helen.fielding@exeter.ac.uk

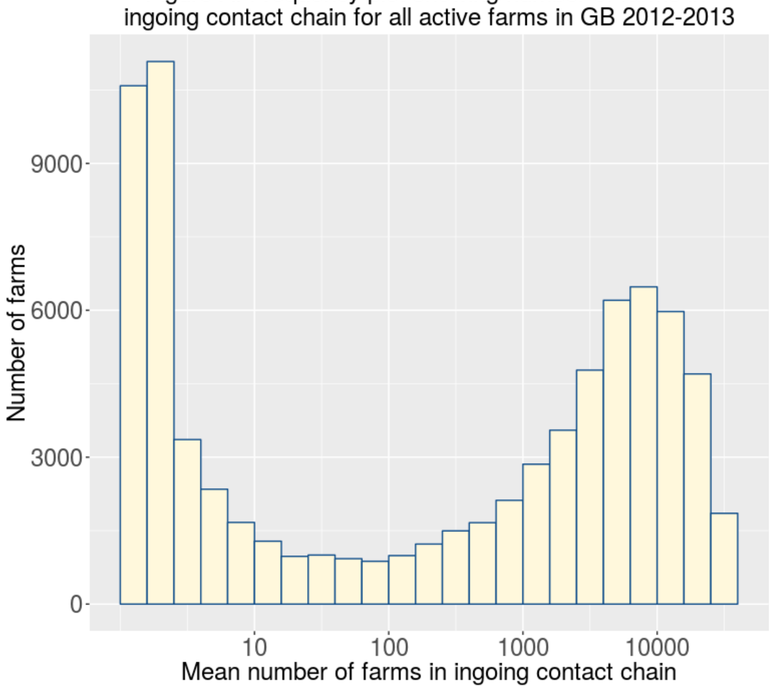
Revealing contact chains of cattle farms

Helen R. Fielding[a], T.J. McKinley[a], Richard J. Delahay[b] , Robbie A. McDonald[a]

[a]*University of Exeter,* [b] *Animal and Plant Health Agency (APHA)*

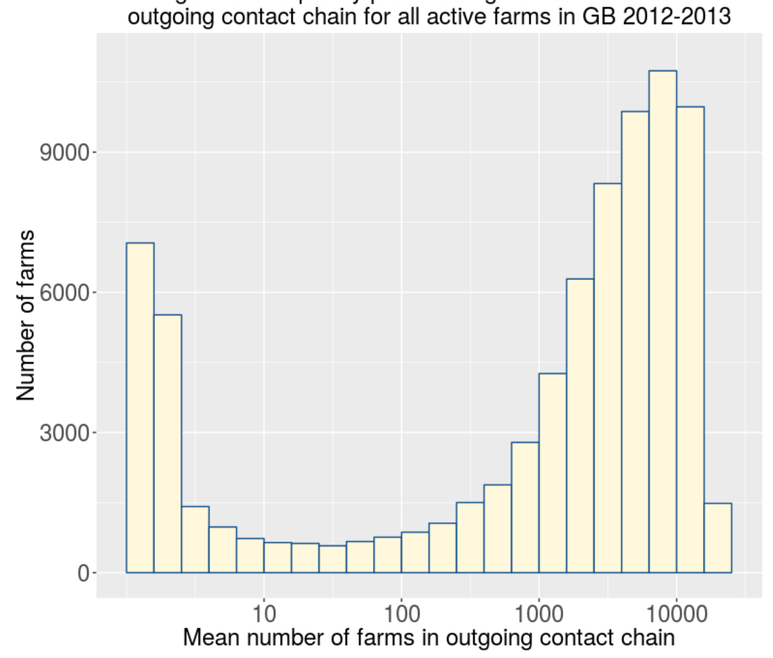
With acknowledgements to the **APHA Data** and **Epidemiology teams** for providing data and assisting with data processing and to **Matt Silk** and **Stefan Widgren** for their help and advice.

Figure A: Frequency plot showing number of farms in ingoing contact chain for all active farms in GB 2012-2013



Figures A and B: Mean number of farms from 24 x 12-month time windows. Whilst most farms contact only a few other farms in their ingoing contact chain, some connect to tens of thousands of farms, encompassing large proportions of the whole cattle farm network. Through outgoing contact chains, some farms 'reach' over 70% of farms in the network and could therefore potentially be highly influential in disease spread.

Figure B: Frequency plot showing number of farms in outgoing contact chain for all active farms in GB 2012-2013



Temporal variation

- Contact chains of a single farm can be highly variable
- Some rapidly increase/decrease between monthly time windows
- These temporal fluctuations may be important in understanding disease dynamics

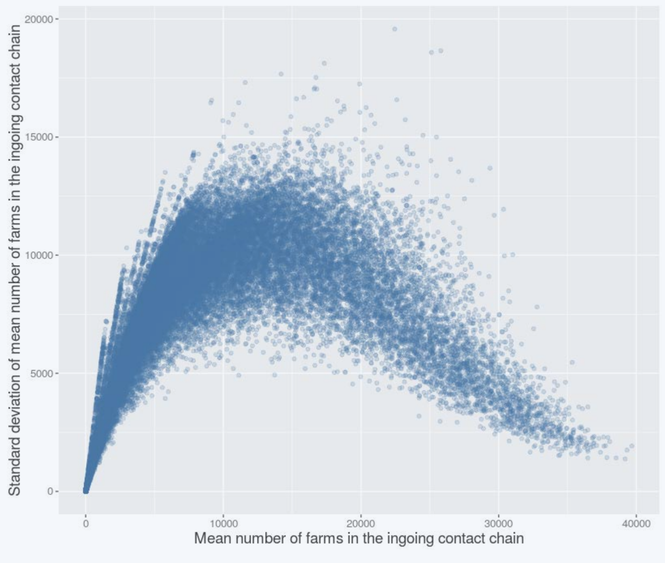
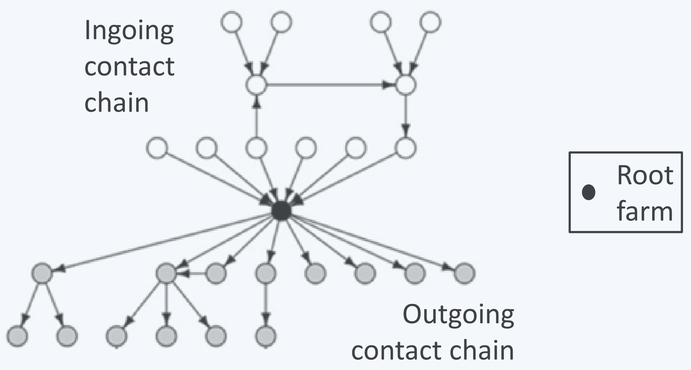


Figure E: Farms with a low and high mean number of farms in their contact chain typically have low variation in chains, however, those with numbers of farms in the mid-range have much higher variation.

Introduction

A contact chain is a sequence of farms linked by sequential movements either from (outgoing chain) or to (ingoing chain) a root farm. We count the number of farms connected through which disease transmission may occur, usually corresponding to the time period a certain disease may persist undetected. We look at ingoing chains with respect to susceptibility to infection, and the role of outgoing chains in disease spread.



Plot reproduced from Nöremark and Widgren, 2014

Materials and methods

- In and outgoing contact chains calculated for 77,985 animal holdings active in Great Britain over period 2012-2014
- Movements to slaughter, markets and showgrounds were removed leaving only farm to farm movements
- One year time windows taken for 24 consecutive months (i.e. Jan-Jan, Feb-Feb, etc.) for each farm location
- Used the mean number of farms occurring in a chain as a summary measure
- R packages 'EpiContactTrace' and 'data.table' used

Figure F: Location of farms in ingoing contact chain of one root farm

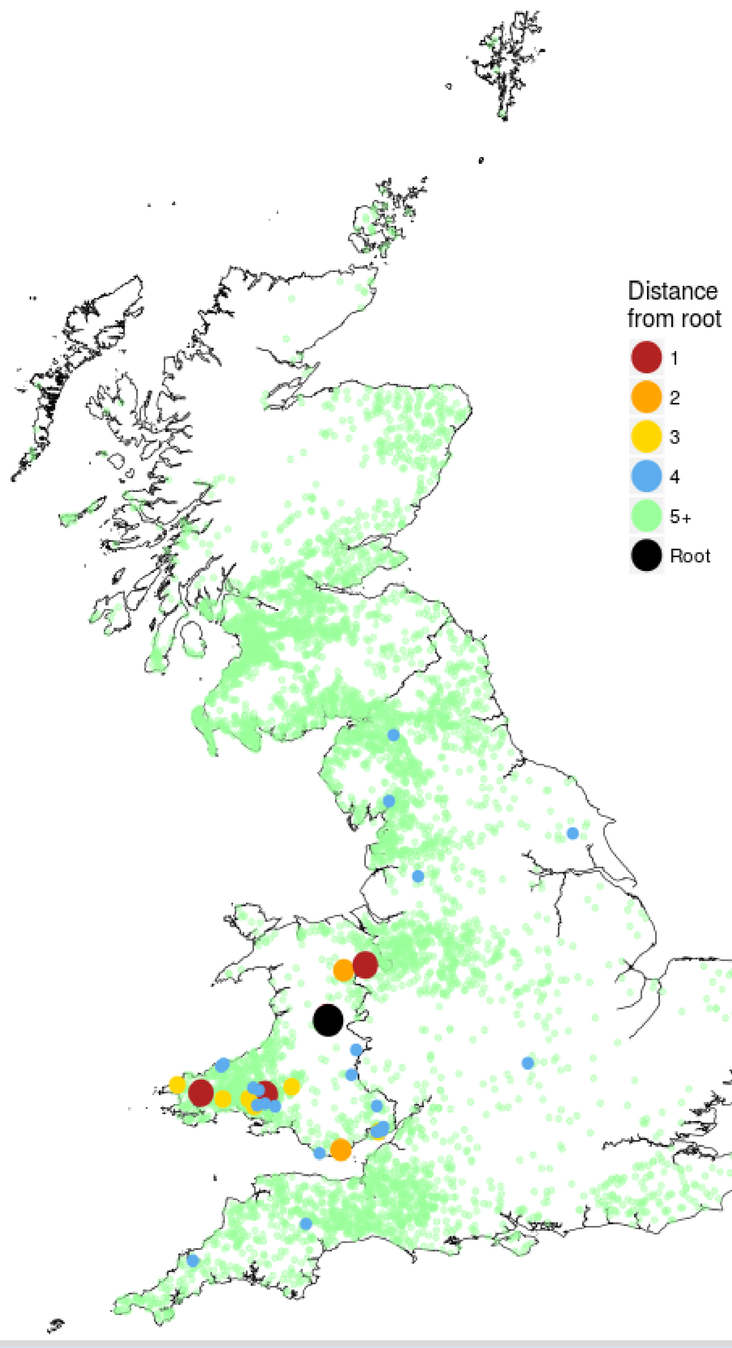


Figure F: Map of Great Britain showing locations of farms in the ingoing contact chain of one single 'root' farm, coloured by the number of movements away from the root farm.

Figure C: Boxplot of mean number of farms in ingoing contact chains of farms by different herd types

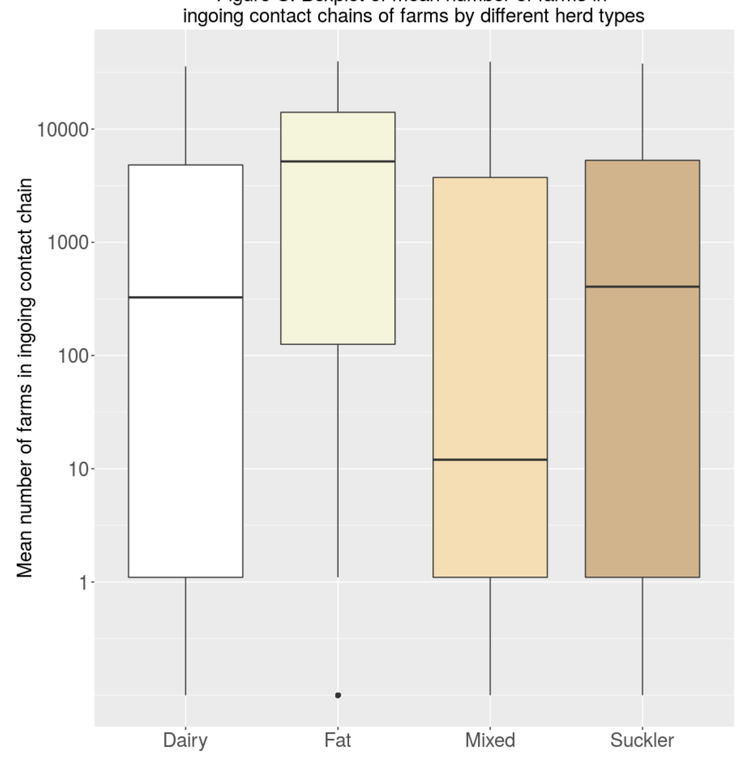
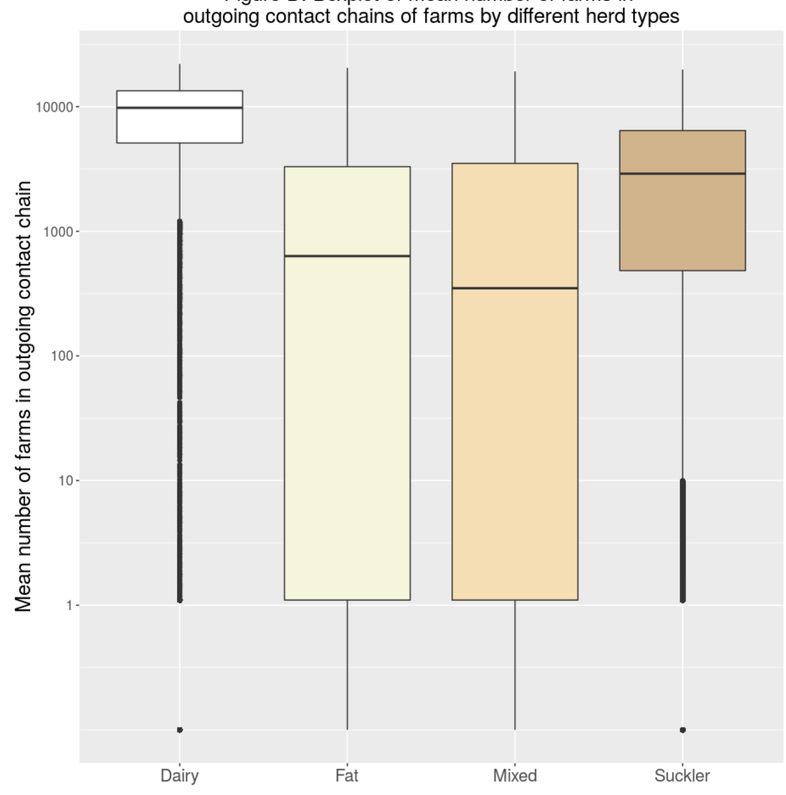


Figure C: Fattening farms have more farms in their **ingoing** chains than breeding (suckler and dairy) farms.

Figure D: Breeding herds, particularly dairy have much higher **outgoing** contact chains than fattening or mixed farms.

Figure D: Boxplot of mean number of farms in outgoing contact chains of farms by different herd types



Summary

- Understanding cattle movements beyond immediate network connections is important
- Some farms become rapidly connected to a large proportion of cattle farms
- Contact chains are complex but provide opportunities for improved disease management

Further work

- Investigate temporal variation to identify potential correlates with subsequent disease
- Characterising spatial component of chains
- Prediction of individual risk through contact chain structure
- Estimating risk of disease transmission and spread based on disease history, type and size of farms in chains and root farms