | |
| Clustering coefficient | Clustering coefficient (CC) can be either a local or a global network attribute. In this study CC is expressed as a global measure, corresponding to the probability that any two nodes *j* and *k* are connected to a node *i* and nodes *j* and *k* are in turn connected to each other (Kiss et al., 2006). As a global measures CC quantifies 'cliquishness' within the network (Watts and Strogatz, 1998). |
| Strongly connected component | The section of a network where any node could be reached from any other node by following the direction of existing paths (Christley et al., 2005). |
| Weakly connected component | The section of a network where all nodes are linked to each other irrespective of the direction of the path (Christley et al., 2005). |

#### 2.2.1. Consistency of the contact pattern over time

Networks are dynamic structures, therefore evaluating the consistency (or the lack of it) of global and individual network properties can reveal important evolutions in the network topology (Kossinets and Watts, 2006; Robinson et al., 2007). Year to year

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