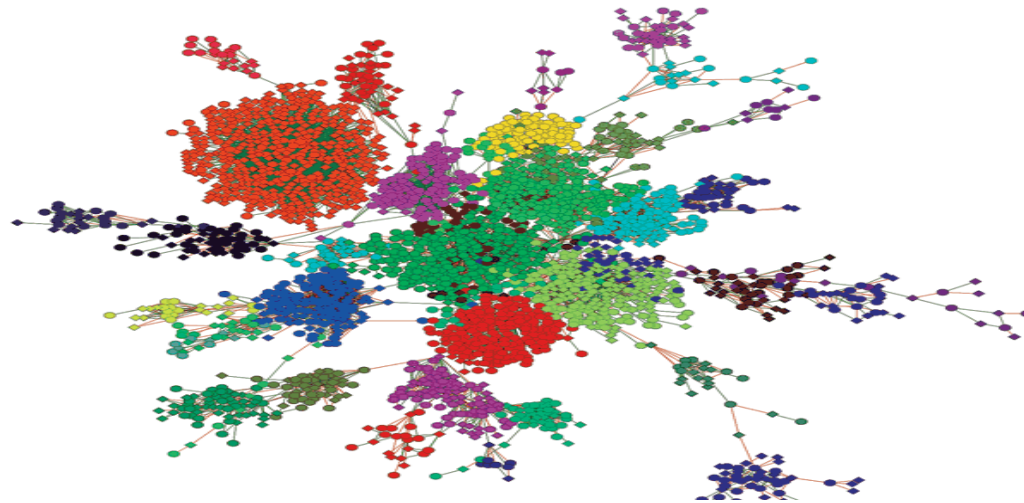


United States Network Modeling Initiatives:

Characterizing cattle and sheep movements for the purpose of understanding disease transmission dynamics



Colleen T. Webb, Colorado State University

Agricola Odoi, University of Tennessee

Katie A. Portacci, USDA, Center for Epidemiology and Animal Health

Ryan S. Miller, USDA, Center for Epidemiology and Animal Health



❑ Cattle movement and bovine tuberculosis

- ❑ NIMBioS (University of Tennessee)

❑ Sheep movement and scrapie

- ❑ Center for Infectious Disease Dynamics, Pennsylvania State University - Dr. Shweta Bansal
- ❑ Webb Lab, Colorado State University - Dr. Colleen Webb

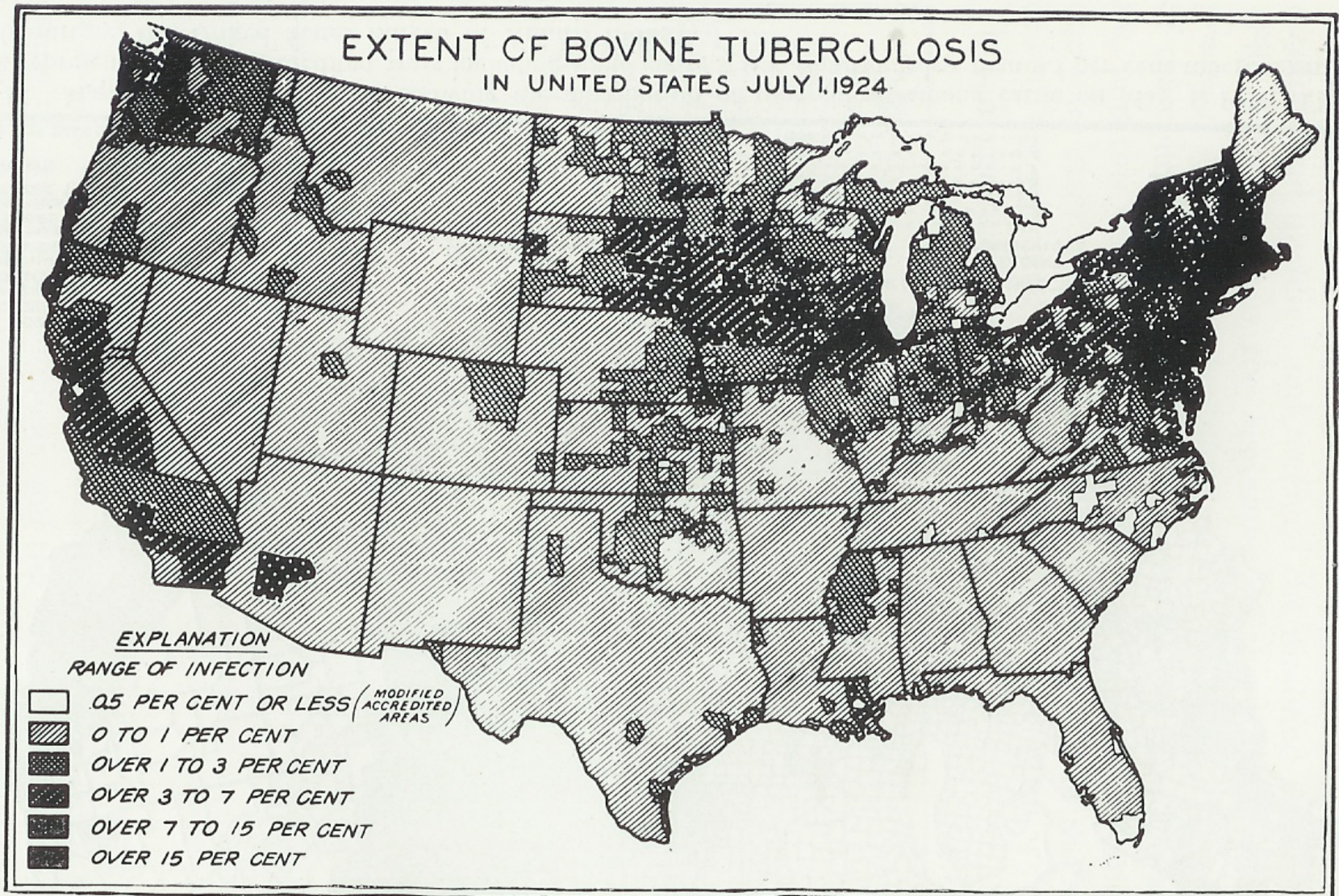


FIGURE 54. Map of the United States showing the distribution of tuberculosis among cattle on July 1, 1924. The darker the area, the higher the incidence of tuberculosis. Note the few counties in white which had received the modified accredited rating, having reduced tuberculosis among cattle to 0.5 per cent or less. (Courtesy, the United States Bureau of Animal Industry.)

Slide courtesy of Dr. Susan Jones



- ❑ Arose from a collaboration between:
 - National Science Foundation
 - U.S. Department of Homeland Security
 - U.S. Department of Agriculture

- ❑ Specific goal to maintain safe food supply, avoid economic disruptions caused by emerging infectious diseases, and evaluating methods to better manage disease outbreaks

- ❑ Investigated by integrating modeling and mathematics with the biological studies

- ❑ Focuses the talents of researchers from around the world to collaborate across disciplinary boundaries

Project Scoping

- ❑ Modeling Bovine Tuberculosis Workshop, July 7-9, 2009
- ❑ Brought together 37 experts from North America and Europe
- ❑ Identified issues related to bovine tuberculosis modeling
- ❑ Included presentations from European scientist on efforts to model cattle movement and TB transmission



Cattle movements and bovine tuberculosis in Great Britain

M. Gilbert¹, A. Mitchell², D. Bourn³, J. Mawdsley², R. Clifton-Hadley² & W. Wint³

For 20 years, bovine tuberculosis (BTB) has been spreading in Great Britain (England, Wales and Scotland) and is now endemic in the southwest and parts of central England and in southwest Wales, and occurs sporadically elsewhere. Although its transmission pathways remain poorly understood, the disease's distribution was previously modelled statistically by using environmental variables and measures of their seasonality¹. Movements of infected animals have long been considered a critical factor in the spread of livestock diseases, as reflected in strict import/export regulations, the extensive movement restrictions imposed during the 2001 foot-and-mouth disease outbreak^{2,3}, the tracing procedures after a new case of BTB has been confirmed and the Government's recently published strategic framework for the sustainable control on BTB⁴. Since January 2001 it has been mandatory for stock-keepers in Great Britain to notify the British Cattle Movement Service of all cattle births, movements and deaths⁵. Here we show that movements as recorded in the Cattle Tracing System data archive, and particularly those from areas where BTB is reported, consistently outperform environmental, topographic and other anthropogenic variables as the main predictor of disease occurrence. Simulation distribution models for 2002 and 2003, incorporating all predictor categories, are presented and used to project distributions for 2004 and 2005.

BTB, once almost eradicated from Great Britain, has been spreading since 1984, and the number of detected BTB cases continues to rise exponentially (Fig. 1). Because BTB transmission cycles remain poorly understood, the causes of this epidemic are keenly debated, with various possible explanations including transmission from wildlife reservoirs, inadequate control measures, agro-environmental factors and movement of infected animals⁶⁻⁸. Previous work has shown the value of environmental variables and measures of their seasonality⁹, as encapsulated in Fourier-processed satellite imagery⁹, in modelling the distributions of BTB in Great Britain¹. The pattern of spread of BTB between 1984 and 2003 shows an expanding core area with outlying foci (Fig. 1). Such a pattern is commonly described in invasion ecology by stratified dispersal models that combine short-distance spread with long-distance dispersal events^{10,11}. For infectious diseases of livestock, short-distance spread can be viewed as contagion to adjacent or nearby farms located within a few kilometres, by direct contact or borne by wind, insects, rodents or alternative hosts, and generally resulting in the local spatial clustering of cases. Long-distance jump-spread can be viewed as contagion occurring between locations separated by large areas of disease absence, and caused by movements of infectious individuals or infected material. The present study sought to evaluate the relative importance of cattle movement as a predictor of BTB distribution and invasion in Great Britain, and to use the established models for short-term predictions.

Two sets of analyses were undertaken. The first was designed to

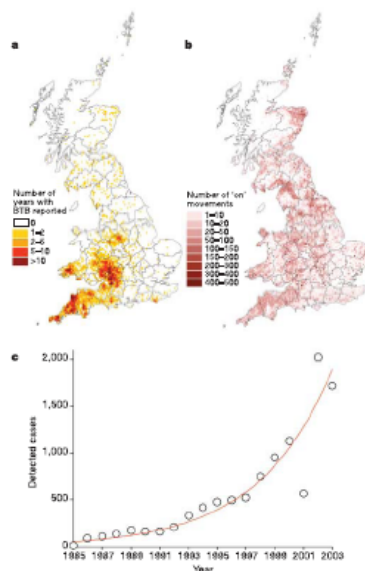


Figure 1 | Distribution and spread of BTB in 1985-2003 and distribution of annual cattle movements. **a**, Distribution of the number of years in which BTB has been reported. **b**, Distribution of cattle inward movements in 2002 by 5-km cells. **c**, Change in the number of BTB detected cases. Note that the number of cases recorded for 2001 was relatively low, probably because of the reduction in testing during the outbreak of foot and mouth disease. They seem to have been compensated for by a comparative increase in 2002. The equation of the curve are: $y = 8.70 \times 10^{-14} e^{0.196x}$, $R^2 = 0.876$, $n = 19$; $P < 0.001$.

¹Biological Control and Spatial Ecology CP160/12, Université Libre de Bruxelles, avenue F.D. Roosevelt 50, B-1050 Brussels, Belgium. ²Veterinary Laboratories Agency, Weybridge, New Haw, Addlestone, Surrey KT8 3NS, UK. ³Environmental Research Group Oxford Limited, PO Box 346, Oxford OX1 3QE, UK.

Representing the UK's cattle herd as static and dynamic networks

Matthew C. Vernon* and Matt J. Keeling

Department of Biological Sciences, University of Warwick, Coventry CV4 7AL, UK

Network models are increasingly being used to understand the spread of diseases through sparsely connected populations, with particular interest in the impact of animal movements upon the dynamics of infectious diseases. Detailed data collected by the UK government on the movement of cattle may be represented as a network, where animal holdings are nodes, and an edge is drawn between nodes where a movement of animals has occurred. These network representations may vary from a simple static representation, to a more complex, fully dynamic one where daily movements are explicitly captured. Using stochastic disease simulations, a wide range of network representations of the UK cattle herd are compared. We find that the simpler static network representations are often deficient when compared with a fully dynamic representation, and should therefore be used only with caution in epidemiological modelling. In particular, due to temporal structures within the dynamic network, static networks consistently fail to capture the predicted epidemic behaviour associated with dynamic networks even when parameterized to match early growth rates.

Keywords: dynamic networks; transmission; infection; livestock movements

1. INTRODUCTION

The movement of animals within the UK is vital to the economics of the livestock industry, but carries with it the risk of transmitting infectious diseases across substantial geographical distances. Data on the movement of all cattle in the UK are collected by the Department for Environment Food and Rural Affairs (DEFRA), as part of the Rapid Analysis and Detection of Animal-related Risks (RADAR) system, itself part of the Veterinary Surveillance Strategy (Lysons *et al.* 2007).

This movement data may be abstracted into a directed contact network in which agricultural premises are nodes, and the movements of cattle between premises are edges. The resulting network may be analysed using a range of techniques, including those developed for handling social networks (Wasserman & Faust 1994; Carrington *et al.* 2005). A common approach has been to consider all the movements within a fixed period (typically 7 or 28 days, or a year) as a static network, and then to analyse the properties of the resulting network (Christley *et al.* 2005; Biggs-Poulin *et al.* 2006), or to repeat this process for a consecutive sequence of such periods and look for trends in the properties of the resulting networks (Robinson *et al.* 2007). Indeed, most social network analysis concentrates on static networks, and there is a paucity of strategies for addressing the structure of dynamic networks (Wasserman & Faust 1994). Research into dynamic networks has concentrated on models based on how individuals create or change their ties in a network, in response to their perception of that network's structure (Snijden 2005), how popular other individuals in the network are (Bambai & Albert 1999), their social distance from and shared activities with other individuals (Kossinets & Watts 2006) or how the other individuals

perform in a game-theoretic framework (Skyrms & Pemantle 2000; Zimmermann *et al.* 2004). The dynamic pattern of movement between farms is also likely to be governed by some underlying set of rules linking livestock population dynamics with economics; however, given the comprehensive nature of the recorded movements, our aim is to understand how they influence disease transmission.

The UK cattle movement data, and the network of connections that can be derived from it, are one of the most detailed datasets available on dynamic network structure. As such, these data have provided an ideal test of many theories and concepts from network theory. What is more, the presence of information about infection on cattle farms (Wint *et al.* 2002; Gilbert *et al.* 2005) provides a real-world comparison with the ideals of network theory. Obviously predicting the spread of actual infections through the cattle movement network requires models that can accurately capture the epidemiology and natural history of a particular pathogen, and produce results that are specific to the particular infection studied. Here we adopted an alternative, and more generic approach, using simple disease models to understand the implications of dynamic cattle movements, as opposed to static network connections. These simple models treat the farm as a single epidemiological unit.

In this paper, a range of static and dynamic network representations of the UK's cattle herd are considered. Since the purpose of constructing network models of cattle movement is to understand the impact of movements upon the dynamics of infectious disease, simulated disease processes were employed to assess the suitability of the different network representations. More specifically, a stochastic, discrete-time susceptible, infectious, recovered (SIR) disease model was developed, and the dynamics and final epidemic size of simulations run upon

* Author for correspondence (m.c.vernon@warwick.ac.uk).

Working Group



Not Pictured:
Dr. Michael Tildesley

Working Group Members

Shweta Bansal	<i>Pennsylvania State University</i>
Michael Buhnerkempe	<i>Colorado State University</i>
Matt Farnsworth	<i>USDA</i>
John Kanenee	<i>Michigan State University</i>
Jason Lombard	<i>USDA</i>
Ryan Miller (Lead)	<i>USDA</i>
Agricola Odoi (PI)	<i>University of Tennessee</i>
Katie Portacci (Lead)	<i>USDA</i>
Michael Tildesley	<i>University of Edinburgh</i>
Matthew Vernon	<i>University of Warwick</i>
Colleen Webb (PI)	<i>Colorado State University</i>
Uno Wennergren	<i>Linkoping University</i>
Folashade Augusto	<i>University of Tennessee</i>

Project Goals: Policy and Regulatory

Provide tangible benefits to the Bovine Tuberculosis Program and to management of other diseases in cattle.

Specifically:

- Improved traceability
- Foundation for disease control zones
- Benefits for market access in the face of an outbreak
- Improved response in the face of an outbreak
- Enhanced surveillance

Scientific and Policy Questions

- ❑ Which sectors of the cattle industry pose significant risks of bTB transmission?
 - ❑ How important are markets, feedlots and other sectors where mixing occurs?



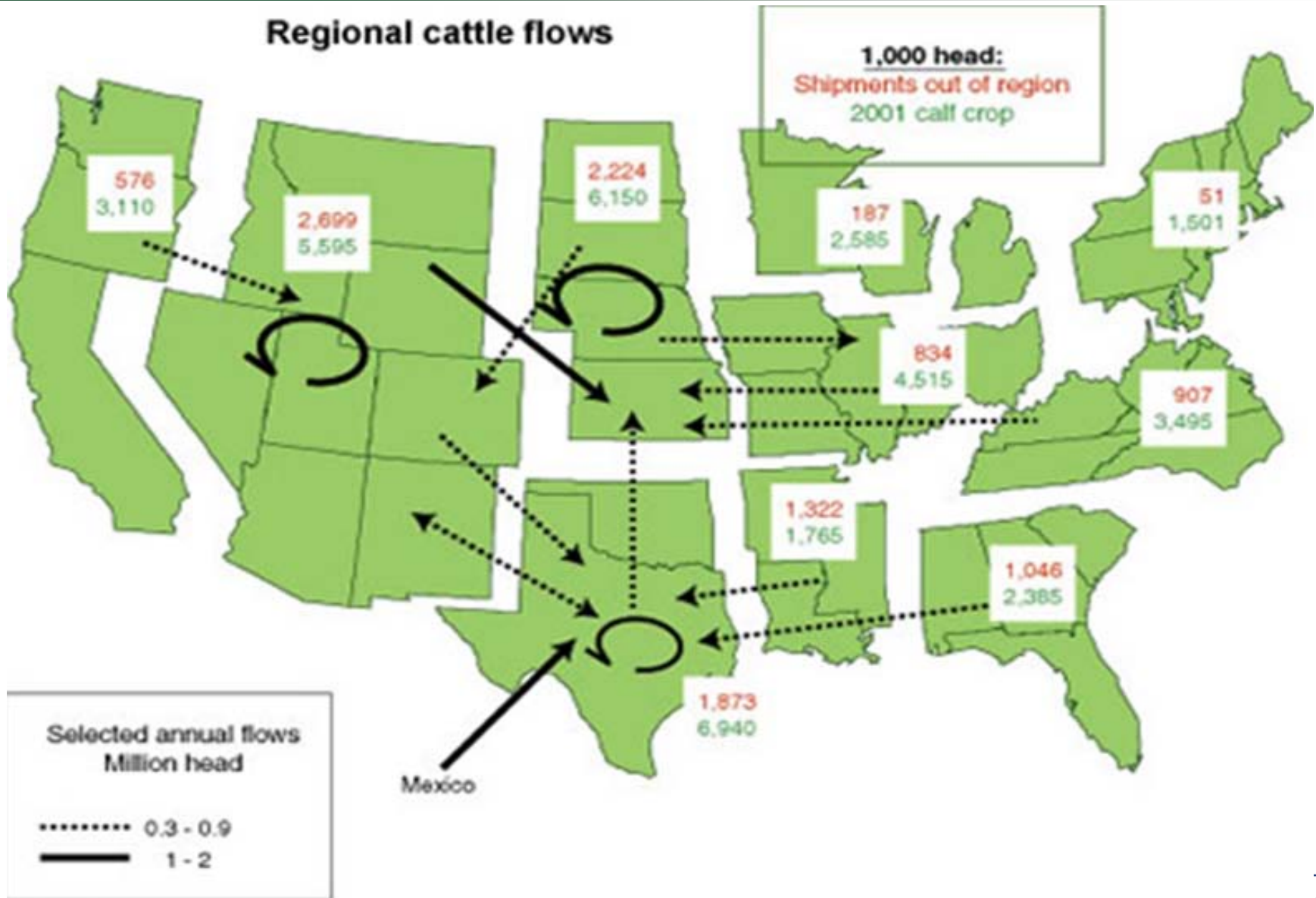
Scientific and Policy Questions

- ❑ Can United States cattle movement data be leveraged to support specific regulatory functions and optimize surveillance and mitigation of bovine TB (and potentially other diseases)?
 - ❑ Two major difficulties in controlling bovine TB include the chronic nature of disease and the lack of test sensitivity which necessitate improved program efficiencies to aid in eradication efforts.

Scientific and Policy Questions

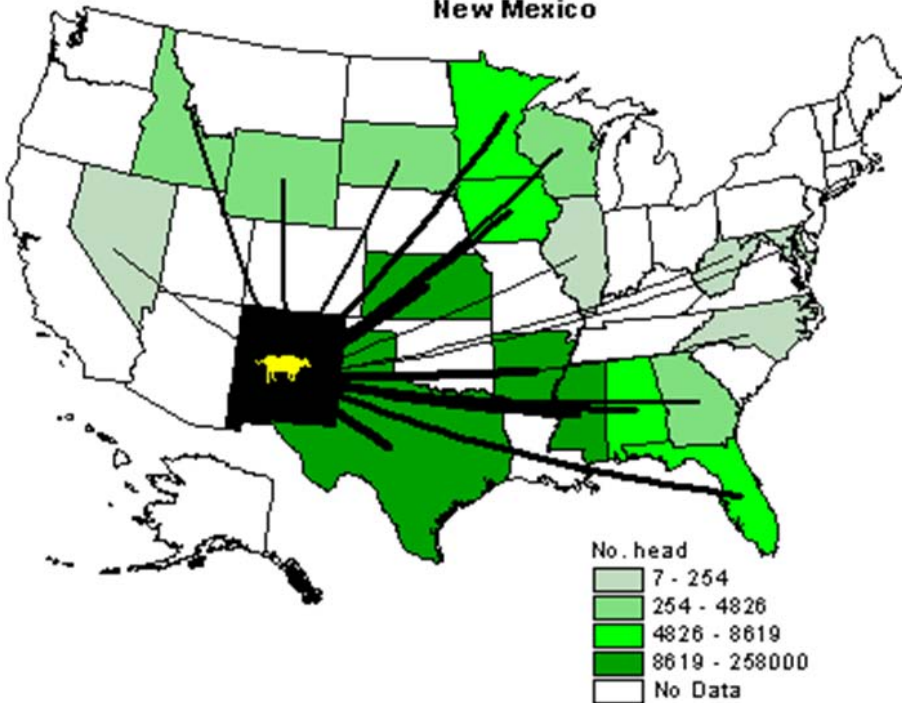
- ❑ How does uncertainty of cattle movement impact model predictions and the efficacy of control and eradication strategies?
 - ❑ Modeling approaches that incorporate an explicit contact structure are based on a completely characterized cattle network
 - ❑ In the United States only a partially observed network is available.

Regional cattle flows

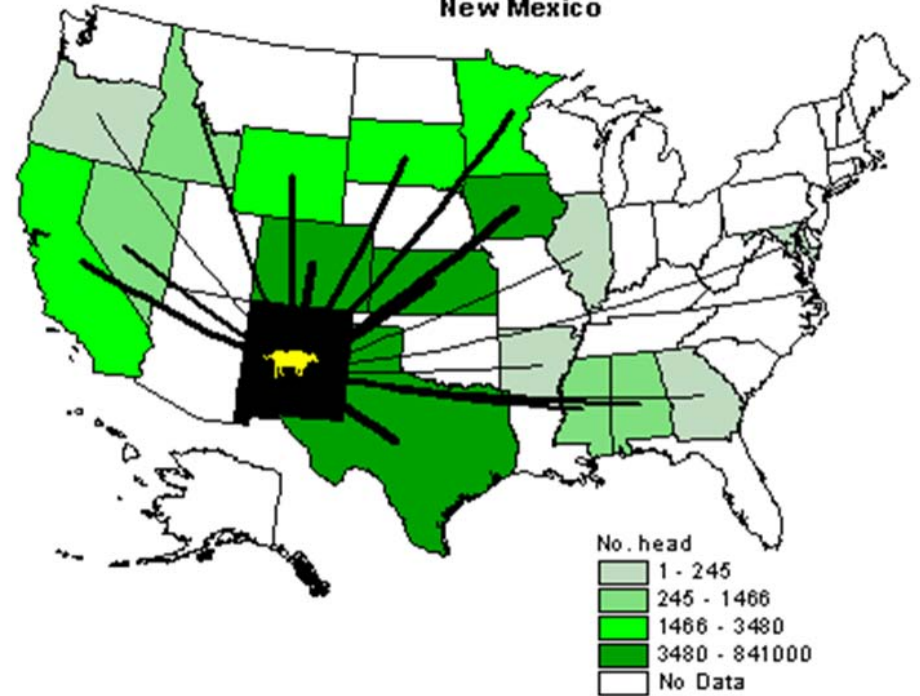


Source: State certificate data (generally 2001) compiled by Economic Research Service, USDA.

**Cattle inflows
New Mexico**



**Cattle outflows
New Mexico**



Source: State certificate data (generally 2001) compiled by Economic Research Service, USDA.

Project Goals: Analytical

The project has two core tasks:

- 1) Develop national cattle movement model
 - contact network
- 2) Use contact network to model bovine tuberculosis from a data driven perspective (not a simulation model).
 - Slaughter surveillance data
 - Positive herd data

Regulatory Functions Supported

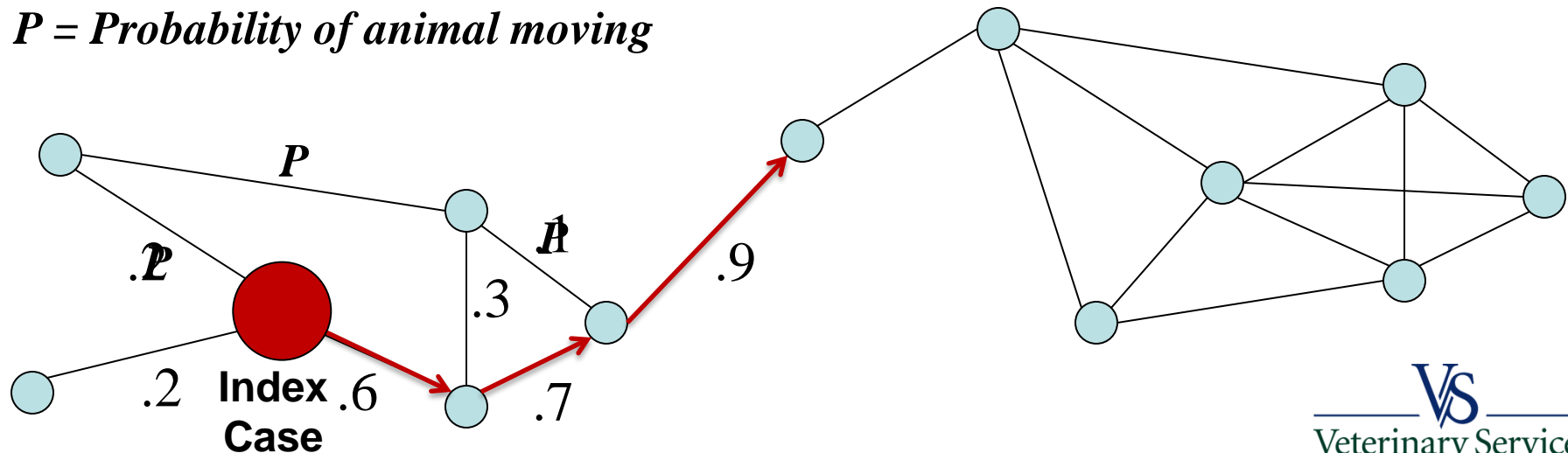
- Traceability
 - Improved traceability when data is limited
 - Optimization of tracing when faced with large numbers of movement events
- Regionalization
 - Greater defensibility
 - Benefits for market access in the face of an outbreak
- Surveillance
 - Enhanced surveillance
 - Optimized surveillance to improve first detect

Traceability

Improve traceability by providing empirical data driven understanding of the probability an animal originated from a geographic location.

- Fundamental regulatory issue is a lack of data describing the movements of individual animals.

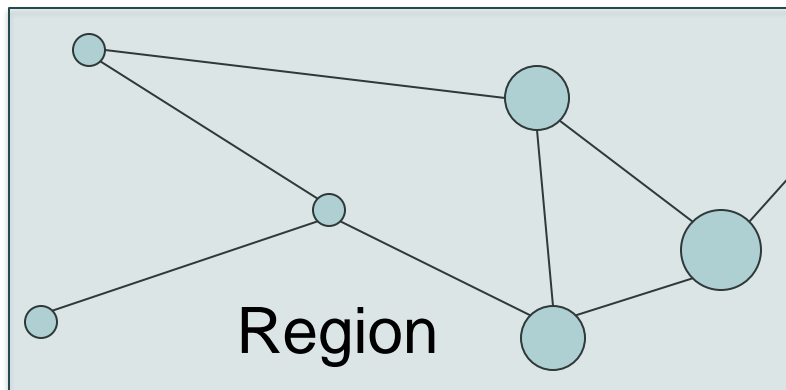
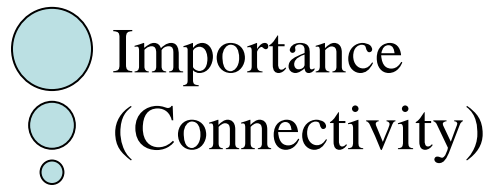
P = Probability of animal moving



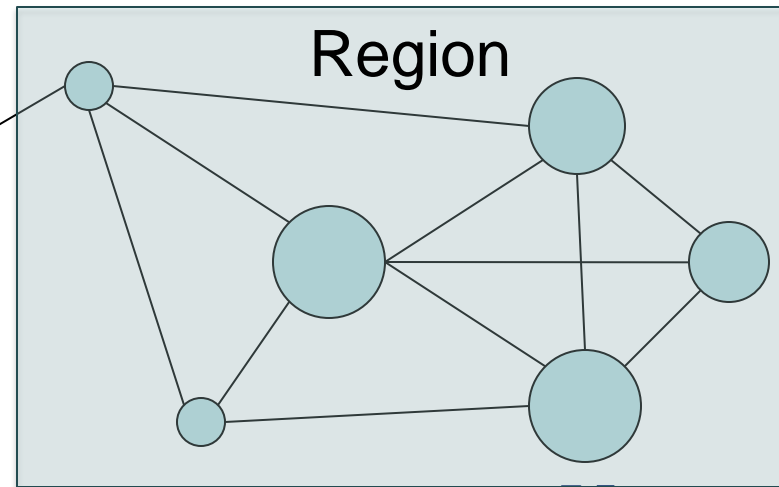
Regionalization

Improve regionalization by developing an empirical data driven understanding regions that are connected via animal movements.

- Benefits are a more defensible method for establishing regions if animal movement is important for disease spread.



Bridging Node

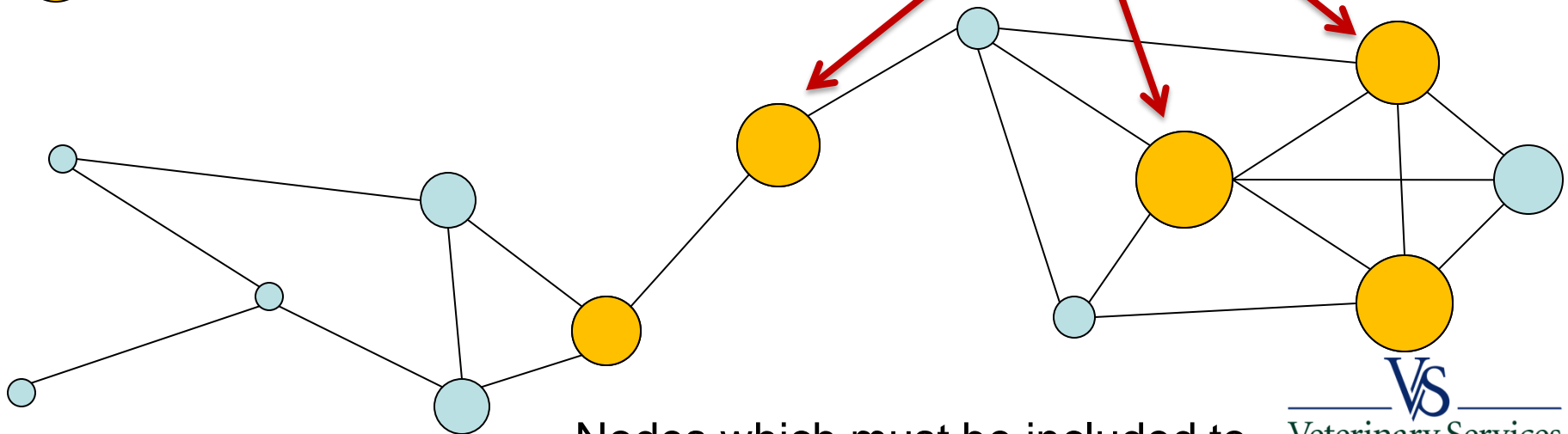


Surveillance

Improve surveillance by developing an empirical data driven understanding locations accounting of the greatest connectivity in the network.

- Benefits are an optimized surveillance that maximizes first detection while minimizing cost.

● Minimum Spanning Nodes



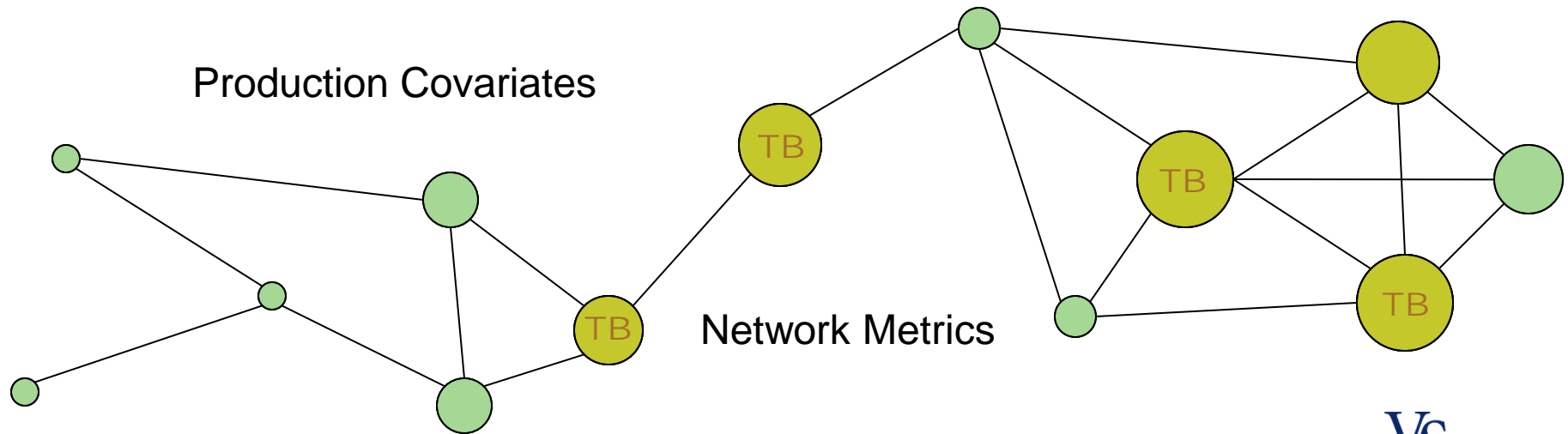
Nodes which must be included to maintain the network structure

Disease Spread

- Does animal movement describe the current and historic occurrence of bovine TB?
- If so can animal movement be used to improve our predictive abilities and improve program activities?
- Can animal movement be combined with other risk factors to describe occurrence of bovine TB and in turn identify areas at risk?

Disease Spread

Incorporate network measures (minimum spanning tree, bridging metrics, flow, others) along with covariates (density of markets, density of off site heifer raisers, sector, etc) to describe occurrence of bovine TB using empirical model based inference.

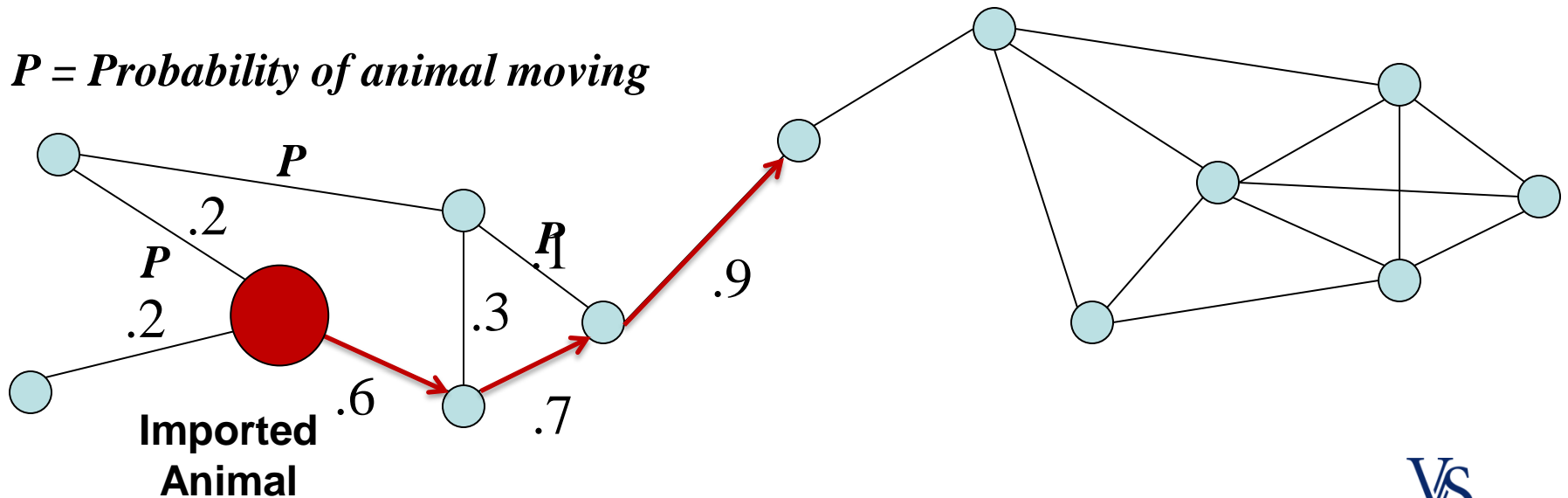


Disease Spread

Support for contributions (risk) of known reservoirs of bovine TB - foreign imports, wildlife reservoirs, etc.

- Provides support for import regulation, testing and marketing of animals moving from areas with endemic TB or with a current outbreak.

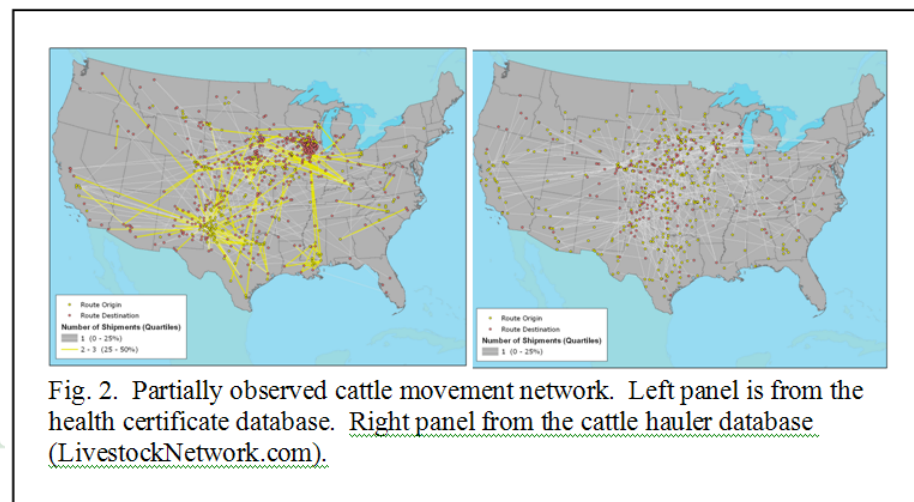
P = Probability of animal moving



Specific Activities of the Working Group

1) Evaluate bias in USDA Digital Certificate of Veterinary Inspection (i.e., health certificate) database.

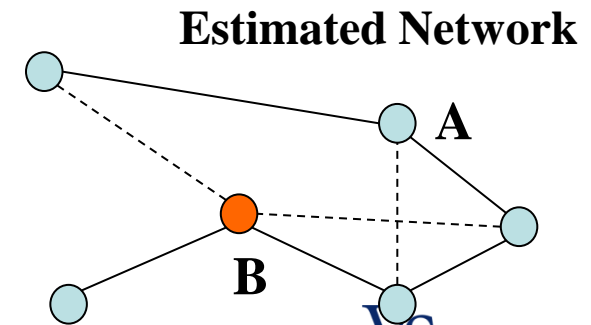
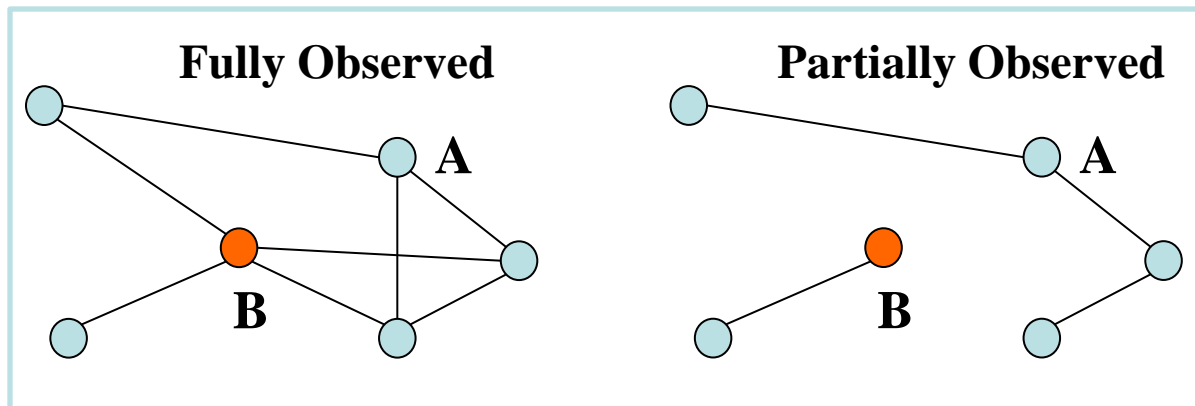
- Best electronically available data on individual cattle movement
 - Health certificates required for interstate movement (except slaughter).
- This data only represents a fraction of all cattle movements, which may introduce potential biases.
 - We will investigate the potential for bias by comparison to other cattle movement databases.



Specific Activities of the Working Group

2) Investigate how partial observation impacts inference.

- For many European livestock models, the network is completely known.
- Use cattle movement data for the United Kingdom to develop methods for estimating cattle movement when the network of movement is only partially observed.



Specific Activities of the Working Group

3) Develop a local network model for Michigan (high TB prevalence)

- Michigan - most comprehensive animal movement data for the United States.
- Develop a network model of cattle movement and TB spread for Michigan
 - understand the relative importance of cattle mixing versus the TB reservoir in wild White-tailed deer
- Use model to understand control and eradication strategies
 - how these strategies impact the potential for transmission to other parts of the country (by linking the Michigan model to the national model).

Specific Activities of the Working Group

4) Develop a network model at the national level for the US.

- We cannot assume that the Michigan model can be scaled to the national level.
- Develop a national scale network model of cattle movement and TB spread
 - Identify the production sectors of importance for driving dynamics
 - Identify production sectors at greatest risk
- Use model to investigate control and eradication efforts
 - Investigate diagnostic testing uncertainty
 - Relate results from the partially observed network to the national scale

Current Status

Data Collection Phase:

- To date 49 states have provided data
- Data entry is nearly completed

Analysis Phase:

- Has begun with descriptive analysis
- Development of a model structure will begin January 2011

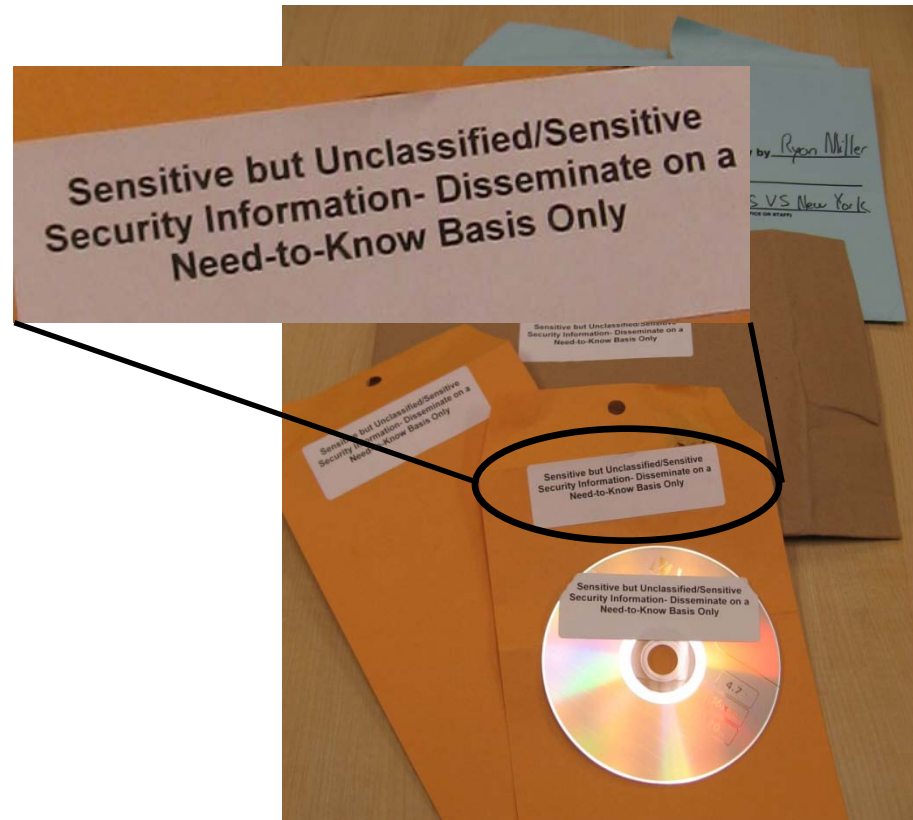


Challenges

Logistical Feasibility

**COPY OF EVERY CVI
BEFORE IT WAS NO
LONGER FEASIBLE AND
WE SWITCHED TO
PULLING EVERY TENTH
ONE.**

Data Sensitivity / Confidentiality



Current Status

Sampling Paper Records:

- 10% sample of supplied records

Data Entry:

- 8 students until September
- High priority states first
- Second level states will be entered as resources are available



frm_SwitchBoard : Form

Today's Date: 5/30/2010

Certificates of Veterinary Inspection Database

ENTER NEW CVI

CHANGE OR REVIEW CURRENT DATA

QUICK STATISTICS:

Total Records Entered:	3
Number States Entered:	3
Dairy:	0
Beef:	0
Records Per Day:	4.3333

Record: 1 of 1

Vs Veterinary Services
Safeguarding Animal Health

Colorado State University
Safeguarding Animal Health

NIMBioS
National Institute for Mathematical and Biological Synthesis

Colleen Webb

Colleen.Webb@ColoState.edu

Katie Portacci

Katie.A.Portacci@aphis.usda.gov

Ryan Miller

Ryan.S.Miller@aphis.usda.gov

