



An estimation of cattle movement parameters in the Central States of the US



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ABSTRACT

The characterization of cattle demographics and especially movements is an essential component in the modeling of dynamics in cattle systems, yet for cattle systems of the United States (US), this is missing. Through a large-scale maximum entropy optimization formulation, we estimate cattle movement parameters to characterize the movements of cattle across 10 Central States and 1034 counties of the United States. Inputs to the estimation problem are taken from the United States Department of Agriculture National Agricultural Statistics Service database and are pre-processed in a pair of tightly constrained optimization problems to recover non-disclosed elements of data. We compare stochastic subpopulation-based movements generated from the estimated parameters to operation-based movements published by the United States Department of Agriculture. Our novel method to estimate cattle movements across large US regions characterizes county-level stratified subpopulations of cattle for data-driven livestock modeling. Our estimated movement parameters suggest a significant risk of a disease successfully invading the US cattle systems.

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1. Introduction

Livestock systems serve significant roles for many regions across the world, yet past outbreaks of disease have demonstrated that they can possess a number of vulnerabilities (Brester et al., 2003; Ferguson et al., 2001; Keeling et al., 2001; Green et al., 2006; Kao et al., 2007; Bajardi et al., 2012). The livestock systems of the United States (US), though strictly regulated, may yet be found susceptible to foreign diseases such as Rift Valley Fever (Xue et al., 2013). The successful modeling and analysis of livestock epidemics for any region relies heavily on an understanding of the underlying system components. The three most critical elements in a practical epidemic model are the disease progression model, the geo-spatial characterization of the susceptible populations, and the spatial-temporal description of the interactions of individuals within the system (Colizza and Vespignani, 2008; Balcan et al., 2009). The models of disease progression are several and often independent of the region studied (May and Anderson, 1979; Barrat et al., 2008; Vespignani, 2012). Data-driven, spatial characterizations of populations are available through regularly conducted censuses (censi) (US census bureau, 2013; USDA-NASS,

2013). The third element, the interactions and movements of individuals within the system, has been shown to be as significant as that of epidemic parameters in metapopulation models (Balcan and Vespignani, 2012). Domestic livestock systems are well-suited for metapopulation models as the movements of livestock are controlled and the individuals are restricted to reside within populations rarely defined by their choice. Within the US, livestock movements are controlled by the cattle industries, primarily beef, dairy, breeding, and showmanship.

Within Europe, motivated by outbreaks of Foot and Mouth Disease, a number of governments have designed and implemented animal tracking systems, even to the resolution of individuals' daily movements. The databases created by these studies have generated very detailed characterizations of livestock movements for a number of European nations (Green et al., 2006; Kao et al., 2007; Bajardi et al., 2012; European Council, 2000; Bigras-Poulin et al., 2006; Brennan et al., 2008; Keeling et al., 2010). No similar program has yet to be mandated for the United States, although the National Animal Identification System has long been in preparation (Animal and plant health inspection service, 2015). In the US, a cultural appreciation of personal privacy, competition between meat production companies, and a U.S. Federal privacy protection law restrict the ability of the government to collect and release livestock data at a finer spatial resolution than is currently done through the United States

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Department of Agriculture's (USDA) Census of Agriculture (USDA-NASS, 2013). To address this challenge, a number of survey-based methods have been used to study livestock movements across small regions (Bailey et al., 1995; Forde et al., 1998; Bates et al., 2001; Dominguez, 2007). However, the national scale of US cattle trade and the potential for livestock diseases to impact the entire country necessitate movement data, models, or estimates to be determined for larger regions. Recently a study has been published of a nation-wide movement estimation based on a 10% sample of veterinary records from State border-crossing cattle shipments (Buhnerkempe et al., 2013). These confidential records were acquired from each State and measures were taken to protect the anonymity of the operations involved. This study could only capture shipments of cattle that crossed state borders and was unable to capture the livestock movements within each state. Further studies with these veterinary records have produced a model for generating model cattle networks and characterized a theoretical disease outbreak in the U.S. (Lindström et al., 2013; Buhnerkempe et al., 2014).

We formulate a large, convex optimization problem to estimate parameters describing the movements of cattle within 10 Central States of the United States. We collect cattle population and aggregated movement data from the United States Department of Agriculture's database and optimally estimate anonymous data points to construct a database of inputs for an estimation of cattle movement parameters. We design the estimation method to produce a high resolution of cattle demographic and movement parameters and to include the minimal set of assumptions. Our results produce county-to-county movement probabilities among stratified subpopulations as well as birth, slaughter, and expiration

rates of cattle for 1034 US counties. In Section 2, we describe the USDA data structures and challenges present in the database. We estimate non-disclosed data points and discuss the mapping of USDA data to inputs for our formulation. In Section 3, we formulate the estimation problem and describe the maximum-entropy objective and the flexible set of linear constraints with minimal assumptions. We solve the optimal estimation problem, display a subset of the results, and compare the results to both summary USDA data and a null model in Section 4. Section 5 summarizes this paper with a discussion of the results and a calculation of critical movement thresholds that demonstrate the potential for a disease outbreak in this region.

2. Data collection and structure

Every five years, the United States Department of Agriculture (USDA) conducts the United States Census of Agriculture (USDA-NASS, 2013). The National Agricultural Statistics Service (NASS) of USDA then summarizes and publishes a large set of data covering livestock, crops, operator demographics, and much more (USDA-NASS, 2013). As the most comprehensive database of US livestock statistics, the NASS database is used for our estimation of cattle movement parameters. In particular, we use data from the 2007 Agricultural Census as the 2012 data was not published at the time of this study. The data of interest to this work comes from section 13, titled "Cattle and Calves", on page 10 of the 2007 Agricultural Census. Section 13 also has a set of related instructions located on page 2 of the instruction sheet appended to the Agricultural Census (USDA-NASS, 2013). From the U.S. Census Bureau and their 2010 Census (of humans) in the United

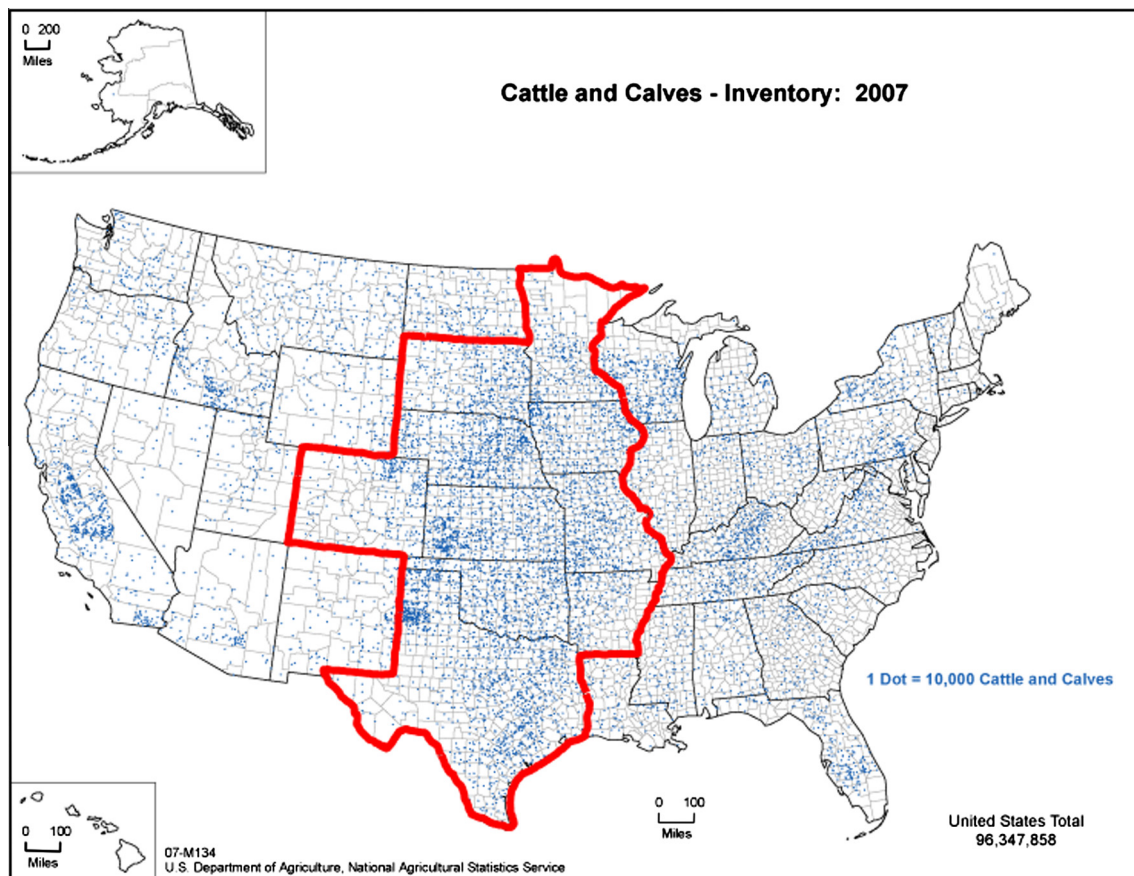


Fig. 1. The 10 Central States of interest are outlined with a red trace over the population distribution of cattle in the United States as provided from the United States Department of Agriculture (USDA-NASS, 2013). Each blue dot represents 10,000 head of cattle. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

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