Assessment of the demographics and network structure of swine populations in relation to regional disease transmission and control

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This dissertation is dedicated to my patient wife (Suzanne) and loving daughters (Ava and Molly) who, along with me, gave up our time together as a family.

Abstract

Commercial swine production has steadily evolved the into interconnected multi-site production systems of today. As a result, large numbers of growing pigs and breeding animals move from one location to another on a daily basis. The health of the national swine herd has improved dramatically, due in large part to this new production structure; but the increased network size and the long distances travelled pose obvious threats to swine health. As animal agriculture has become more sophisticated, our government resources have not kept up. Available datasets are inaccurate, fragmented, and offer limited definition of the population at risk and its nature. National efforts to improve livestock population data have met considerable public resistance, and as a result, progress has been limited. Knowledge of the populations at risk is of primary importance when trying to define the potential for disease to spread within and between these populations. Disease spreads by non-mechanical means (as in aerosol transmission of PRRS virus) potentiates the need for knowledge of the neighborhood. Given the dynamic and transient nature of our swine populations, the neighborhood's health status is constantly challenged by the most recent delivery of pigs into the neighborhood.

The following dissertation seeks to expand the knowledge of swine populations. Current geographic datasets were assessed for accuracy and reliability. In the event of a foreign animal disease outbreak the usefulness of these datasets would be of prime importance, as they will dictate the distribution of resources. Additionally, the use of satellite-derived thermal imagery to verify the presence of commercial swine is described, along with its estimated sensitivity and specificity. Any regional disease elimination program must consider all swine populations, therefore non-commercial populations (specifically, 4H exhibition pigs) are analyzed. Population size, seasonality, caretaker knowledge, presumed and measured health status, and relationship with commercial swine are defined. The physical movement of infected animals across the landscape allows rapid spread of a pathogen to occur. Volume, frequency, and geographic scale of movements will dictate how quickly and thoroughly an epidemic will proceed. For this reason, these are defined and displayed for pig producing areas at different scales.

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Introduction: Evolving challenges in swine disease management

Facilities and management methods for swine production have changed dramatically in the USA and other developed countries over the last 50 years. Many changes were specifically instituted with the goal of improving animal health [e.g., all-in/all-out (AIAO) management; multiple site production]. Several factors have changed in US swine production and are likely to influence disease rates. Included would be herd size, population structure, and dynamics; sources and health status of incoming stock; area density of pigs and other species; biosecurity practices; group sizes and animal density; replacement practices in breeding herds; pig flow (e.g., AIAO vs. continuous flow); housing systems; ventilation systems and air quality; sources, quality, and delivery systems of feed and water; hygiene and effluent management; nutritional programs; weaning age; and specific health interventions (e.g., vaccines)[1].

The fundamental principles of epidemiology dictate that these substantial changes in production systems should alter the patterns of disease occurring in swine populations. Indeed, previously prevalent pathogens including *Sarcoptes scabiei* var. *suis*, *Brachyspira hyodysenteriae*, *Trichinella spiralis, Toxoplasma gondii* and *Taenia solium* have been either eliminated or substantially reduced in modern systems[2-6]. On the other hand, the swine industries of developed countries have experienced two substantial pandemics over the last 20 years: PRRS virus[7] and Porcine Circovirus type-2 associated diseases[8]. The viruses involved appear to be highly host specific for swine and caused major economic losses to affected swine industries worldwide. Other agents that have become more prominent as swine production has intensified include *M. hyopneumoniae, H. parasuis, S. suis*, and *Lawsonia intracellularis*[9]. In the USA, for over 20 years PRRS has been unquestionably the most problematic disease confronting the modern swine industry. The capacity of the virus to spread locally among farms despite intensive biosecurity measures is arguably the most challenging feature of the disease, and has led to calls for cooperative efforts to control the disease at a regional level. The goal of the work conducted in this thesis is to enhance efforts for regional control of PRRS virus, focusing on the application of geographic information systems, spatial analysis, and the role of animal movements.

Use of Geographic Information Systems in livestock disease control and eradication

Understanding disease in a spatial context

There are many benefits to incorporating a spatial component in analysis of health information. Geographic knowledge of the locations of animal populations is vital to containing epidemics through identification and quarantine of high-risk populations and movement restrictions. Advances in information technology and software based geographical information systems have greatly increased the potential for capturing and utilizing spatial data in livestock disease management. This in turn has lead to advanced methods of spatial analysis, including recognized approaches for analyzing health data such as cluster detection, diffusion studies, interpolation, risk factor identification, and various types of regression analysis[10]. Cluster detection encompasses nearest neighbor analysis and cell count methods to assess the area density of disease events compared those expected if the disease were randomly distributed in space; this is performed using either unique points or contiguous areas on a landscape. Diffusion studies include line analysis (approximation of a disease 'front'), trend surface analysis (method of interpolation), and most notably network analysis which focuses heavily on the relationships between entities. The methods listed above do not require the use of a GIS, but rather make good use of data captured and maintained within a GIS.

Advances in techniques in sophisticated analysis still give present imperfect methods for understanding a disease process occurring on a geographic landscape. In a critical review of spatial analysis in disease research, Mayer[11] cites three areas of weakness in spatial analysis of disease- not enough is known about the nature of disease to assign causality, there are so many candidate risk factors that logic cannot point clearly to causality, and the methods used often do not properly address issues of scale. As more data is available for analysis, these three failings become increasingly important, as they will only be corrected by the researcher's analytic approach.

When a new or poorly understood disease occurs in a region, the spatial, temporal, and disease event data are presented using a GIS to both describe and analyze the situation. Bovine Spongiform Encephalopathy (BSE or 'Mad Cow Disease') is a non-contagious disease, with a long incubation period, that destroys the brains of cattle and is spread predominantly through prion-contaminated feed. Large numbers of cattle were affected in several European countries during the 1980's and 1990's and the epidemic continued even after bans on high-risk feed ingredients (particularly meat and bone meal) in ruminant diets. Because pigs and poultry are not affected by BSE, these ingredients continued to be fed to monogastrics. In Great Britain, Stevenson found that before the feed ban, the unexplained geographic risk was uniformly distributed across the county (there was significant clustering along a North-South gradient). However, after the ban, the same analysis showed that the unexplained risk was now clustered in part of the country - potentially due to some specific cause[12]. The author used a "pig/cattle" ratio, derived from government registers, as a proxy for the degree to which pig feed was manufactured and fed in various regions. Subsequently, a similar analysis in France found that after the feed ban, cattle were at significantly increased risk of BSE if they were in a pig dense area of the county[13]. In both cases the authors postulated that cattle feed was likely contaminated by hog feed containing ruminant tissues that was being manufactured at the same feed mills. Since that time, all feeding of meat and bone meal to any species (including swine and poultry) has been banned throughout Europe.

Postweaning Multisystemic Wasting Syndrome (PMWS) is a recently emerged disease (now known to be caused by Porcine Circovirus type-2) that gained recognition in major pork producing countries for its severe effects and its mysterious etiology[8]. In Denmark, the disease appeared first in late 2001. Researchers carefully identified and confirmed the diagnosis at case farms as they occurred[14], and performed a descriptive study to identify temporal and spatial clusters of disease. The results did, in fact, indicate two distinct spatial clusters and one spatio-temporal cluster. Since the study was performed as a retrospective case-control study, the clusters and additional descriptive information lead the authors to the conclusion that a new disease agent was emerging in Denmark, versus a systemic, national change in husbandry method. Although no etiologic agent was identified in this study, the clinical signs described are now largely attributed to some Porcine Circovirus type-2 (PCV2) associated disease and are generally preventable by vaccination for PCV2. These examples demonstrate how using GIS to visualize spatial patterns of disease and basic descriptive statistical methods lead researchers to a more refined understanding of the epidemiology of poorly understood livestock diseases.

Use of GIS in control and eradication of swine diseases

Mapping of affected farms has always been an essential component of disease control programs. Over the past few decades, computerized mapping tools have become more widely available to academic researchers, government agencies, and the general public. These geographic information systems (GIS) have allowed large amounts of data to be compiled, analyzed, and related across representations of the physical landscape. There are numerous examples of how a GIS has been incorporated into practical, functional tools to manage and/or eradicate swine disease. In Norway, zone level risk of swine *Mycoplasma hyopneumoniae* infection was evaluated simply by extracting basic information from a GIS (ArcView 3.1). The data were then used to run simulations with stochastic modeling software (@RISK), using basic assumptions about transmission potential over space[15].

In Hungary, a country with endemic Pseudorabies Virus (PRV), Solymosi, et al. developed a system called VetEpiGIS, to integrate epidemiologic methods and spatial data[16]. In this example only vector type data was employed. Closer to home, the state of Minnesota began using a GIS in the early 1990's to manage data and visualize disease status of farms and zones in their PRV eradication program[17].

In New Zealand, epidemiologists at Massey University have developed a suite of software products useful to increasing the understanding of livestock epidemics. Most notable is the EpiMAN program. This software incorporates components from multiple disciplines into a single decision support system. The software compiles descriptive geographic data (on an ESRI ArcInfo substrate), visually presents the mapped progression of epidemic progress, and creates pertinent reports for the various parties involved in disease control[18]. Furthermore, this software includes a database management system, incorporates expert systems input, and has a built in statistical analysis package. Besides the ability to manage a real-time animal disease scenario, EpiMAN also allows the user to simulate and forecast near and long-term conditions based on the available disease information[19]. The EpiMAN software met real-life field conditions during the 2001 Foot and Mouth Disease (FMD) epidemic in Great Britain. Stevenson sought to quantify the predictive performance of the software. It was found that EpiMAN was able to accurately forecast events during the first two weeks after initial cases were found. After that, too many confounding variables reduced the precision. This experience, however, does indicate the usefulness of a GIS based decision support system in controlling a costly disease epidemic[12]. Using the same software package with an additional module called Interspread, Morris[20] created a model using the 2001 UK FMD epidemic data. His model demonstrated the necessary impact of timely pre-emptive slaughter and the potential benefit of pre-emptive vaccination. An important feature of this article was that it was written and published during the 2001 epidemic, when the model was being used actively by government officials to help manage the disease crisis on a daily basis.

Disease dispersal via animal movement

The self evident risk of spreading livestock disease via livestock movements has been frequently documented. Rinderpest virus of cattle was repeatedly introduced, eliminated, and reintroduced in Europe, India, Asia, and Africa. The scale of these rinderpest epidemics was largely responsible for the establishment of the first veterinary school in Lyon[21]. The first detailed discussion of the specific risk that modern transportation plays in disease risk was published in 1970[22]. The author identified four key components that contribute to risks inherent in animal movements: 1) vehicles, 2) carrier animals, 3) route or travel corridor, and 4) time for exposure and stress. Since that time, livestock industries in developed countries, and particularly swine industries, have only increased their reliance on multi-site production, often over broad geographic areas. A set of papers published by Karsten, et al. describe the creation and validation of a model to simulate Classical Swine Fever (CSF) infection[23, 24]. The model did not track the specific risk a source farm presents to the receiving farm, but it did consider vehicle contact frequency along with several other modifiable stochastic parameters such as pig-pig contact frequency. While it included transportation risk, the sensitivity analysis of the model was more geared towards understanding the effects of incubation period, basic movement control, and different pre-emptive slaughter strategies.

Understanding how disease could propagate, spread, and be sustained in an environment made up of farms and villages was the purpose of a study in 2003[25] in which cats infected with Feline Leukemia Virus (FLV) were the subject. The author used a matrix to quantify relationships amongst cats, and their local community and this example considered the animals to be moving only locally and on their own volition.

Boots and Sasaki created a model to demonstrate the effect that spread over long distances had on increasing a pathogen's virulence[26]. Their work mostly focused on vector and water-borne diseases, but if the same principles held true for livestock diseases, one could infer that long distance movements of livestock between locations could broaden the mix of pathogens and give rise to the emergence of more virulent pathogens. This is a troubling prospect, considering that in North America large numbers of pigs and cattle are moving across both state and international borders every day of the year.

Shortly after the peak of the 2001 UK FMD epidemic, animal movement data was analyzed in a thorough descriptive epidemiologic summary[27]. Investigation into the early spread strongly implicated livestock markets and dealers in facilitating the spread of FMD through animal movement. The rapid geographic spread of the virus over most of the Great Britain was aggravated by a seasonal increase in sheep movement between farms, dealers, and markets. In another paper using data from the 2001 FMD outbreak, a point level disease spread model was used to assess the importance of animal movement[28]. While movement data was incorporated into the model, it was acknowledged that movement patterns in the UK were not well characterized in their livestock movement database.

Aerosol transmission in area spread of disease

Like transportation, aerosol transmission of livestock pathogens has great potential for spreading disease. In a very clear and informative summary, Stärk presents the aerosol spread potential for several different swine disease pathogens as well as their sensitivity to relative humidity. She suggested that producers focus on disease control methods (i.e. filtered air) that extend beyond basic biosecurity measures which do not mitigate risk of aerosol transmission[29]. Danish researchers wanted to study the risk factors for pig farms becoming infected with *Mycoplasma hyopneumoniae*[30]. The Cox regression model supported the hypothesis of airborne transmission of *M. hyopneumoniae* between pig herds as well as spread through movement of subclinically infected animals. Subsequent studies to assess the likelihood of aerosol transmission of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV)[31] also supported the aerosol transmission hypothesis. In a review of PRRS area spread research, Lager, et al.[32] indicated that the probability of local area spread via aerosols likely depended upon the characteristics of an infected animals' viremia (virulence and viral output) as well as the number of susceptible animals in an area.

More recently, researchers at the University of Minnesota[33, 34] have established a facility and protocols to study the potential for airborne spread of PRRS virus. This research setting, located in an agricultural area with few other pig farms, relies on a perpetually viremic (PRRS positive) population juxtaposed approximately 100 meters from barns employing different biosecurity protocols and containing naïve pig populations. The naïve populations are monitored intensively to detect new infections and the biosecurity protocols (air filters, coverall, gloves, etc...) are compared for effectiveness at preventing transmission of PRRS. Furthermore, this viremic population has been evaluated as a source for long-distance spread of both PRRS and *Mycoplasma hyopneumoniae*[33]. By collecting air samples at varying distances downwind from the infected populations, and by recording the relevant weather conditions, new knowledge of the long distance spread potential is coming to light. The published study revealed infectious aerosols collected at 4.7 kilometers away. Subsequent to this publication, Otake was able to collect infectious PRRS and *Mycoplasma hyopneumoniae* in air samples collected at 9.1 kilometers and 9.2 kilometers, respectively[35].

Shortly after the 1967-68 British FMD epidemic, a spatial analysis was presented to refute previous hypotheses about the spread of FMD after the initial case[36], and proposed the pattern of spread was consistent with unusual climatic events supporting the creation of 'lee' waves. This refers to the wind's ability to carry viral particles over the landscape, depositing them at regular intervals. The climatologic variables lined up in accord during the infective period to support his hypothesis. This and the other examples above demonstrate the potential issue that aerosol transmission presents to swine disease control efforts. Research on the 2001 British FMD epidemic showed that geographic (Euclidian) distance was more predictive of infection than the shortest or quickest driven route[37]. This would support the contention that aerosol transmission was a frequent mode of transmission, although the study also revealed a protective effect of natural boundaries (water bodies). Even though premises were geographically close, a narrow body of water seemed to offer protection from infection. This suggests some impact of common land borders but the specific components of this could not be defined.

Area spread of PRRS virus

PRRS virus is the most important endemic disease affecting pig farms in the US, with an estimated cost of over $560 million per year[38]. In a 2002 paper[32], indirect area spread was defined as disease transmission that results from vectors, fomites, or aerosols as opposed to direct horizontal or vertical transmission. The same author[39] put forth observational evidence of area spread of PRRS taken from recent field investigations. In that report, common viral genetics (ORF-5) among farms located close to each other suggested some mode of area spread. Indirect area spread has been increasingly identified in importance in the transmission of PRRS virus as herd biosecurity standards have improved. Several routes of indirect area spread have been investigated. They include insects, boots and coveralls, personnel vehicles, contaminated equipment and transportation trailers, and infectious aerosols.

Insects are prevalent in all swine facilities, but are also known to travel between different livestock facilities. Otake, et al.[40] in 2003, examined the potential for mosquitoes to harbor and transmit PRRS and showed that mosquitoes remained potentially infectious for up to 6 hours after feeding on an infected pig. Houseflies have also been identified as potential vectors of PRRS virus. Otake, et al.[41] determined that PRRS virus could remain viable and infectious in the digestive tract of houseflies for up to 12 hours. In 2009, a study[42] evaluating the potential for houseflies to transmit PRRS virus from an infected pig population to a neighboring naïve population reported PRRS transmission in two out of seven replicates, demonstrating the potential for housefly transmission events in commercial pig production settings. In this same Minnesota research setting, another author[43] was able to recover virus positive (therefore potentially infective) houseflies at distances up to 2.3km away from an infected pig population. These flies were verified to have originated from the experimental source facility, by both insect and viral genetic markers.

Use of genetic tools (restriction enzyme patterns and gene sequencing) to determine relatedness of viruses has also been employed to investigate area spread, with the hypothesis being that geographically proximate farms would have genetically similar strains of PRRS virus. Mondaca, et al.[44] found a significant negative correlation between geographic distance between farms and genetic similarity of PRRS viruses using data from one Minnesota county. While the route of spread of infection was never established, this study suggested that viruses were spread and maintained locally in that study setting. Given the high prevalence of multisite production (separate sow herd, nursery, and finishing) in current industry, local clustering of animal movement, offers a potential explanation for this local effect. This same effect of was not demonstrated in a second, similar study[45] of a large production area in Illinois. The author attributed the lack of local genetic homology to the impact of long-distance pig transportation events (i.e. new viruses were coming into a site and area via the movement of infected piglets, not aerosols or local fomite effects). However, in comparing these two studies, the contrasting observations likely arise from the different geographic scale of the study areas. The Minnesota study area was much smaller (farms located in a single county). The Illinois study area, by contrast, was much larger- most of the state of Illinois. A more recent and more thorough study by Shi et. al[46] pealed apart the lineages of PRRS virus isolated found over time from different areas of the county (states). Using standard viral alignment techniques and Bayesian coalescence analyses, the author was able to define the lineage of certain strains. After viral lineages were determined, estimates of viral exchange (transmission frequencies) were calculated between states. This analysis represents and important step towards understanding patterns of viral emergence over time and space.

In 2000, Amass, et al.[47] sought to determine the impact of people as potential vectors for PRRS. In her study, human nasal secretions, fingernail washings, and saliva were evaluated for the presence of PRRS as well the potential for contaminated clothing to transmit the virus. The study was not able to demonstrate infection in negative sentinel pigs, but did identify viral RNA (not necessarily infectious) in both fingernail washings and saliva in the hours and days following exposure to infected pigs. A later study[48] was able to demonstrate the truly infections nature of contaminated clothing and boots. Contact with PRRS infected pigs followed directly by contact with PRRS uninfected pigs results reliably resulted in transmission. This latter study also demonstrated the effectiveness of simple biosecurity steps (changing clothes and shoes and washing hands) to reduce the risk of infection. More recently, Pitkin, et al.[49] reevaluated the risks of boots, coveralls, and hands. As before, simple mechanical vectoring of PRRS occurred via boots, coveralls, and equipment. The multiple mechanisms for PRRS transmission support the need for comprehensive biosecurity measures to prevent introduction of the virus into herds.

In the US swine industry, it is not unusual for a single trailer to be used for livestock transportation to multiple locations. Additionally, a single truckwash facility may be used to clean multiple trailers after their use. Contaminated vehicles were investigated as a potential source of new PRRS infections by Dee, et al.[50]. In this 2004 study a scale model trailer was used to simulate field conditions in which PRRS could contaminate a trailer. Contaminating trailers with known quantities of PRRS virus successfully produced infection events in most replicates. Additionally, this study looked at the impact of commercial disinfection processes to kill PRRS virus. Results showed that only trailers that were washed, disinfected, and dried were safe to use, demonstrating the importance of proper trailer sanitation and drying for the prevention of PRRS infection.

In a series of studies, Dee, et al.[51, 52] evaluated the potential for PRRS to be conveyed on personal transportation vehicles and ultimately infect pigs. PRRS contaminated snow and mud were the initial source of PRRS infection that was then subsequently tracked through several locations, ultimately ending up in a simulated barn environment. Swine bioassay was used to evaluate the contamination status at multiple locations and to confirm the viability of the virus. These studies clearly demonstrated the high potential for fomite transmission, particularly in winter.

The capacity of PRRS virus to spread locally among farms despite good biosecurity measures has led to the opinion that collaborative efforts are necessary to control the disease. Regional programs for the control of PRRS have been attempted for some time. A regional disease program for PRRS in one French pork producing region demonstrated some success in control (limiting further spread) but not elimination of the virus shortly after its initial introduction[53]. This program relied heavily on producer participation (albeit incomplete). Besides identification of infected sites, highly influential sites were identified and given priority for diagnostic resources. Information was presented in 2004[54] about a regional PRRS control program in one South-central Minnesota county. A similar program was also initiated in a West-central Minnesota county and has since progressed to involve a large part of Northern Minnesota[55-57], currently known as the “North of 212” project.

The importance of data validity in understanding area spread of disease

Data Accuracy

In “Data Quality: The Field Guide”, Redman points out the hazards of dealing with inaccurate data[58] and lists 4 ways to deal with ‘polluted databases’: 1) deal with the downstream impact, 2) conduct periodic mass cleanups, 3) conduct routine point in time error catches before they are entered, or 4) find and correct the source of the error. The last option presents the greatest savings of time and money, and would be the choice for anyone striving for data accuracy. Rytkönen warns of misapplication of GIS in spatial epidemiology if data are not valid, accurate, and complete, and at the same time advocates the need to develop solid quantitative applications with the data to more fully understand influential covariates in epidemics[59]. It is important to note that most point-level disease models assume perfect positional accuracy for farms, while there may be considerable error present. Modeling efforts using 2001 FMD epidemic records[28] and a poultry disease control project on the Delmarva Peninsula[60] revealed significant point-level inaccuracy of farm locations. In poultry disease project, 88% (212 of a sampled 240) of database-known farms were in fact functioning poultry farms. Furthermore, the mean point-to-point error distance was 990 meters.

A question that arises invariably is where to establish the farm locations, a topic addressed by Peter Durr [61]. He posits the question out as a choice between various polygons (the area of the farm), the polygon(s) centroid, or the specific location of buildings (barn or residence). In another article on this topic[62], 500 different farms were studied to determine what method best represented ‘the farm’. The metric for judgment was distance of various points to the farm centroid and percentage of farm areas captured by selecting specific points. He determined that the ‘main building’ on the farm was the best point for geo-referencing the farm. The study also illuminated the potential weakness of using any of several methods or data sources to approximate the locations of the farms, and call for a consistent classification algorithm to define the various geographical entities of a farm. The differing situations of grazing animals and animals raised in confinement would also need to be taken into account in developing a standard approach.

Data availability

Acquiring geographic data is becoming increasingly easier. Various government agencies maintain data on farm specific locations or at least present aggregated zone-level data. Whether it is the use of agriculture census data related to population census data in Canada[63], farm locations found in the Agriculture Property Registry in Norway[15], the Danish Central Husbandry Register[64], the Belgian Identification and Registration (I&R) database[65], the German HI-Tier[66], or the USDA[67], large standardized datasets exist throughout the developed world. In addition to farm location information, in some countries there are ancillary datasets collecting animal movement information, which can be used in constructing farm-farm networks.

Recently, the US began the process of creating and implementing a system that will identify every livestock premises w/ coordinates as well as identifying every animal or animal group that moves between these locations during its lifetime[68]. The system is call the National Animal Identification System (NAIS) and was planned to be fully implemented by early 2009, with the ultimate goal of identifying all animals and sites that have had disease contact within 48 hours of discovering foreign animal disease infection. Most recently, due to poor support at the state and farm level, this program has been modified to be more flexible and more ambiguous, allowing more state-level enforcement and implementation and initially only requiring records for interstate animal movement[69]. Whether, strictly enforced as initially intended or modified to appease detractors, this is an important development, because it presents the first time that farm location and animal movement data will be collected for use in future disease control or elimination efforts. Disease control projects such as the Minnesota Cooperative Mapping Project for swine disease can utilize such a refined location dataset for the purposes of farmer driven disease elimination[70].

Resolution

As important as availability, the spatial resolution of the data determines its suitability for different analyses. A review by Graham, et al. describes some of the issues concerning data resolution in epidemiology[71], and called for modeling and analysis to be performed at the scale true to the function of the data. For example, early in the Minnesota pseudorabies (PRV) eradication program the farm level resolution was set at a 40 acre area[17], an artifact that still persists in the system today. During the PRV eradication program in Illinois, county level measurements were used to understand the PRV epidemic in the larger scope of the state[72]. In Sweden, a study of foot-pad dermatitis in broilers (poultry) was performed using data aggregated to a very large level, the Swedish two-digit zip code. Results showed that when the individual farm effect was removed, this coarse resolution failed to provide significant results[73]. In a California study on deep muscle abscesses in horses, it was noted that using the centroid of zip codes to identify and characterize horse locations was not accurate enough to understand the animal-animal disease spread dynamics that drive an epidemic event[74].

Characterizing swine populations

Effective regional control of animal disease requires an understanding of all reservoirs of infection and of mechanisms and risks of pathogen transmission. For highly host specific agents such as PRRS virus, the at risk populations are limited to the family Suidae. In addition to commercial swine herds (meaning herds kept with the primary objective of income generation from pork production) many other swine populations exist. These include feral or wild pigs, pet pigs, hobby farm pigs, and pigs reared in youth education programs (e.g., Future Farmers of America and 4-H).

Feral Swine

Feral swine, or “wild pigs”, are not native to the US. They exist as a mixture of escaped domestic swine and true wild Eurasian swine released intentionally for sport hunting. A report[75] summarizing US feral swine populations and the potential risks they pose to US commercial swine populations puts forth recent population estimates of three million animals in Texas alone and four million for the entire US. If accurate, this is approximately 6.2% of the size of the US commercial swine population[76] (September 2010 estimate of 65 million head). The same report indicated that feral swine populations were known to exist in 39 states in 2004, mostly spread throughout California, the Deep South, and the Southeast US. Ongoing expansion of feral pig populations in the USA is depicted in maps generated by SCWDS (Southeastern Cooperative Wildlife Disease Study)[77], which show feral swine ranges steadily progressing from 1982 to 2004

(Figure-1). The authors give four reasons for this marked increase in range- 1) intentional release of animals into habitat, 2) effects of population growth, 3) escape from domestic production, and 4) habitat alteration by humans and global warming.

The critical importance of feral swine populations lies in their potential for disease transmission to commercial swine populations. Thirty important bacterial and viral pathogens and 37 parasites are known to be carried by feral swine. Much attention has been paid to the importance of feral swine in Europe, where classical swine fever (CSF) has been a constant threat to commercial production. In 2000, in Germany, 59% of index cases from the previous decade were due to primary contact with infected wild-boars[78]. Fortunately the US has remained free of both CSF and FMD. However, the US wild pig population has long been known to be endemically infected with brucellosis and PRV which have been eliminated from the US commercial swine herd.

In 1993 and 1994, Gipson, et al.[79] examined and tested twenty feral hogs in Kansas and found no strong evidence of PRV, Brucellosis, or PRRS infection. This wild pig population was relatively isolated from other wild pig populations and likely did not have the same disease pressures as would be found in other geographies. In 1996[80], a sampling of 120 Oklahoma feral swine tested for evidence of leptospirosis, brucellosis, PRRS, PRV, SIV, TGE, and vesicular stomatitis virus (VSV). These samples revealed previous exposure to Leptospirosis, PRV, and SIV, with all other test results (brucellosis, PRRS, TGE, and VSV) being negative. Gresham, et al.[81] tested 227 trapped feral swine in South Carolina in 1999 with similar findings. In this study, 61% of animals tested were seropositive for PRV and 44% were seropositive for brucellosis. In 2001 and 2002, Corn, et al.[82] sampled feral swine at 10 sites in the Southeaster US. The authors found pigs seropositive to PRV at all 10 sites with an overall seropositive percentage of 38%. In previous samplings at these sites going back as far as 1979, feral swine have consistently been shown to be seropositive to PRV. A unique study in Texas[83] (from 2004 to 2006) demonstrated the real interaction patterns between feral and domestic swine. By placing GPS collars on 37 feral swine, the authors demonstrated overwhelmingly that feral swine will regularly approach commercial swine facilities to within 100 meters. The associated serologic testing demonstrated seropositivity for PRV and brucellosis, but not for PRRS or CSF. More recently, in 2006 and 2007, Corn, et al.[84] tested serum from feral swine in North Carolina and South Carolina for PRRS, PRV, Brucellosis, PCV2, and multiple types of SIV. These feral swine populations were shown to exist in close proximity to concentrated commercial hog production areas. The results demonstrated consistent exposure to SIV and PCV2, and a lack of exposure to PRRS in both states. Interestingly, the feral swine tested in NC did not possess antibodies to PRV or brucellosis. A 2008 study[85] of SIV exposure in 875 feral swine located in six states demonstrated low but detectable seroprevalence (1% to 14.4%) for the H3N2 type of SIV in three states and only one county with antibodies against the H1N1 type of SIV. In 2010, Baker[86] tested 50 feral swine trapped in Oklahoma and found the population to be significantly seropositive for *M. hyopneumoniae* (32%), PCV2 (42%), and H3-SIV (40%). Only one animal tested positive for PRRS or H1-SIV, consistent with the expected rate of false-positive results with the tests performed.

The body of evidence concerning feral swine in the US allows for some reliable assumptions about the population. Both Brucellosis and PRV are established, albeit inconsistently, throughout the national population. When investigated, H3-SIV appears to be the dominant circulating strain of SIV. Finally, the almost total absence of antibodies to PRRS, in multiple samplings, would suggest very little circulation in feral swine populations. The biggest risks that feral pigs likely pose to commercial production are PRV or brucellosis.

Exhibition Swine

Livestock exhibition is a colorfast component of the cultural fabric throughout the US, but very little has been formally published about the disease risks linked to exhibition swine populations in the US. Many of these animals are purchased in the spring to be shown during summer at “county-fair” type livestock shows through 4-H programs or the like. The annual tallies for 4-H swine program participants have ranged from 140,000 to 212,000 (1996-2003)[87] and since participants usually obtain multiple swine for use in these programs, the expected number of 4-H swine would not be less than 200,000. In addition to 4-H, swine are exhibited as part of other programs such as FFA or they may simply be exhibited as “open-class” entries, not affiliated with a youth program. Swine used for exhibition may have very little in common with swine for commercial production, since traits desirable for show are often not desirable in commercial production. As a result, exhibition swine often exist parallel to commercial swine and constitute a substantially different industry.

A study to demonstrate the risk presented by large livestock shows[88] reported information from 556 of 753 households that showed pigs at the 2002 Indiana State Fair. The authors were able to determine the approximate destination of only around 61% of the animals. There was no comprehensive system in place to track movement of the show pigs and the author concluded that such livestock shows are an effective means to rapidly disseminate a livestock disease epidemic.

One-hundred and thirty-seven exhibitors at the 2005 California State Fair responded to a biosecurity and animal movement survey[89]. The average number of exhibitions that had been attended during past 12 months was three (ranging from one to seven). Ninety-seven percent of the animals being shown would return home after the fair, and of the 73 swine shown, 66 (90%) would be returning home. Only 26% of the returning animals would be kept in some type of quarantine away from other animals. This survey presented further evidence of inherent risk associated with exhibition animals.

An observational study[90] of Australian livestock shows in 2006 showed that over 30% of at-show feeding events were "swill" feeding. It was also discovered that many shows relied on only the owners to monitor the health of their animals; of the staff charged with this task, only three percent had training on disease recognition. This study demonstrated potential for infection and dissemination of swine diseases due to laxity of biosecurity at exhibition events.

These studies collectively demonstrate the current dearth of animal health education and logistic documentation involved in exhibition swine both in the US and abroad. Development and refinement of disease control programs must include this sub-population of mobile, disease-susceptible animals to be comprehensive.

Pet Pigs

A further segment of non-commercial swine populations is pet pigs which are kept as domestic pets and not raised for food. Typically they are categorized as either "miniature pigs", "potbellied pigs", or "tea-cup pigs"[91, 92]. In California, 400 pet pig owners were surveyed[93] with questions about their demographics, husbandry, animal movements, and contact with humans, other pet pigs, or livestock. Respondents (106/400) indicated that usually only one or two pigs were kept in a household, that one third of respondents owned other livestock, and that three percent of owners kept commercial pigs. Veterinary care was almost exclusively provided by small animal veterinarians and post-mortem examinations were unlikely to be performed. Additionally, forty percent of owners reported feeding food waste to their pigs.

Caretaker Knowledge and Behavior

Disease prevention, by definition, is driven by a caretaker's preventive actions. These actions likely reflect both the attitudes and education of the caretaker. These in turn affect caretakers' implementation of biosecurity steps and interactions with veterinary service providers and government officials.

The attitudes of farmers are a likely influence on the success or failure of biosecurity programs. A 2008 study[94] in the United Kingdom sought to characterize attitudes and opinions of farmers, veterinarians, and industry professionals. The results showcased obvious differences in opinion. Farmers felt that government would need to do more to ensure successful disease control. Veterinarians thought farmers' willingness to invest in biosecurity methods was the most important.

Ellis-Iversen, et al. [95] surveyed 43 cattle farmers surveyed in the United Kingdom from 2005 to 2006, using human behavior theory to understand attitudes towards biosecurity. She found that more proactive farmers identified the economic constraints that hindered implementation of practices; and also that less active/proactive farmers said they would rely on their own veterinarians for advice on uptake of these practices. These results demonstrate the potential importance of veterinary input in motivating less proactive farmers.

Among 421 of 609 pig farms surveyed in 2005, responses were used to describe biosecurity practices in Belgium[65]. It was found that few producers used biosecurity measures such as showering (2.1%) or downtime for people entering their farms (7.1%). The survey also described the Belgian swine farm demography, of which over 8% were hobby farms; these were much more likely to feed kitchen waste. These smaller farms also employed less standard biosecurity practices than larger farms. Exposure to other livestock species was indicated in well over half of respondents, who also kept cattle, sheep, or other livestock on their premises.

A survey of 172 Spanish pig farmers in 2000 and 2001[96] studied the relationship between farmer perceptions and implemented biosecurity practices. The authors found a general correlation between farmers' perceived importance of a biosecurity measure and its implementation at his farm. It could not be determined if the attitude preceded the action or if the action inspired the attitude, but the author concluded that future efforts should be made to educate producers on the true importance of various biosecurity measures, in hopes that changed attitudes would mean improved biosecurity.

A survey of 153 Swedish pig farmers[97] following a 2007 PRRS break sought to better understand how information is disseminated and biosecurity practices are adopted in response to disease outbreaks. Among the author's findings were that proximity to the outbreak was associated with greater awareness; that larger farms were more likely to be aware; and that in general the information communicated by the government to farmers was insufficient. Forty-eight percent of farmers were not aware of how PRRS could spread and only 56% were aware of the clinical signs caused by PRRS. This study clearly indicated the need for more producer education on PRRS clinical presentations and epidemiology to better control any future outbreaks of the disease.

Overview on Methods of Spatial Analysis of Animal Disease

An early instance of using GIS and health data to analyze and understand disease occurred in 1960's. Reif and Cohen approximated the home locations of 1,007 dog owners and determined that a significantly greater proportion older dogs living in an urban environment developed severe lung changes[98]. In addition, they overlaid data from the Philadelphia Department of Health of dust concentrations in various parts of the PA landscape that supported the association between disease and this environmental risk factor.

Hungerford lists three basic issues regarding the use of spatial statistics in animal disease: 1) is disease clustered?, 2) do diseases and risk factors have the same geographic distribution?, and 3) do relationships exist between the variables at different geographies?[99] In a comprehensive review of spatial and temporal cluster detection techniques, Carpenter reviews and cites several examples of analyses that have been used in human and veterinary medicine[100]. These include methods for detection of spatial clusters (linear, aerial, and point clusters), temporal clusters, and simultaneous time-space clustering. Some examples of these are given below.

Time-Space interaction

Methods that consider the effects of time and space in disease spread are extremely useful and are commonly engaged to determine if there is space-time interaction, which is a hallmark of infectious disease. These include use of the spatial scan statistic for cluster detection and the space time K-function. Region-specific survival analysis is yet another method by which different geographies could be compared.

The Barton & Knox method was used to analyze the space-time interaction in Swedish poultry flocks[73] and Corynebacterium infection in California horses[74]. The Barton method relies on point-level data (or data that has been aggregated to a centroid point). In analysis similar to ANOVA, time interval data are treated as covariates in evaluating the physical distances between cases. One weakness of this method is that smaller distances (important for contagious disease spread) bring less weight to bear on the test statistic (Q). The Knox method requires the user to set cut-off values for time and distance prior to running analysis, and so is somewhat subject to user bias[100, 101]. Barton's method was used by Singer et. al[102], but failed to detect spatial-temporal clustering of antimicrobial-resistant bacterial isolates in California.

Ederer-Myers-Mantel (EMM) method of time-space cluster analysis can be used to confirm the temporal clustering at a specific location and is often preceded by a spatial test method such as Moran's I. Fosgate et al.[103] studied cases of human brucellosis in California using this method. This analysis demonstrated significant time-space clustering, which the author suggested was attributable to ethnic population effects. In order to better understand how Bovine Spongiform Encephalopathy (BSE, 'Mad Cow Disease') spread, the Ederer-Myers-Mantel time space cluster test was used to confirm clustering of disease events over time[104]. This information was used to understand the origin of infection (potentially contaminated feed).

Space-time K-function was used to compare actual case occurrences with the number expected during the recent British FMD epidemic[12, 105]. This adequately differentiated unusually high disease occurrence over a region and showed differences between regions. The space-time K-function has also been used by French, et al. to understand the occurrence of Equine Grass Sickness[106] and Sheep Scab[107] in the UK. In both cases they were able to identify strong evidence of space-time clustering. These were important findings, because the epidemiologies of these two diseases are poorly understood. In the case of Equine Grass Sickness, the analysis supported the notion that the disease was spread via some contagious contact between infectious horses or some localized risk factors, rather than some general environmental condition. For Sheep Scab, the disease agent is a mite, but impact of government control programs and season in general was not well understood. This work demonstrated multiple cyclical time-patterns (time clustering signals) and definite neighbor effects (spatial clustering signals). Additionally, the effect of space-time interaction could be shown for the disease events.

The scan-statistic is repeatedly seen in epidemiologic studies and can be thought of as a “moving window” that travels looking for statistically unusual numbers of events within its border. Using the scan-statistic in regions of low pig density, Italian researchers were able to identify a single significant cluster of PRV infected herds. This cluster helped to characterize the infection as being driven by persistence in the region vs. individual farm effect[108]. In a case where livestock was the suspected source of human giardiasis in Ontario, the spatial scan-statistic revealed clustering in several regions[63]. Two of the regions had clusters that could be associated with livestock, while others had no explanation (low livestock density). In this case the scan-statistic was useful in identifying unusual occurrences and relating them to known and unknown causes. The author suggested the use of the spatial scan-statistic in a regular program for monitoring of several endemic disease conditions.

Regression methods

In an effort to more completely understand the impact of multiple factors (including location or proximity) on disease risk, regression methods are often employed. To understand the factors involved in PRV infection in Hungarian swine operations, simple regression methods were used to examine associations between spatial attributes and the presence of antibodies to PRV. In this case, proximity to lakes and highways was significant, but nearby uninfected hog farms were not a significant risk factor[16].

Another common approach is survival analysis (time to event data) using Cox proportional hazard regression analysis. This method was used on a dataset of PRV infected hogs farms in Minnesota[109] and significantly elevated risk was found for locations close to lakes or rivers and the density of herds within a 5km radius. In another study of PRV in Illinois, Cox proportional hazards regression analysis examined factors associated with time under quarantine[110]. Again, regional farm density was a significant factor, but only when considering vaccinated herds. Cox regression was used after the 1997-98 hog cholera epidemic in The Netherlands where neighbor's herd size and distance to neighbor were found to significantly influence disease risk of farms[111].

In Denmark, Cox regression has been used to evaluate a farm's risk of becoming infected with *Mycoplasma hyopneumoniae*[30]. The results supported arguments for airborne transmission of this pathogen, since proximity to infected farms was significant in a model including another non-spatial risk factor (purchasing pigs from multiple sources). A different Danish study focusing on infection with PRRS virus used Cox regression to analyze several potential risk factors[112]. In that model, infected neighbors presented a clear increase in risk. When their model was expanded to include approximate distance, size of neighboring farms, and exposure time, the risk of proximity was even more apparent.

Kernel Estimation

The kernel function in mapping is the process of compiling the density functions (kernel estimates) of individual points on a raster landscape, to create a smoothed, continuous landscape. Kernel estimation was used by Mintiens, et al. in a Classical Swine Fever risk analysis in Belgium[113]. A kernel estimate was derived for each farm to determine the density of the local neighborhood. This, in turn was referenced against the actual disease events from historical record, revealing that the higher the kernel estimation for neighborhoods on a raster surface, the higher the risk of infection. Similarly, in Argentina, kernel function was used to gauge FMD outbreaks per square kilometer[114]. Here, 127 counties were divided into 3085 individual cells to allow user to establish differential risk across a surface. The raster surface of this density was used to find significant correlation between herd size and FMD transmission activity during three different stages of the 2001 FMD epidemic. Later, FMD transmission potential was determined using data from the 2001 UK FMD epidemic[37]. The authors calculated a transmission kernel for shortest route, quickest route, and simple Euclidean distance. These were compared for their predictive validity, revealing that a simple Euclidean distance-based kernel was the most appropriate risk parameter to use. One exception to this was the observation that some natural boundaries (water bodies) were protective.

Social Network Analysis

Social network analysis (SNA) examines social structures- connections among related parties and their association with, or impact, on the characteristics of those parties. Hawe[115] lays out several basic terms used in understanding the components and analysis of social networks. There are two elements- the "actors" (individuals) and their "relational ties" (the relationships between individuals). Networks can be defined by a relationship type within a fixed set of similar actors, or they may range outward by including multiple relationship types among different groups of actors. The ties between actors are used to generate descriptive statistics for the individual actors. There are several types of measurement each with its own computational rules. "Centrality" measures are commonly used, referring to an actor's connectivity to other actors; and these range in their specific focus (closeness, betweenness, etc…). The size and complexity of networks (components, isolates, cliques, etc…) is also a common nomenclature in the study of social networks. The directionality of networks is reflected more specifically in terms like outdegree (number of nodes that are receiving from the node in question), indegree (number of nodes that are sources for the node in question), betweenness (how often a node lies on the shortest path between other nodes), strong component (directed network in which all nodes are accessible), and weak component (undirected network in which all nodes are linked).

SNA has even been used in the investigation of terrorist networks. Krebs[116] described the social network of the 9/11 terrorists. He also differentiated prospective/predictive use from retrospective analysis, describing the difficulty of predictive use due to the difficulty of obtaining detailed network data in a timely manner. This concern may also hold true for predictive animal disease modeling. Another interesting observation from this paper was the intentional fragmenting and isolation of smaller individual networks, to isolate them from the "contagious" risk of being discovered by authorities. This risk isolation concept could also be directly applied to the control of animal disease.

Recently there has been an increased interest in using tools from the social sciences to understand and predict animal disease risk. Social network analysis (SNA) has been used in understanding human disease issues. In a paper describing this application, Friedman and Aral define three types of potential networks in health-focused scenarios[117]. Risk-potential networks show a pattern of risk linkages between individuals. Ego-centric networks consider the linkage relating to only one individual at a time. Sociometric networks consider a large number of individuals and all of their linkages. Wasserman lists two mainstays of SNA- visual display and creating a probabilistic model of outcomes[118]. Furthermore, he describes the usefulness of SNA as providing a vocabulary for thinking of interconnected networks, allowing the mathematical analysis of relationships, and the ability to prove theorems about social structures[119]. Social network analysis has found heavy usage in epidemiology purely as a visualization tool.

Social network analysis for studying human disease

Network analysis methods have been applied to HIV transmission research. David Bell, et al. worked extensively to model the transmission of HIV amongst defined populations[120]. As part of this research, the social characteristics of different subpopulations were studied to understand their impact on disease transmission using classical statistical methods[121]. A study was designed to evaluate SNA as a tool to understand and identify transmission risk[122]. The results of model simulated disease spread were compared to measures of centrality from SNA. The network analysis applied to the same set of actors but with addition of relationship matrices. Since there is a fairly accurate estimation of several behavior-associated risks (i.e., risk of infection during unprotected sex), a model simulation could be created to estimate the risk of infection given a set of behavior patterns. This same set of behavior patterns was analyzed with UCINET[123] software for SNA. The results of the two were compared and it was found that the output from UCINET was a very good approximation for the risk estimated by the complex disease simulation. To evaluate HIV risk, model simulations were performed with different risk assumptions[124], and then evaluated the social network analysis output to compare methods. This modeling exercise suggested that the simple use of "degree centrality" to identify high risk individuals was as valid as other methods. These reports suggest that when considering risk of infection for an individual actor/agent (and by analogy- animal or farm), SNA may be a valid method.

Network structure appears to be important in disease spread. In 1999, one paper[125] evaluated structural elements in two social networks and their impact on sexually transmitted disease prevalence. While no statistical measures were presented in the paper, the author indicated that as the groups were measured over time (during the 80's and 90's), as networks intensified and grew disease transmission went up (for syphilis), but as they fragmented disease transmission went down (for HIV). Following a network study in Colorado and Manitoba, Jolly, et al.[126] suggested that smaller, peripheral network structures outside of core networks could be the cause of "endemic" disease patterns, compared with rapid rises in prevalence seen in more intense, larger networks. These observations indicate the likely importance of overall network structure in contrast to an individual actor's network characteristics.

Work with SNA and human disease has also incorporated geographic distance between agents. In a study of 595 HIV at-risk people living in Colorado Springs, CO [127], geographic distance between actors was positively associated with social distance and it was concluded that individuals had a greater chance of becoming infected because of the increased probability of an infective contact living in their proximity. SNA was applied to the study of *Chlamydia* infections in a sexual network[128]. The authors defined the social distances in standard SNA terminology, but also applied geoanalytical techniques to the data. The results showed areas of case clustering that correlated with the measured sexual network. SNA provides a formal structure for describing and analyzing relationships amongst actors in the context of disease transmission, and can be analyzed in tandem with geographic distance in disease modeling.

Going beyond infectious diseases, obesity has also been studied using social network analysis methods. In 2007, obesity was evaluated[129] as a "contagious" condition and followed the spread of obesity between individuals in a social network. Using individuals enrolled in the Framingham Heart Study, BMI (Body Mass Index) was recorded for individuals. The study showed clustering of obesity within the larger network. Using successive time intervals as a proxy for causation, the author was able to conclude that a person had a (statistically significant) 57% percent chance of becoming obese if their friend had previously become obese. Similar observations were also reported for siblings and spouses. Because of the intense data collection efforts of the Framingham study over successive years, this study was able to perform good causative speculation on a non-infectious disease condition. It is likely important that the very large datasets of the Framingham study enabled significant relationships to be detected. Difficulty in obtaining comprehensive data sets on network relationships may limit the application of these approaches in veterinary medicine.

Use in animal disease study

Dube[130] reviewed the use of social network analysis in livestock disease modeling and analysis. In this work, the author translated much of the standard nomenclature of SNA for application in understanding livestock disease transmission. For example "Nodes" are farms, and "arcs" can represent livestock movements between farms. Indegree measures the number of shipments, animals, or farm relationships that send animals to a given farm. Outdgree is the opposite. Within the study population, weak components are undirected networks consisting of nodes that may not have reciprocal ties. Strong components, on the other hand are networks in which all nodes are mutually accessible, having no isolated elements.

The movement of animals is arguably the most relevant component farm-to-farm relationships. A study commissioned by the International EpiLab in Denmark attempted to apply the concepts of SNA to swine and cattle disease risk[64]. In this project, farms were considered as nodes and animal movements were considered as links in the network. The paper stopped short of performing any formal network analysis functions and the resultant output was mostly descriptive and not analytically interpretable. Network analysis is by its nature is a visual method, so there was good visualization of farm networks, but no quantification. Further discussion in the paper demonstrated the variable farm density across Denmark, but there were no connections drawn between geography and the network analysis. There was, however, a detailed description of animal travel distances, based on a census of livestock movements maintained by the state. This dataset was a complete census of all livestock animal movements (origin, destination, and date) in Denmark.

A further attempt at applying SNA in animal disease modeling focused on the potential for hog cholera transmission in Sweden[131]. Graph theory is the mathematical study of directional graphs and is the mathematical foundation for social network analysis. The authors used the term "graph theory" to describe the system of matrices which described the relationships between actors (farms) in the model. In addition, a model simulation for hog cholera spread was created. Again, in that paper there was no true use of network analysis methods to describe the risk other than for visualization. As in Denmark, Sweden maintains a complete tally of animal movements between their farms.

An advanced application of SNA in epidemic modeling addresses the initial outbreak data from the 2001 UK Foot and Mouth Disease (FMD) epidemic[132]. In this example, actual farm-level outbreak data were obtained. Retrospectively, SNA was applied to animal movement events from the beginning of the disease epidemic. These data were then analyzed by several SNA methods, including 'relative betweenness', k-neighbors, and structural equivalence. Attributes were applied to nodes which were then grouped by dissimilarity with a hierarchical clustering method. The author found that several SNA attributes were able to identify nodes that were determined to be epidemiologically important early in the outbreak.

Consider the impact of farm location and routine contact (direct or indirect) between animals through livestock shows or human disease vectors. Webb studied sheep populations in Great Britain using matrices and graph theory to demonstrate the risks to individual sheep farms from being a member of a network[133]. In this study two networks were created. One network was of farmers who attended the same show, and the second was comprised of farmers that were close to each other - clusters of geographic proximity. Risk could be assigned to membership in either network. This study also linked the two networks to create a third, comprehensive, network by way of secondary calculated matrices. This study did not evaluate the data based on measures of centrality, but rather focused on selected descriptive statistics for the basic network. These included geodesic distances, number of disconnected components, diameters, and fragmentation indices. This work also offered good visualization of networks overlain on geography. Another use of sheep population and movement data[134] defined various network structures (giant strongly connected component; giant weekly connected component; giant out component; and giant in component) using a complete network matrix. While not explicitly using these components as part of the analytic method, the author used them to define the size and dimensions of the Scottish sheep population to validate her study population, which in turn was being used to define and understand disease reproductive rate (R_0) for epidemic modeling.

In California, a three-county region was analyzed to determine FMD disease risk amongst several species of livestock with varying direct and indirect contact rates[67]. This work was unique in that it included several species and incorporated human activity (visits by managers, veterinarians, and others). The authors obtained data from a mailed questionnaire. They then calculated approximate travel distances based on some assumptions and together with the specific farm information, created descriptive summaries. The strength of this paper, again, was mostly in its descriptive visualization of farm locations and transportation routes. It did offer insight into the potential importance of non-animal network factors that might be captured for analysis. In a paper showing results from a similar type of survey in New Zealand, Sanson[135] investigated movement patterns on sheep and cattle farms during busy and quiet times of the year. The movements included animals, people, and other items. This data did not lend itself to SNA, but it did (as in the previous example) describe the interconnectedness of modern farming operations in that country.

Social network analysis can be used in predictive modeling. Natale, et al. [136, 136, 136, 136, 137] examined the movement patterns of cattle in Italy to calculate values for social network analysis parameters. The author then performed several disease spread simulations, by successively removing certain farms from the population, based on various network characteristics. These simulations revealed that significant reductions in disease spread resulted by targeting farms with higher network values. Specifically, removing the nodes (farms) with the highest 1% of degree centrality values resulted in an 88% reduction in infected farms. Compare this with the random elimination of 20% of farms, which only offered a 47% reduction in infected premises. This analysis suggests that use of knowledge of network relationships and the characteristics of individual farms to direct strategic responses targeting specific farms of epidemiological significance could be a powerful approach for containing epidemics of animal disease.

Values for network attributes generated by social network analysis give insight the nature of farms being studied. In 2010[137], social network analysis methods were used to evaluate the movements of cattle in Italy. In this publication, the author proposed a new centrality measure called Disease Flow Centrality as a more useful tool. However, in simulations using traditional centrality measures compared with Disease Flow Centrality, no advantage was seen and the author concluded that this measure was generally not advantageous to use. Regardless of the lack of findings, however, the new measurement was a logical integration of disease transmission characteristics found in farm-to-farm relationships (animal movements). Geographic proximity was incorporated into the model, but only at the beginning of the simulation during the "seeding" process. Another descriptive and analytic study[138] of cattle movement networks demonstrated the use of network measures (outdegree centrality, weak component, and strong component) alongside an infection chain model for three consecutive years of cattle movements. In this study the author found relatively small median travel distances (ranging from 33km to 55km) with some movements of more than 1,000km. This study determined that outdegree centrality values would be useful in determining the size of an unrestricted epidemic when compared with the infection chain results as a standard. The strong and weak components both overestimated the potential size of an epidemic, using infected sites as the result.

Network data can also be used to evaluate the farm landscape and understand natural patterns that should be incorporated into future control efforts. Livestock often travel long distances between locations. Without specific knowledge of these transportation events, disease management becomes more difficult. Bigras-Poulin, et al.[139] concluded, in a paper on the Danish cattle industry's movement patterns, that the heterogeneous nature of cattle livestock transportation would make non-network driven models ineffective. The authors also emphasized the importance of timely and accurate updating of network data. A later publication by the same first author[140] described Danish pig movements over a part of a year. Results demonstrated great heterogeneity of movement patterns and the author concluded that homogenous movement model assumptions were only valid for large scale risk evaluation efforts and that network data would be critical to any local disease control efforts. A study of Scottish sheep movements[134] from 2003 to 2007 demonstrated great heterogeneity in movement patterns (both the variance and covariance of animals on and off farms). A descriptive analysis of cattle movements in Argentina[141] revealed a seasonal pattern of movements as well as characterizing the distances involved. Median travel distances in different areas ranged between 88km and 218km. Descriptive studies of this sort are important to underpin modeling efforts but in general display heterogeneous farm-to-farm relationships. These studies repeatedly demonstrate the potential importance of animal movements between farms, that these may not follow normal distributions, and are likely to be variable over time. Furthermore, a single long-distance transportation event may have great significance to epidemic spread.

While not performing standard social network analysis, a 2010 study[66] used trade information in tandem with locational information to define and describe different trade regions in Germany. This resulted in 9 distinct trade communities that interacted with each other as well a overlapping each other to some degree. This technique relied on a neighborhood seeking, modularity function (Q), to analyze historical trade patterns between locations. Rather than rely on political boundaries or natural geographical features, Lentz's technique created natural groupings based upon the actual movements of animals. In Spain, the use of spatio-temporal cluster analysis along with social network analysis measures[142] concluded that a regional approach for surveillance and prevention would be best, versus a national approach. The methods employed were useful in determining where the high risk regions were located. A survey of 421 Belgian pig herds in 2005[143] determined direct and indirect contact rates between farms. Results showed that a few pig herds in Belgium had a very large number of direct contact links with other farms. This knowledge would be the basis for risk assessment in a region. The type of pig production at a location will likely dictate its importance in disease transmission. A 2010 article[144] broke Swedish pig movement patterns down by production type. This analysis showed the differences of contact rate and magnitude between the different types of premises. The results clearly demonstrated that "source" farms (e.g. breeding herds) have a much greater impact on epidemic size than "sink" farms (e.g. fattening herd). In their model exercise, an infected nucleus herd resulted in a median of more than 2,000 infected premises (out of a possible 3,084) while an infected fattening herd resulted in a median value of one infected premises (itself). Clearly the type of production will dictate its movement patterns, which in turn will dictate its potential role in epidemic disease spread.

Network analysis and modeling was used to understand wildlife interactions and disease spread. The brushtail possum (*Trichosurus vulpecula*) was the subject of a study to determine the implications of social networks regarding TB infection rate[145]. Groups of possums were observed and manipulated during the trial while they were being observed for infection with TB. This study used classical Social Network Analysis methods and calculations to describe the output. UCINET software was used to calculate 'flow-betweenness and 'closeness' values. The author then used non-parametric methods to determine that transmission rates were significantly influenced by an individual animal's social network analysis attributes. Drewe[146] studied TB wild meerkats in South Africa. By observing interactions (grooming for example) and their directionality, the author could determine the relative importance of network measures on transmission of TB. He reported findings supporting strong directional impact of relationships; for example, grooming outdegree (vs. indegree) and aggression indegree (vs. outdegree) were correlated with TB infection. This study points to the importance of relationship direction in disease transmission. Another study[147] of social networks in wildlife demonstrated a lack of impact in controlling disease by targeting individuals. In this study the authors used radio collars to understand movement patterns of the Tasmanian devil (*Sarcophilus harrisii*), which are known to carry a contagious "facial tumor" disease[148]. However, the findings demonstrated a lack of aggregation in this population, and high risk individual were not easily identifiable and therefore feasible intervention strategies were not defined.

Animal Disease Modeling

Once epidemic data have been analyzed, and hopefully some insight has been gained about the behavior of a disease, a logical next step is to try and predict the occurrence of disease before it happens. Some examples of using predictive models have already been mentioned[19, 149, 150]. Other examples of using models to predict disease spread are seen in efforts to anticipate disease behavior for FMD and CSF during outbreaks. Tildesley, et al. used the fine-scale spatial and temporal data from the 2001 UK FMD epidemic to develop a model[151]. The authors showed the beneficial effects of vaccinating specific at-risk premises (versus simple ring vaccination) as well as supporting the theory that reactive vaccination and pre-emptive culling are effective disease control strategies. This model showed the critical importance of having accurate farm location data, since it relies on specific farm-farm geographic relationships.

Bates, et al. used very straight-forward Monte Carlo simulation to create a predictive model for predicting FMD infection in a region of California[152, 153]. Their model incorporated multiple host species, defined farm locations, various contact types and rates, and expert opinion. The purpose of this model was to evaluate the impact of additional control measures beyond those defined in the baseline response strategy for the state of California. The results of model simulations suggested that delay in the diagnosis of FMD in the index herd was most highly sensitive to the site of the farm and the authors stressed the necessity of having an active surveillance program in place to reduce time to detection.

Similarly, Jalvingh et al. simulated the potential spread of CSF in The Netherlands based on data from the 1997-98 CSF epidemic[149, 150]. This model used a software module called InterCSF, which was adapted from Interspread (part of EpiMan package mentioned earlier). This model is spatial, temporal, and is driven by stochastic calculation processes. The outcomes of interest were the size and duration of a CSF epidemic. This model included specific farm coordinates as well as farm attributes (size and type). The model was run using Monte Carlo simulation (similar to the one listed above) to evaluate the outcomes from different control approaches. A unique feature of this work was the incorporation of economics. When cost of disease and intervention were examined on a dollar basis, it was concluded that appropriate pre-emptive slaughter was cost justified while simply enlarging movement control restriction rings became very costly. These models are enlightening, but given the broad financial implications they present, more work to validate their reliability needs to be performed.

Other applications of GIS into animal disease control

Use of habitat data to define livestock disease risk

A number of innovative approaches have been explored using GIS to gain insight into transmission and control of animal diseases. These approaches present the possibility of incorporating greater geographic content to exploit the strength of GIS- the ability to assemble and integrate diverse and disparate data for the purpose of risk analysis in a spatial context.

In New Zealand, bovine tuberculosis (caused by *Mycobacterium bovis*) remains a major and problematic disease. A national eradication effort has been impeded by the presence of a several wildlife reservoirs, particularly the brushtail possum. Research done at EpiCentre, Massey University, demonstrated a relationship between of environmental variables measured using remote sensing and livestock disease risk [154]. This analysis incorporated land slope, tree height, and vegetation cover which were classified from satellite imagery. They were then able to demonstrate clustering of TB-infected possums in suitable habitats and the clustering was positively associated with clusters of TB-infected cattle.

Ticks are known vectors of numerous diseases affecting both animals and/or humans (Lyme disease, Erlichiosis, Rocky Mountain Spotted Fever, etc…). To better understand the potential impact of climate and geography on the spread of tick-born disease, a Canadian study modeled tick population growth based on their life-cycle, the effect of cumulative environmental temperature, and presence of tick-carrying mice[155]. Results suggested that slight changes in the environment, may greatly increase the tick-borne disease risk for parts of Canada.

Cellular Automata Models and Wild Pigs

Cellular automata models utilize a raster landscape comprised of stationary individual cells. The cell is the unit of concern and its state is a function of the states if its neighbors. These raster cells interact with their immediate neighbors and contagious effects are exhibited as step-by-step, local neighborhood effects are amplified. A cellular automata model simulating a FMD outbreak was developed in Australia[156]. Parts of Australia have significant wild pig populations whose size and activity are a function of geographic features. The investigators used land cover and terrain data in a GIS to generate variable habitat options (depending upon season and region). A simulated introduction of FMD was monitored and the different model endpoints were compared. The sensitivity analysis demonstrated the potential effects of wet vs. dry season, different probability thresholds, and variable latent-infectious periods. The authors also incorporated interactions with domestic livestock. Manipulation of all the variables described had very unique characteristics in the model output and could be useful in understanding the impact of season and environment on potential disease spread.

Remote-Sensing

Remote sensing is the technology and techniques of using remotely-captured measurements of the Earth's surface to estimate the current status of its functions and processes. Airplanes and satellites are used to capture various types of data from the earth's surface.

Remote sensing technology has been used to predict animal disease occurrence by understanding and defining the environmental conditions that foster disease propagation, such as habitat suitable for parasites known to transmit vector-borne diseases. The use of remotely sensed data to understand the epidemiology of Trypanosomosis and Bluetongue (two vector-borne livestock diseases) has been described by De La Rocque, et al.[157] in 2004. In 2007 Guis, et al.[158] were able to create an accurate model for Bluetongue using high resolution landscape imaging to predict infections at specific sheep farms on the island of Corsica, in the French Mediterranean. In 2006, Bouyer, et al.[159], described a significant correlation between disease risk for African Animal Trypanosomosis (a vector-borne, protozoal livestock disease of genus *Trypanosome*) and specific vector-supporting habitat in Western Africa. Leblond, et al.[160], in 2007 described significant relationships between French landscape characteristics and the risk of confirmed cases of West Nile virus infections in horses.

Remote sensing has been assessed as a tool to identify livestock populations. A previous attempt to identify and catalog commercial swine populations was made in a swine dense region of North Carolina[161, 162]. Using IKONOS 4 meter resolution satellite visual imagery, a semi-automated classification routine was performed using GIS software. Using defined criteria, the program identified locations that were possible lagoons or swine barns. Using a known dataset of verified farm locations, the semi-automated process resulted in a detection accuracy of 76% for barns and 79% of the waste lagoons. However, this technique was highly non-specific, as many non-farm sites were identified as barns or lagoons (44% and 47% respectively). The purpose of this study was to explore the possibility that remote sensed data of surface temperature can be used to predict the existence of current populations of pigs in farm buildings, which could enhance the efficiency of efforts to control outbreaks.

Visualization

Even without formal analysis of geographic data, or model building, GIS is being used as a visualization tool. In a formal government report on PRV status, maps of feral swine populations illustrate the ever-increasing spread of this biosecurity risk to commercial swine populations[163]. When decision-makers are trying to understand a situation, no amount of statistics would have the same impact as being able to visualize the population expansion across the national landscape

(Figure-1). Again, focusing on PRV and feral swine, Thulke, et al.[164] used detailed epidemiologic data from past PRV epidemics in Germany to demonstrate the power of visualization. In this work, the point specific information was used to create interpolated prevalence/risk maps. These maps were created in a time-series, and then compiled in a 'movie' to illustrate the spread of the disease. A person viewing the 'data movie' can readily appreciated distinct temporo-spatial patterns of disease spread. However, a previous geostatistical analysis had not detected these patterns. In both cases mentioned above, visualization lends itself to initial hypothesis formulation by giving the user a 'birds eye' impression of epidemic evolution.

The power of visualization for understanding animal disease spread is further demonstrated in an on-line article in Nature[165]. The author, Declan Butler, has regularly reported on the spread of Avian Influenza for Nature. Animal disease data from FAO, OIE, and other government organizations was compiled and overlain as a "mash-up" on the Earth's surface using Google Earth[166]. The extreme visual appeal alone is impressive, but this event is important because nearly real-time information is being presented to the masses in a way that effectively portrays the scope of the problem (Figure-2).

Particular to PRRS, the impact of visualization adds power to ground-level control efforts. The American Association of Swine Veterinarians[167] and the recently formed Minnesota PRRS Elimination Task Force[168] both have formal position statements supporting efforts of PRRS virus elimination from the US swine industry. The National Pork Board[169] and National Pork Producers Council are currently considering language for similar position statements. Regional PRRS elimination efforts are also underway throughout the US and Canada[170]. All of these efforts rely on the foundation of farm-mapping tools to describe landscapes and guide actions for testing and elimination. To assist in these efforts, the University of Minnesota has developed a tool to assist veterinarians and produces in individual and corporate PRRS elimination efforts[171] (Figure-3). Mapping tools are critical to convey the dynamic landscape to audiences.

Conclusion: Going forward

The US swine industry has become increasingly dispersed across the landscape as it has intensified and evolved over the past several decades. Farming locations are becoming more integrated into the connected webs of production systems. As complexity increases, new opportunities will arise for government agencies, academia, and veterinarians to prevent and control disease spread. In the US, GIS has been employed in disease control and elimination programs for some time now, but only at the governmental level and only for documentation purposes. Many other developed countries possess and maintain sophisticated livestock databases. In the US, the inventoried population has been exclusively commercial swine but other swine populations exist and would be susceptible to major swine diseases as well.

Tools and methods are rapidly developing for use by government, academia, private business, and producers and knowledge of disease transmission (aerosols, fomites, etc…) continues to grow. When detailed disease information is loaded applied to population data, these methods can be applied to understand disease spread over the landscape. This results in more accurate epidemiologic description and more valid prediction of disease spread during a future epidemic. In addition to this, use of Social Network Analysis techniques incorporates the increasingly complex network of farm sites.

Opportunities exist to better understand the impact of farm-to-farm relationships along with other new potential technologies. A more complete population at risk should be defined and the accuracy of the data available also needs to be assessed to accurately assess local and large-scale disease risk. The work presented on the following pages will address these concerns and point to further areas for improvement.

Chapter-1: Assessment of the adequacy of available spatial data of the demographics of swine populations in Minnesota, USA

Introduction

The ability to analyze disease patterns in a geographic (spatial) context is contingent upon knowledge of the demographics of the species of concern (population at risk). For transmissible diseases, the proximity of livestock populations might influence the probability of transmission between farms, and the presence of diseased animals at a given location might influence the risk of infection for susceptible populations within its vicinity. Consequently, knowledge of locations and disease status of neighboring farms influences animal health decisions made by public or private veterinarians and producers.

In many countries, including the USA, government policy stipulates response measures to an incursion of a foreign animal disease[172-174]. Geographic knowledge of the locations of animal populations is integral to containing epidemics via identification and quarantine of high risk populations and movement restrictions. Spatial modeling techniques can be applied to predict the likely spread of disease and support resource allocation and decision making[19]. The efficiency of emergency responses is therefore partly a function of the quality of spatial data of the populations at risk. These principles equally apply to efforts to control endemic diseases. In the USA, Porcine Reproductive and Respiratory Syndrome (PRRS) is widely acknowledged as the major swine health problem. The ability of the PRRS virus to spread locally between farms, despite substantial investments in biosecurity, has prompted calls for 'regional' control efforts to reduce the impact of the disease[167, 168].

The purpose of this study was to assess available sources of data on the demographics of swine populations in Minnesota to support planning of disease control initiatives. Specific objectives of the study were: 1) to compare publicly available datasets of the spatial distribution of swine farms in Minnesota; 2) to assess the positional accuracy of farm locations in two of these databases in relation to verified farm locations; and 3) to describe the spatial distribution of a non-commercial swine population (4-H pigs) in relation to commercial swine production.

Materials and Methods:

Data Sources

Five available datasets recording the demographics of swine holdings in Minnesota were identified and obtained from their respective sources. These were:

1) National Agricultural Statistics (NASS) Census – 2002: The United States Department of Agriculture (USDA) conducts a national survey of agricultural activities every 5 years. Data are obtained by farmer surveys and aggregated at the county level for analysis and publication. For this analysis, the most recent (2002) data for swine production were downloaded from the NASS website (http://www.nass.usda.gov/Census/). The NASS census data does not include point coordinates for individual farm premises and could include multiple sites as a single "farm", because data was collected at the owner level (a single owner may operate more than one site).

2) The Minnesota Board of Animal Health (MBAH) is responsible for the control of regulated animal diseases in the state of Minnesota. The MBAH maintains data on locations of premises producing livestock, for all major livestock sectors, specifically for the purpose of supporting disease control activities. The MBAH swine farm locations data has been compiled over many years and most recently was used in the pseudorabies virus (Aujesky's disease) eradication campaign. The data do not indicate the type of production (for example, farrowing, nursery, finishing) nor the number of animals reared at a premises. For the purposes of this analysis, data on swine operations obtained in 2004 were used. A farm's county location was not recorded in the database, but was derived by using farm coordinates data spatially joined to counties data (ArcGIS version 9. ESRI Inc.).

3) The Minnesota Pollution Control Agency (MPCA) is responsible for regulating potential sources of environmental pollution in the state of Minnesota. These include livestock operations, for which the agency issues permits for manure management. Farms recorded in the MPCA database are those farms holding valid feedlot permits. Data on feedlot operations are compiled and maintained by county and state offices. They include the species and total number of animal units for which the permit is issued (measure of herd size). Exceeding a threshold capacity of 50

animal units necessitates registration with MPCA (equivalent to 125 pigs weighing greater than 136 kg each). Data for premises registered as producing swine in 2004 were used for analysis.

4) The 4-H program is a youth educational program that commenced in the late 1800's in several US states to provide an introduction to agricultural industries[175]. Typically, 4-H youth livestock programs allow for an annual experience that involves purchasing one or more young pigs that are reared to market weight and exhibited at various show events. Data on registered 4-H participants in Minnesota were obtained from the state 4-H office. The data included the county, but not the geographic coordinates, of premises. Additionally, a survey was sent to a random sampling of 200 4-H swine program participants that were at least in 7th grade of school (approximately 12 years old or older). This survey tool was designed to assess the husbandry practices of 4-H swine participants as well as their attitudes about and knowledge of swine diseases and biosecurity measures.

5) To evaluate the accuracy of the individual farm locations data in the MBAH and MPCA databases, recent field verified data (2006) provided a reliable 'gold standard' for specific farm locations (R. Morrison, E. Mondaca pers. comm.). The data were collected as part of a pilot PRRS control project in Stevens County and the eastern half of Rice County, Minnesota. Based on NASS survey data among Minnesota counties, Rice County and Stevens County rank at the 83rd and 65th percentiles, respectively, for pig farm density and at the 76th and 57th percentiles, respectively, for number of pig farms per county.

Software

MS Office Access 2003 was used for data aggregation and reprocessing for further analysis. ArcGIS 9.0 (ESRI, Redlands, CA) was used for warehousing and presenting the geographic data. Statistix 8.0 (Analytical Software, Tallahassee, FL) was used for general statistical analyses, and GeoDA 9.5 (Luc Anselin, IL) was used for county-level comparisons.

Analyses

1) Comparison of spatial distributions of swine farm premises by county in Minnesota, as recorded in the NASS, MBAH and MPCA databases.

For all three datasets, descriptive statistics were generated and Spearman's rank correlation was used to estimate correlation of county farm counts among databases. To demonstrate the agreement among datasets, GeoDA was used to create a series of descriptive maps. Each dataset was graphed as pig farm density per county (number of farms per 100 square kilometers) and quartiles of farm densities were mapped. County rates were then smoothed using a 1st order Queen's contiguity weighting file in GeoDA. A 1st order weighting matrix was selected because of its inherent simplicity and the relatively large size of the counties compared to the expected range of local disease spread from individual farms.

Spatial Clustering

GeoDA was used to test for spatial clustering and to compare differences in farm counts among databases. The Univariate Local Indicator of Spatial Autocorrelation (LISA) with Empirical Bayes (EB) rate procedure in GeoDA was used to determine clustering of farm density. Univariate LISA demonstrates how values for contiguous areas are spatially similar or dissimilar, and the EB rate was used to standardize the county counts over county area (100 square kilometers). Moran's I value (with the associated pseudo P-value) was calculated following smoothing with 1st order Queen's contiguity weighting. Graphical representation of clustering was displayed for High-High, Low-Low, High-Low, and Low-High patterns.

Clustering of Differences between datasets

In order to better understand possible regional biases in datasets, the differences in counts between the three datasets (NASS minus MBAH, NASS minus MPCA, and MPCA minus MBAH) were calculated for each county. The Univariate LISA with EB Rate was again used to describe the spatial distributions of these differences. Since none of the three datasets is a "gold standard", this analysis will reveal potential regional bias in one dataset relative to another. The over or underestimation of a regional difference cannot be precisely known, but the regional trends in variation will be better understood.

2) Evaluation of the accuracy of farm location data in the MBAH and MPCA databases in two Minnesota counties

In two Minnesota counties (Stevens and the Eastern half of Rice) exact farm locations are known for all active swine operations (81 in Stevens County and 53 in Eastern Rice County), as of 2006. The geographic coordinates for farms in the MBAH and MPCA datasets are also known. A system relying on common-name (either owner name or premises name) and proximity (points located within 10 kilometers of each other) was used to create a common index for farms identified in all three datasets. Farms were manually matched, using knowledge of local names, potential misspellings, farm-coding differences, and ownership changes. While imperfect, this method allowed for a more complete site-by-site matching than might a rigid application of validation rules. The overall outcome of processing was that farms listed in multiple databases and possessing a common index number could be linked and compared across datasets. To evaluate the completeness and accuracy of the datasets, missing farms (existing farms not recorded in a database) and false-positive farms (recorded in a database but not currently active) of MBAH and MPCA datasets were used to derive two probability values. These were the probability that a dataset includes an actual, existent farm site and the probability that a farm listed in either the MBAH or the MPCA dataset was actually a current swine operation. For farms listed in all three datasets, the geographic error was calculated as the Euclidean distance between sites with the same index number. Basic descriptive statistics were generated including mean, standard deviation, mean center, and standard distance. After all possible sites in the three databases were indexed, all verified farm locations were assigned identical X,Y coordinates to fix the true farm location to a single point in space. The corresponding matched farm locations from the MPCA and MBAH datasets were likewise transformed such that their derived coordinates accurately represented their location relative to the respective verified ‘true’ farm location. This enabled both visualization of the positional error for all commonly indexed farms in the MBAH and MPCA databases; and calculation of positional accuracy and precision for each dataset relative to the true farm location.

3) Spatial distribution of a non-commercial swine population (4-H pigs) in relation to commercial swine production.

Data on six years of 4-H swine program participation were collected and compiled by county. Descriptive statistics were generated for these data. Spearman's rank correlation was performed to measure the county-level association between the six year average 4-H participation (average participants per county) and commercial swine production (number of swine farms in the NASS dataset) at county level. In GeoDA, 4-H participation density (raw rate and smoothed rate) was graphically rendered for evaluation. Spatial clustering of 4-H density was assessed with Univariate LISA with EB Rate modification and bivariate LISA analysis was performed to test for spatial correlation of 4-H participation and spatial correlation of 4-H participation with commercial swine production (NASS data). A 1st order Queen's contiguity weighting file was used for spatial smoothing. Bivariate LISA allows the value of one polygon (county) to be related to the different values of surrounding polygons to determine whether 4-H participation is spatially correlated clustered with commercial production.

Results:

1) Comparison of spatial distributions of swine farm premises by county in Minnesota, as recorded in the NASS, MBAH and MPCA databases

At the coarsest level, estimates of the total number of swine farms in Minnesota ranged from 5,499 in NASS database to 10,768 farms recorded in the MBAH database (Table-1). Significant positive correlation ($P<0.0001$) was observed among county counts of swine farms among all three databases (Table-2).

All three datasets indicate that swine farms are geographically clustered in the state. Moran's I values ($P<0.001$) were 0.79 for the NASS data, 0.68 for the MPCA data, and 0.69 for the MBAH data. All datasets indicated that the density of swine farms is greater in the southern counties of Minnesota (Figure-4). The raw density maps and spatially smoothed density maps both reveal that MBAH data has relatively higher numbers of swine farms recorded in the central portion of the state than the other datasets. Univariate LISA with EB Rate revealed clustering of high density counties with other high density counties, and vice-versa (Figure-5). NASS and MPCA data show clustering along the southern border, while MBAH density clusters in the southern and central portion of the state. The maps indicate that the three datasets have different spatial clustering patterns for swine farm density.

With respect to the numeric differences in county counts of farms between datasets, very clear evidence of regional differences between datasets was seen (Figure-6). The Moran's I values were moderate in range for the three comparisons (0.54 for NASS-MBAH, 0.47 for NASS-MPCA, and 0.40 for MPCA-MBAH) and were all significant (pseudo $P<0.001$). MBAH overestimated farm density in central Minnesota and underestimated density in northern Minnesota (relative to NASS data). MPCA overestimated farm density in the south and underestimated density across a portion of the north (again relative to NASS data). Relative to the MPCA data, MBAH data record more farms in the central portion of the state and less in the south.

2) Evaluation of the accuracy of farm location data in the MBAH and MPCA databases in two Minnesota counties

A substantial proportion (16%, for MBAH and 25% for MPCA) of operational swine farms in both counties were not recorded in each database (Tables-3, Table-4), with the probability that a dataset includes an actual, existent farm site being fairly consistent between counties and datasets. In contrast, the probability that a farm listed in either the MBAH or the MPCA dataset was actually an existent swine operation was highly variable (36% and 74%) among databases and counties with no evident pattern. These observations demonstrate considerable inaccuracy in both available databases of swine farm location with respect to the presence of operational swine farms. Although the NASS data did not include farm identities, the NASS database recorded 69 farms in Stevens County where 81 current operations were identified.

Regarding the positional accuracy of farm coordinates, the MBAH data overall was less accurate in locating farms (greater 1 Standard Deviational Ellipse) than the MPCA data (Figure-7, Figure-8). In these two figures, we see all matched farm locations plotted in reference to their true farm location. The direction and distance from the "True Farm Location" represents the error for every farm that was matched and commonly indexed to its true farm location, assuming no bias in those farms that were successfully matched. In Rice County, the MBAH data included two points that deviated similarly in magnitude (approximately 9.8 kilometers) and direction from the verified sites and are likely attributable to errors in data entry. Removal of these two points would greatly reduce the average error in MBAH dataset and reduce the obvious N-S axis of the Standard Deviational Ellipse. Histograms of the error distributions show the MBAH data to be right skewed in both counties (Figure-9). The MPCA data appeared to have a more uniform distribution. Nearest neighbor analysis indicated that MBAH points were clustered around the verified sites and MPCA points distributed randomly (Table-5).

3) Spatial distribution of a non-commercial swine population (4-H pigs) in relation to commercial swine production

Participation in 4-H programs in Minnesota varies among counties. The 6-year mean participation per county ranged from 0 students to 112 students enrolled per year (mean of 30 participants per county per year). Analysis of year-to-year participation numbers by county revealed very little variation. Much of the variation in county-level participation can be attributed to the previous year's participation, with correlation coefficients ranging from 0.83 to 0.98 (Table-6). We used the six-year mean number of 4-H swine participants per county to visualize the spatial distribution of the 4-H swine population in the state (Figure-10). The 4 quartiles of density presented on the map show an increase in density for southeastern counties. The smoothed county-level farm density map suggests regional concentration in the Southeastern corner of the state. The spatial clustering of 4-H density seen with Univariate LISA w/ EB Rate modification further supports the observation that there is a general trend for increased 4-H participation density in the southeastern counties (Figure-11). Clustering was significant but the spatial autocorrelation was less than seen with commercial production (Morans I = 0.48 vs. 0.79 for NASS data). Using the Bivariate LISA with EB Rate method, it was observed that high density 4-H counties co-cluster geographically with high-density commercial production counties along the south-central portion of the state (Figure-12). 4-H production was significantly, but only moderately, correlated with commercial production (Table-7).

The response rate for the 4-H survey was 61% (121/200). Thirty-six percent of respondents kept 4-H pigs at the site throughout the year, and 39% indicated that their family also raised pigs commercially. Of these, 83% responded that the commercial pigs were within 0.5 miles (~0.8

kilometers) of their 4-H pigs, and 32% reared their 4-H pigs in the same barn with commercial pigs. For respondents whose families did not raise commercial pigs, 20% of respondents indicated that the nearest commercial pigs were located within 0.5 miles.

Discussion:

Accurate data on the spatial distribution of susceptible populations is an invaluable resource for planning and executing emergency responses or other programs to control or eradicate animal diseases. There are logistic difficulties in maintaining high quality spatial databases, particularly for rapidly evolving industries such as the swine industry in the USA. Until recently, the USA has not attempted to establish a national system for registration of premises raising animals. This responsibility has historically rested with the individual states. Current efforts led by the US Department of Agriculture to establish a national premises database as part of the National Animal Identifications System aim to address this shortcoming, but completion of this task is unlikely in the short term. The accuracy of existing spatial farm databases is likely to vary considerably among states, and our observations in Minnesota cannot be extrapolated beyond the state.

For an infectious disease in a geographic area, the relevant populations at risk include all susceptible animal species. This study was limited to swine because the predominant swine health problems (notably PRRS and Porcine Circovirus Associated Disease) affecting the US industry appear to be highly host specific. For logistic reasons, this study was restricted to commercial swine enterprises and a single non-commercial sector (4-H pigs) for which relevant data were accessible. This dataset demonstrated not only that a niche swine population (4-H pigs) was geographically correlated with commercial production, but also that this niche swine population was relatively stable over sequential years. Further, the 4-H survey findings demonstrate the potential interaction between commercial and non-commercial swine populations. In this, they emphasize the likely importance of non-commercial swine populations as reservoirs of swine pathogens and the need to assess the risk that such populations present when planning regional control programs. Clearly, when investigating disease control options, all commercial and non-commercial swine populations (e.g., feral, backyard, pet, etc.) in a region need to be included.

It should be noted that the sources of data that we evaluated were compiled for very different purposes. Adequacy of data is therefore a relative concept, and standards for data quality according to use are arguably more appropriate than absolute measures of accuracy. The clustering of error points in the MBAH dataset (Figure-7, Figure-8), suggests they are 'seeking' to be accurate to the true location. The MPCA error point-pattern, in contrast, does not intensify at its cluster center- the points exist randomly in the study area (Figure-7, Figure-8). This is likely an artifact of the respective data collection procedures. For MBAH data, farm locations are assigned to locations deemed to be the actual farm location. This fits with the data element coding laid out for APHIS surveillance data standards on their website (http://www.aphis.usda.gov/vs/nahss/resources.htm). However, these definitions of data elements delineate methods of geographic data collection (GPS, address geocoding, etc…), but no standards for precision or accuracy in reference to actual livestock locations are presented. In contrast, MPCA farm locations are assigned to the centroids of the quarter-section (square administrative unit equal to approximately 65 hectares) or full section, depending on county. Since actual farm sites may be anywhere within a quarter-section, the relationship between the actual location and the MPCA assigned location appears random within the study area. Further, geographic correlation and autocorrelation of county-level farm density among datasets indicate that differences among datasets are not spatially random and that one data resource may under or overestimate the density of swine farms in a multi-county region of the state.

The databases that we obtained for this project were not accompanied by metadata files that normally would convey some data quality parameters and document procedures used to compile the data. Appropriate metadata should provide timely information to facilitate data sharing across organizations that could be critical in managing emergency responses. Therefore, future consideration of data quality standards for spatial databases to support animal health activities should include metadata standards.

Our study primarily considered completeness and positional accuracy. In comparing the three databases of swine production across Minnesota, we were limited by the absence of a true 'gold standard'. The unique purposes of each dataset and their differing definitions of what constitutes a "swine farm" will, no doubt, be cause for differences. However, when used for the purposes of estimating the true locations of swine farms, it can logically be concluded that there are significant accuracy concerns in at least two of the three databases (only one can be accurate). Furthermore, the existence of spatial correlation in the patterns of discrepancies among these databases suggests local administrative factors, such as local office compensation for enrollment, or regional shifts in livestock production over time, may influence the accuracy of data. Substantial variability in the adequacy of available data can be expected even among counties within the state. This was confirmed in the analysis of verified 'gold standard' locations in Stevens and Rice counties where the probability that a farm listed in either the MBAH or the MPCA dataset was actually a current swine operation (and to a lesser extent the probability that a dataset includes an actual, existent farm site) calculated for the MPCA and MBAH databases varied substantially from county to county. We consider that the completeness of these databases observed in these two counties is substantially below what should be achievable and necessary to support effective emergency responses or other animal health programs.

Similarly, with respect to positional accuracy of individual farms, deviations of the order of 10 kilometers observed for a small number of farms would be problematic when managing emergency responses. The positional inaccuracy observed in the MPCA data could largely be attributed to the system for recording locations (by section rather than specific location), and could be considered acceptable for the purposes of their responsibilities (i.e., the management of livestock waste and air quality). However, the greater positional inaccuracy of the MBAH locations is of greater concern as locations are intended to indicate specific farm locations that would be used in cases of emergency response to foreign disease outbreaks. In the two counties considered, 10% of farms had a positional error of more than 900 meters, a radius which would typically include multiple other farm sites. If resources were to be allocated to improve the accuracy of this database, priority should first be given to improving the completeness of the data more so than the positional accuracy of recorded farms. The current inadequacy of reliable spatial data of commercial swine enterprises in Minnesota is compounded by the presence of substantial populations of swine in non-commercial arenas. Planning for emergency response preparedness should include formal assessment of non-commercial populations and their potential role in disease transmission within a region.

Chapter-2: Demographics of Minnesota Swine Populations – Evaluation of Remotely Sensed Data as a Potential Tool for Identifying Swine Populations

Introduction:

With the advent of new technologies comes the possibility of using novel tools to improve essential processes. The National Animal Identification System of the United States Department of Agriculture aspires to inventory all swine premises in the county[68]. The use of mobile GPS instruments and the availability of high resolution orthophotographic images can allow users to identify farm buildings and locations with a high degree of accuracy and precision. However, there are difficulties in maintaining currentness and completeness of spatial farm databases. This is the result of a dynamic agriculture system, with some farms ceasing to raise pigs while others construct new production facilities. Unused facilities may return to active use and facilities may change ownership over time. Some imperfections in livestock databases are inevitable, and the degree of inaccuracy will be a function of the measures employed to maintain data accuracy despite the volatility of the livestock populations of interest. In the face of a foreign animal disease outbreak, methods to rapidly verify the presence of livestock at registered farm sites could improve resource allocation for the implementation of emergency response measures. Sites in the vicinity of infected premises that could be confirmed to be populated should be given priority for site visits, herd testing, and forward and backward tracing of animal movements.

In Minnesota, most commercial swine are confined in buildings that are easily visualized with orthophotographic imaging that is now freely accessible. Pigs produce heat as part of the metabolic processes of maintenance and growth. Ventilation of swine confinement buildings is an important factor in optimizing the ambient conditions in confinement operations. Overheating and increased levels of dangerous gases can overwhelm and kill pigs if ventilation systems are not adequately managed. However, not all heat is removed from the building as exhausted air. Some of the heat is transferred to the exterior surfaces of the building (walls and roof) and is lost from buildings by radiation, conduction and convection.

Remote sensing is the technology and techniques of using remotely-captured measurements of the Earth's surface to estimate the current status of its functions and processes. Webster's New Millennium Dictionary[176] defines remote sensing as "the technique or process of obtaining data or images from a distance, as from satellites or aircraft". Remote sensing satellites capture various types of data from the earth's surface. These data include radiation of various wavelengths, as well as thermal surface signatures. The resolution of data collected varies between type of satellite and information band. At the time of this writing, LandSat ETM+ data presented the highest resolution of thermal image data available for MN that can be purchased by the public. It presents surface temperature data at a comparatively crude resolution. Temperature is given as 30 X 30 meter blocks compared with 1 meter photographic resolution from available airplane overflight orthophotography.

Remote sensing technology has previously been used to predict animal disease occurrence by understanding and defining the environmental conditions that foster disease propagation. Generally, this has centered on monitoring the habitat range for parasites known to transmit diseases – vector-borne diseases. The use of remotely sensed data to understand the epidemiology of Trypanosomosis and Bluetongue (two vector-borne livestock diseases) has been described by De La Rocque et al.[157] in 2004. In 2007 Guis et al.[158] were able to create an accurate model for Bluetongue using high resolution landscape imaging to predict infections at specific sheep farms on the island of Corsica, in the French Mediterranean. In 2006, Bouyer, et al.[159], described a significant correlation between disease risk for African Animal Trypanosomosis (a vector-borne livestock disease) and the presence of specific vector-supporting habitat in Western Africa. Remote sensing has been used to study West Nile, another vector-borne disease spread by mosquito. Leblond et al.[160], in 2007 described significant relationship between French landscape characteristics and confirmed cases of West Nile infections in horses.

Remote sensing has been assessed as a tool to identify livestock populations. A previous attempt to identify and catalog commercial swine populations was made in a swine dense region of North Carolina[161, 162]. Using IKONOS 4 meter resolution satellite visual imagery, a semi-automated classification routine was performed using GIS software. Using defined criteria, the program identified locations that were possible lagoons or swine barns. Using a known dataset of verified farm locations, the semi-automated process resulted in a detection accuracy of 76% for barns and 79% of the waste lagoons. However, this technique was highly non-specific, as many non-farm sites were identified as barns or lagoons (44% and 47% respectively). The purpose of this study is to explore the possibility that remote sensed data of surface temperature can be used to predict the existence of current populations of pigs in farm buildings.

Hypotheses

The following hypotheses were considered:

- Sites identified as active swine farms emanate more heat, which can be detected by remote sensing, than randomly selected points in the same geographic region
- Sites identified as being active swine farms emanate more heat, which can be detected by remote sensing, than non-swine farm sites in the same geographic region
- Season impacts the magnitude of differences detectable by remote sensing

Specific Objectives

- Obtain surface temperature data for Rice County during cold and warm seasons and define the recorded surface temperature at each verified active swine farm in the region.
- Determine the relationships of site-type and season with remotely sensed surface temperatures in Rice County

Materials and Methods:

Two surface temperature datasets were obtained from Dr. Marv Bauer and Fei Yuan of the Forest Resources Department. The datasets had been processed and georeferenced to a UTM15 projected coordinate system. The first dataset (cold weather period) was captured on 2/27/01 and the second dataset (warm weather period) was captured on 5/21/02. Both datasets originated from LandSat ETM+ satellite imagery giving 30 meter by 30 meter resolution thermal bands (Figure-13). Data were presented as raster image files with the temperature attribute given in degrees Kelvin. Both datasets were captured by the satellite during the daylight hours.

The two raster files were imported into ArcGIS software package (v9.X) as two projected layers. Other data layers imported were a county land-cover raster; county-level boundaries; county roads; county orthophotograph; and specific farm location points. The locations of verified farm locations were defined very precisely, with each point being either the centroid of multiple clustered buildings or the centroid of a building itself.

The Eastern half of Rice County was circumscribed by a rectangular polygon which defined the study zone. In this domain, two additional sets of points were created. The first was a set of "sister" farms. These were the centroids of building sites from neighboring locations (farm sites) that were not identified as hog farms. These assumptions were based on a visual survey of orthographic images with a thorough, census-level knowledge of active swine populations in the county. The third dataset was composed of randomly selected points within the study zone. The random points were generated using a bounded random number generator employing the coordinate limits of the study zone. Figure-14 displays all three point datasets in Eastern Rice County.

In ArcGIS, a script was created and run in ArcInfo Workstation that assigned the value (temperature Kelvin) of the 30x30 raster cell to every farm point. The end result was an attribute table with temperature values for every point (in all three point datasets). Frequency distributions and histograms were created from the data for visualization. ANOVA analysis (General AOV/AOCV- Statistix 8.0 software, Analytical Software, Tallahassee, FL) was used to determine significant differences by Season, LocationType, and a Season X LocationType interaction variable. The type of hog farm (Farrowing, Nursery, or Finishing) was also analyzed. A diagnostic threshold point (cut-off temperature) was selected which represented an approximate average for each season, the geographic data points were assigned corresponding indicator variables, and Logistic Regression analysis was performed (Statistix 8.0 software) to determine the odds of LocationType with regards to point temperature. Further, Receiver Operating Characteristic (ROC) curves were created to assess the diagnostic usefulness of point temperature in determining the presence of a livestock population.

Results:

Frequency distributions show the temperature patterns for the three datasets (Figure-15 and Figure-16). During the winter period, there appears to be three potentially different temperature distributions, with hog farm sites (Farms) being the warmest, non-hog farm sites (NonHog) being next warmest, and random locations (Random) being the coldest. In the summer period, the random locations are warmest, with the hog farm and non hog farm locations appear to be similar.

ANOVA

Using the AOV/AOCV ANOVA procedure in Statistix, the variables Month, LocationType (hog farm, non hog farm, or random), and an interaction term were selected for analysis. Results indicated that Season, LocationType, and their interaction term were all significant predictors of surface temperature (Table-8). Individual analysis for each season shows that mean temperatures were only significantly higher during the cold weather period (Table-9). Surface temperature did not differ significantly by type of hog farm- Farrowing, Nursery, or Finishing (Table-10).

Logistic Regression

Indicator variables were added to the datasets to designate locations that had temperatures greater than or equal to the cutoffs of 10.13°F in the February dataset and 67.73°F in the May dataset. A logistic regression model was created in Statistix for the dependent variable HogFarm (0 or 1), using the temperature cutoff indicator (0 or 1) as the independent variable. Results (Table-11 and Table-12) show a significantly increased odds ratio during the winter (OR= 3.72; 95CI= [1.71, 8.11]), but not during the summer (OR= 1.41; 95CI= [0.68, 2.92]), using these cutoff values.

Diagnostic Performance

Given the distributions of swine farm (Farms) and non-swine farm (NonHog), temperature would not appear to be a reliable, differentiable characteristic during the warm season (Figure-16). Receiver operating characteristic (ROC) curves for these two diagnostic threshold cut-off points were created to determine their usefulness in detecting the presence of swine at a specified location (Figure-17 and Figure-18). Using a cut-off of 10.13°F (Feb dataset), the resulting sensitivity was 56% and specificity was 75%. Using a cut-off of 67.73 °F (May dataset), sensitivity was 49% and specificity was 59%. ROC curves were used to estimate area under the curve for both Feb (63%) and May (55%).

Discussion and Conclusion:

The results revealed significant differences in point-specific temperature as measured by satellite, but these differences were not consistent between seasons. Type of hog farm was not found to influence the observed temperatures. The usefulness of using a diagnostic cut-off temperature appears to be limited in both sensitivity and specificity.

One reasons for this limitation is the lack of spatial definition it presents. The data are available as a 30 meter by 30 meter raster. Considering that the average finishing barn is 12 meters by 60 meters, it becomes obvious that the temperature of a raster cell cannot be assigned to a single building and will be a composite of surface temps detected in that larger area (an area larger than the barn).

A second reason could be the relative insignificance of the animals' heat production compared to the influence of the sun on the earth's surface. Crude calculations reveal a multifold magnitude of difference. A 1,000 head finishing barn would typically have roof dimensions of 40 feet by 200 feet (8,000squarefeet or 743squaremeters). Pigs weighing 175 lbs (80kg) would produce 206 W of heat energy (27.58×kg^-0.54)[177]. One thousand pigs would produce 206,480 W, equaling 278 W/m^2. Energy from insolation (solar radiation) changes seasonally and may be calculated by the formula; I (insolation) = S (solar constant of 1,300) cos Z (solar zenith angle)[178]. Values calculated for central Minnesota, on the dates considered, yield 775 W/squaremeter (on 2/27/2001) and 1,180 W/squaremeter (on 2/21/2002)[179]. These values are 2.8 and 4.2 times the pigs' thermal heat production, respectively. This difference would explain both the insensitivity of this method in general and the difference in diagnostic sensitivities for cold and warm weather months (56% in cold weather and 49% in warm weather).

When considering tools that may be employed in disease control efforts, the benefits and draw-backs of each should be considered. While cumbersome, direct communication with farmers and other community members will likely create a solid and reliable dataset for animal population at risk. Novel tools like remote-sensing are interesting because they present the user with new types of information that can be quickly obtained for analysis. Based upon this study, remotely sensed surface temperature data would not be sufficiently predictive of the presence of animals to reliably enhance the efficiency of an emergency response to a disease outbreak.

Chapter-3: Potential role of non-commercial (4-H) swine populations in the epidemiology and control of Porcine Reproductive and Respiratory Syndrome (PRRS) virus

Introduction

A reproductive syndrome of unknown etiology described in the United States in 1989 was the first documented clinical presentation of Porcine Reproductive and Respiratory Syndrome (PRRS) virus infection of swine[7]. The causative arterivirus is now endemic in most swine producing countries and, with an estimated cost of $560 million annually, PRRS is the most economically significant disease affecting the US swine industry. In inflation adjusted terms, this estimate greatly exceeds the estimated annual economic burdens of both hog cholera ($364 million in 2004 dollars) and pseudorabies ($36 million in 2004 dollars) viruses before national programs were undertaken to control those diseases[38]. Like other RNA viruses, PRRS virus displays marked genetic heterogeneity that is reflected in variability in virulence, clinical manifestations and epidemiological attributes. Variants of the PRRS virus in Chile appear to have relatively low virulence, while highly virulent variants have been implicated in widespread and severe disease outbreaks in China[180, 181]. The propensity of PRRS to cause reproductive disease is strain dependent and variants of the virus also differ with respect to their potential for aerosol transmission[182, 183].

The foremost obstacle to PRRS control is the ability of the virus to spread among neighboring farms despite strict biosecurity measures. Elimination of PRRS from individual herds has been regularly achieved using a variety of approaches[184-186], but these efforts are frequently undermined by reintroduction of virus via routes which in most cases are either unknown or speculative. In addition to obvious routes of introduction in pigs or semen, experimental studies have confirmed a variety of potential routes for PRRS virus transmission among herds, including people, fomites, transport vehicles, insects and aerosols[33, 48, 50, 187]. Coordinated efforts to control PRRS in France had qualified success[53], and a government led eradication program in Chile appears to have been successful[188]. Likewise, an emergency government program immediately following the initial detection of PRRS in Sweden resulted in elimination of the virus[189]. However, in each of these countries a low proportion of herds was infected when the programs were initiated. The American Association of Swine Veterinarians has stated a long-term goal of PRRS elimination in the USA[190]. However, in regions with a high herd prevalence of PRRS infection, considerable obstacles need to be overcome before any coordinated control program will be practical[38].

Effective regional control of animal disease requires an understanding of all reservoirs of infection and of mechanisms and risks of pathogen transmission. PRRS virus, like other arteriviruses[191], is highly host specific and it is unlikely that non-porcine species could be reservoirs of the virus. Consequently, when developing regional control strategies for PRRS, attention may be focused entirely on populations of *Suidae*. Although commercial swine herds (meaning herds kept with the primary objective of income generation from pork production) constitute the vast majority of the US swine population, many other swine populations exist. These include feral or wild pigs, pet pigs, hobby farm pigs, and pigs reared in youth education programs (e.g., Future Farmers of America and 4-H). Feral or wild pig populations are important reservoirs of infectious diseases including brucellosis and pseudorabies[81, 82], and are also potentially important reservoirs for PRRS virus[192]. Although widespread in much of the USA, as yet feral pigs are not known to have become established in Minnesota. Youth education programs which include rearing and showing of pigs attract broad participation in many US states including Minnesota. According to the 4-H National Headquarters, the numbers of youth involved in the swine educational curricula ranged from ~140,000 to 212,000 per year from 1996 to 2003. Currently, there is little documentation of the relationships these youth 1 have with the commercial swine industry. The purpose of this study was to characterize the 4-H swine population and to evaluate its potential importance to the epidemiology and control of PRRS.

Materials and Methods:

Demographics of commercial and 4-H swine populations in Minnesota and the USA

Agricultural youth education programs in Minnesota are seasonal activities that are linked to county fairs. To understand the chronology of 4-H swine exhibition in MN, the schedule of Minnesota Federation of County Fairs information for 2004 was obtained[193]. Data of participation in 4-H swine programs in MN from 2000 to 2005 were obtained from the state 4-H office. These data included the name, address, county, and year of participation for each participant. Data were summarized and aggregated by county and year. The data were then imported into ArcGIS 9.0 (Environmental Systems Research Institute, Redlands, CA) for geoprocessing and standardization of data formats. GIS objects were exported as shape (.shp) files for exploratory spatial analysis using GeoDA software[194]. To evaluate the existence of co-clustering of commercial swine production and 4-H production in counties, the spatial distribution of 4-H participation data was compared with that of commercial swine populations described by the National Agricultural Statistics Service (NASS)[195], Minnesota Pollution Control Agency (MPCA)[196, 197], and Minnesota Board of Animal Health (MBAH)[198].

Data of 4-H participation for all states were obtained from the National 4-H Headquarters website[199]. These data included a range of 4-H activities by state, including enrolment in the Animal Science-Swine curriculum. Geographic distribution of average 4-H and 4-H swine curriculum enrolments were visualized as raw quartile maps of membership per 10,000 square kilometers. Using different spatial clustering analyses in GeoDA, the geographic distributions of national 4-H swine program participation and general 4-H enrollment were analyzed and compared with national commercial production data as measured by the 2002 NASS national agriculture survey statistics[195]. Procedures used in GeoDA to assess spatial autocorrelation were univariate Local Indicator of Spatial Autocorrelation (LISA), multivariate LISA, and Moran’s I statistic[200, 201]. The LISA statistic yields a measure of spatial autocorrelation for each individual location examined. Univariate LISA maps show the spatial autocorrelation between one variable (in this case 4H swine program participation) in an area (e.g., state or county) and the same variable in all adjacent areas. Bivariate LISA maps show the spatial autocorrelation between one variable (e.g., 4H swine program participation) in an area and another variable (commercial swine production) in adjacent areas.

Mail survey and interviews of 4-H participants

A 64 question survey instrument (available upon request) was developed to describe 4-H participants’ livestock activities and to assess their knowledge of swine health and biosecurity. In Minnesota in 2005 a total of 2,738 youths registered to show pigs in the 4-H program, of which 1,725 were in the 7th grade or above. The arbitrary selection of 7th grade was chosen to focus on older participants likely to have more experience and education related to swine production.

Using a random number generating function in an MS Excel spreadsheet, a random sample of 200 participants was selected from those students in 7th grade or higher who had mailing addresses in Minnesota, and who were not members of the same household as another selected participant. Students were encouraged to complete the survey without help from others. The initial survey mailing was followed by a reminder post-card mailing after two weeks, and then a second mailing of the complete survey to non-respondents. Descriptive statistics of survey responses were compiled with 95% confidence intervals. Multivariate logistic regression analysis was performed to evaluate relationships between survey responses and participant characteristics including age, gender, and family involvement in commercial swine production. The relative importance of swine diseases as perceived by 4-H participants was ranked as the ratio of number of the respondents rating a disease as important to the number that were unfamiliar with the disease. Two diseases not known to occur in the USA (therefore deemed of negligible importance) were deliberately included for comparative purposes.

Forty-three 4-H participants showing pigs in two Minnesota counties were interviewed when they registered their pigs for exhibition. The questionnaire (available upon request) was administered to 20 participants in Rice County and 23 in Stevens County. The survey explored reasons for participation and also asked participants to list measures that can be implemented to decrease pathogen transmission among pigs. For descriptive purposes, the measures listed were categorized as “Equipment and Facility Sanitation”, “Personal Sanitation”, “Pest control”, “Separation or Isolation”, “Source Health”, “Vaccination or Medication”, or “Other”. In addition, at the Minnesota State Fair in 2005, a convenience sample of 172 4-H participants registered in 9th grade or greater from 53 counties (of 220 participants from 54 counties), was asked a short series of questions regarding the origin and PRRS vaccination status of their pigs.

Seroprevalence and seroconversion to PRRS virus

County officials were contacted to confirm the dates of county fairs and whether the 4-H shows were terminal (requiring pigs to go to slaughter following the fair). The seroprevalence of PRRS infection in 4-H pigs was estimated in pigs from nine county fairs which shipped pigs to a regional slaughterhouse after livestock exhibition. Selection of the counties was by convenience but five of the counties rank amongst the highest hog producing counties in Minnesota (Martin 1st; Nicollet 4th; Mower 5th; Brown 10th; Watonwan 12th). The other counties (Rice, Steele, Le

Sueur, and Fillmore) have less dense commercial swine populations. Samples were collected from the collaborating slaughterhouse on five occasions. Blood samples were collected from individual pigs (n = 661) following stunning without interference with the procedures of the plant. To assess the incidence of PRRS seroconversion following fairs, two counties (Blue Earth and Winona) with non-terminal fairs were selected. At these fairs, participants were invited to participate in the study if they intended to return pigs to their farm for at least two weeks. In accordance with IACUC requirements, participants gave informed consent for collection of blood samples from their pigs. Blood samples were collected from pigs (n = 32) on the day of exhibition and participants were later contacted to arrange collection of a second blood sample two weeks after the fair. The presence of antibodies to PRRS virus was determined using the IDEXX HerdChek PRRS Antibody test kit (IDEXX Laboratories, Inc., Maine) performed at the University of Minnesota Veterinary Diagnostic Laboratory. For the recommended cut-off of a Standard to Positive ratio of 0.4 that we employed, IDEXX provides estimates for sensitivity (97.4%) and specificity (99.6%)[202], which we used with the Rogan-Gladen estimator to calculate true prevalence from apparent prevalence[203]. One-way ANOVA was used to compare mean PRRS Sample to Positive ratios among counties and chi-square analysis was used to compare the proportions of seropositive pigs. Association of seropositivity with hog farm density (using NASS, MPCA, and MBAH data) and 4-H participant density was assessed for these nine counties using Spearman's rank correlation method. McNemar's chi square was used to test for differences in seropositivity in paired samples of serum collected from pigs at fairs and two weeks later.

Results:

Demographics of 4-H and commercial swine populations in Minnesota and the US

All county fairs in Minnesota were scheduled between weeks 24 and 37 in 2005, and more than half of county fairs were held in the month preceding the State Fair in early September. Only seven of 79 (9%) county fair boards contacted required that their shows were terminal (animals required to be sent to slaughter at the end of the fair). In 2005, 2318 students registered to show 4-H pigs in the state of Minnesota, similar to a mean of 2592 over the five preceding years. Participation in 4-H swine programs varied markedly across Minnesota, with the greatest concentration in the southeastern counties. Statistically significant spatial clustering of 4-H swine participation was found in the southeastern corner of the state, using Univariate LISA analysis. Multivariate LISA analysis using either NASS or MPCA data indicated that 4-H swine program participation was geographically correlated with commercial swine production at the county scale (Moran’s I 0.37; bootstrap estimated P = 0.001). A slightly different pattern of co-clustering was observed using the MBAH data, with High-High clustering occurring in both the south-central and central portions of the state (Moran’s I 0.24; bootstrap estimated P = 0.001). Although results of the analysis varied among the databases of commercial swine production selected, all analyses indicated that 4-H swine participation has significant geographical correlation with commercial pork production in Minnesota (Figure-19).

The geographical association between 4-H swine production and commercial production evident in Minnesota was also observable on a national scale. Across the USA, the area density of swine curriculum enrollment (1998-2002) was highest in the traditional corn-belt states of the Midwest and eastern Midwest (Figure-20). The density of 4-H swine participation was correlated with swine farm density (Moran’s I 0.30; bootstrap P=0.001), with significant spatial autocorrelation (“High-High”) throughout the central Midwest and “Low-Low spatial autocorrelation throughout the western US.

Mail survey and interviews of 4-H participants

A response rate of 66.5% (133/200) was achieved for the mail survey of randomly selected 4-H participants. While a majority of participants exhibited pigs at only one show the previous year (median 1, mean 2.5, range 1 to 35), one participant claimed to have exhibited at 35 shows. The mean number of pigs registered for the current year was 4.8 (median=3, minimum=0, maximum=30) and 54% (95%CI:45%, 63%) of respondents intended to show their pigs at locations other than their local county fair in 2005. One-sixth of participants were also participating in the FFA Swine program (FFA is a youth leadership program including livestock projects similar to 4H. In FFA, pigs can be exhibited concurrently with 4H and “open class” pigs at county fairs). About one quarter (24%;17%, 32%) of respondents had contact with pigs other than their own 4-H pigs at least once a week and 77% (69%, 84%) had livestock other than swine kept at the same location as their 4-H pigs (56% cattle, 28% poultry, 26% sheep, 8% goats, 21% other). Approximately three-quarters of respondents (74%; 65%, 81%) obtained their 4-H pigs from off-farm sources, and 13% (8%, 20%) obtained pigs from another state. Of the 82% of participants who purchased pigs, 95 of 111 (85%) purchased the pigs in the months of March to May. Commercial pig production was undertaken by 39% [31%, 48%] of families of 4-H respondents and 36% [28%, 45%] of respondents indicated that other (non 4-H) pigs were kept at the same site as their 4-H pigs. Of 47 respondents from farms rearing both 4-H and commercial pigs, 15 (32%) kept both groups in the same barns. For 74 respondents without any family involvement in commercial production, 55% indicated that other pigs were located within two miles of the site where they kept their 4-H pigs.

With respect to knowledge and attitudes towards biosecurity and swine health, respondents ranked clean transportation and obtaining pigs from sources with good health status to be the most important measures to ensure pig health (Table-13). When asked how important 14 diseases were to commercial pork producers, respondents perceived swine influenza, *E. coli* and *Salmonella* to be the most important diseases of swine, with PRRS ranked fifth (Table-14). Forty-one percent of respondents were not familiar with PRRS, compared with 51% for porcine epidemic diarrhea, a disease never reported in the USA. However, 30% indicated that their pigs had been either vaccinated against PRRS or treated for PRRS infection. Logistic regression analyses indicated that the odds of having regular contact with other pigs, having no other species of livestock, and certification by educational programs beyond the 4-H program all increased significantly for participants from families who raise commercial swine. Awareness of biosecurity and perceived importance of diseases was not influenced by age group, gender, or family involvement in commercial pork production.

Of the convenience sample of 172 4-H participants interviewed at the Minnesota State Fair, most were from southern Minnesota. Thirty-three% of these had registered “home-raised” pigs, not purchased from an outside source, while 15% were exhibiting pigs that originated from other states. Nineteen (11%) of participants stated that they had vaccinated their pigs for PRRS. Survey responses collected from participants at the Rice and Stevens county fairs were similar with respect to grade in school, years in 4-H, whether pigs would return home after the show pigs’, and intended participation in other shows. One third (33%) of exhibitors were planning to show their pigs at other exhibitions and almost half (48%) of Stevens County 4-H swine show participants were bringing their show pigs home from the county fair. The primary motivations for participation were ‘too have fun’ (88%), to learn about pigs and livestock husbandry (54%), and to go to the state fair (30%). Only 16% of participants listed that winning was their motivation for participation.

Seroprevalence and seroconversion to PRRS virus

Across all nine county fairs where 4-H pigs were sampled at slaughter (n = 661), the apparent seroprevalence of PRRS 48% (44%, 52%). Using the Rogan-Gladen estimator, true prevalence was calculated to be 49% (45%, 53%). Both mean S/P ratio and seroprevalence varied significantly ($P < 0.0001$) among counties, with apparent seroprevalence ranging from 29% to 76% (Figure-21). Of the 32 samples from live pigs during county fairs, 19 (59%) were seropositive. Of these, 27 pigs (17 seropositive and 10 seronegative at the fair) were available for follow up sampling. Seven (70%) of the initially seronegative pigs had seroconverted by two weeks after the fair. However, 4 of the 17 previously seropositive pigs tested seronegative at the farm and McNemar's test for symmetry showed differences in seroprevalence at the fair and on farm were not significant (Chi square=0.82; P=0.37).

Discussion:

For over two decades, persistent and severe economic losses from PRRS virus infections in the USA have provided strong motivation to develop and implement effective control programs for this disease. Local spread of virus among farms despite considerable investment in biosecurity is the most frustrating and problematic aspect of PRRS control[204]. Knowledge of the demographics of all potential reservoirs of an infectious agent is an important prerequisite for assessing the feasibility of any regional control or eradication program. From the perspective of the pork industry, the epidemiological significance of any potential reservoir population is a function of its size, the prevalence of pathogens of concern, and its proximity to and interactions with commercial swine populations.

In Minnesota in 2005, the number of registrants in 4-H, raising a mean 4.8 pigs indicates, a total 4-H population of the order of 12,000 pigs concentrated in the period of March to September. This is a trivial population relative to the estimated inventory of 6.5 million, and sale of 14.6 million, pigs in Minnesota in 2005[205]. However, the significance is elevated when one considers that, at both and state and national levels, participation in 4-H swine programs is geographically associated with commercial swine production. Within Minnesota, significant clustering of 4-H and commercial production was found at county level, and 39% of 4-H participants reared pigs on the same locations as commercial pigs. Furthermore, the frequent existence of other swine populations within two miles of 4-H pigs also suggests a real risk of bidirectional transmission of PRRS between 4-H and other pig populations in Minnesota[53].

A national survey of PRRS seroprevalence in US finishing hogs found more than 50% of finishing pigs were seropositive for PRRS[206]. In the same study, 75% of 639 samples from 43 Minnesota hog farms were seropositive, and 36 of 43 (84%) Minnesota finishing herds had at least one seropositive pig (E. Bush, personal communication). Our observations that 49% of 4-H pigs sampled at slaughter, and 59% of pigs sampled at fairs, were seropositive for PRRS virus indicates exposure risks of similar magnitude in both the commercial and 4-H populations. Again, this is unsurprising given the close proximity and interactions we found between these sectors of swine activity. Seropositive results in some 4-H pigs (and also commercial pigs) are likely to be attributable to vaccination, although only 11% of state fair participants claimed to have vaccinated their pigs for PRRS. Based on population sizes alone, it is evident overall that commercial swine farms currently present much higher risk to 4-H populations than the reverse. However, particularly for boar studs, and nucleus or multiplier breeding herds, for which the economic consequences of PRRS outbreaks can be extreme, the risk presented by small non-commercial populations in their vicinity is non-trivial. Investigations of PRRS outbreaks in commercial herds have implicated nearby "backyard" operations or show pigs as sources (S. Daniels, N. Debuse, M. Strobel, personal communications). In both cases, genomic analysis confirmed sequence identity between viruses at the commercial (previously PRRS negative) and neighboring sites. Because of the seasonality of fairs, show pig populations are often transient because pigs are commonly purchased and raised for the express purpose of exhibition. Consequently, risks presented to commercial herds are likely to be highly variable over time.

The limited sampling we conducted of pigs at fairs yielded only 10 seronegative pigs for follow up testing. However, the fact that seven of these animals had seroconverted by two weeks after the fair supports the axiom that congregation of animals from multiple sources is a high risk activity for transmission of infectious diseases. Until Minnesota was officially declared free from pseudorabies, government regulations required that swine exhibitions were terminal. Subsequent to pseudorabies eradication from commercial swine, most county fair boards have opted to hold non-terminal shows, and the frequent intention of participants to show pigs at multiple events is facilitated by such policies. The concentrated seasonal schedule of county fairs, and the repeated mixing of animals at multiple events is likely to facilitate transmission and could present substantial challenges to traceability in the event of a suspected foreign animal disease outbreak[88, 89, 93, 207]. Better information is also important to understand the potential role of other sub-populations of swine that may also serve as sources of entry of foreign diseases or reservoirs of endemic agents[93].

The diseases ranked highest in importance by 4-H participants (swine influenza, E. coli, and *Salmonella*) are all pathogens that attract considerable media attention due to their impact on human health (recognizing that the important distinction between *E. coli* types causing disease in pigs and humans is unlikely to be understood by much of the general public). In contrast, despite its unquestioned primacy among swine pathogens in the USA, as a highly host specific agent PRRS is rarely mentioned in the mainstream media. We infer that the perceptions of the importance of diseases by 4-H participants were probably driven more by media emphasis on zoonotic risks than participants' familiarity and experience with livestock. The low level of awareness among participants of PRRS as the major swine health challenge in swine indicates that education about swine diseases and control should receive more emphasis in youth educational programs. This need is reinforced by the fact that overall participants ranked porcine epidemic diarrhea (an exotic disease never reported in the USA) to be more important than several prominent endemic swine pathogens (porcine parvovirus, erysipelas, *Streptococcus suis*).

4-H youth programs have a proud history of youth education and development related to agriculture. The survey indicated that while respondents indicated familiarity with common biosecurity measures, a large proportion were unfamiliar with diseases common to swine. Although a seemingly negligible population of pigs overall, common practices of 4-H participants including sourcing pigs from distant sources and showing pigs at multiple shows can magnify their importance as potential reservoirs. It is important that many more participants were motivated by the desire "to have fun" and "to learn about pigs and livestock husbandry", than by the prospect of winning. If true, this implies likely receptivity to swine industry initiatives such as provision of 4-H pigs by local producers, which has been encouraged by veterinarians in Minnesota. As the commercial swine industry increasingly looks towards regional strategies to reduce the impact of PRRS[190], the industry should seek to engage with educational programs. Specific education on biosecurity risks and disease control is a necessary component of this engagement.

Chapter-4: Network analysis of pig movements in Minnesota and their potential influence on interherd transmission of PRRS virus

Introduction:

The potential for disease dissemination via translocation of infectious hosts is self evident[22, 208], and restricting human travel or animal transport is a time honored principle of infectious disease control. Government restrictions on cattle movement were an integral component of efforts to prevent the spread of rinderpest in European countries in the 18th century[21]. More recently, movements of livestock were a major factor in geographic dissemination of the 2001 foot and mouth disease (FMD) epidemic in the UK[27, 28, 209]. The introduction of infected animals into herds negates any natural barriers (e.g. distance from other farms) or deliberate biosecurity measures (e.g. fences, gates, air filters) to reduce the risk of agent spread among farms. The implicit risk of disease transmission associated with commerce underpins the international framework for regulating trade in animals and animal products embodied in the World Animal Health Organization[210].

The consequences of introducing infected animals into a region are amplified if an agent is capable of being transmitted between farms despite strict herd biosecurity practices. PRRS is the most economically important disease in the US swine industry and local area spread of the virus among farms is arguably its most problematic characteristic. Research by Dee et al. has demonstrated the spread of PRRS viruses by fomites[48, 51, 52, 211], insects[40, 41, 187, 212, 213], and transport vehicles[50], as well the potential for long distance aerosol transmission[214-219]. Given the apparent facility of PRRS virus to spread locally among farms, the introduction of PRRS-infected pigs onto a farm constitutes a potential risk to all herds in its neighborhood. PRRS is endemic in the USA and is not a regulated disease. Commercial movement of pigs occurs over long distances and largely without consideration of PRRS status, and therefore likely constitutes a major mechanism for geographical dissemination of PRRS viruses. The successful implementation and execution of regional PRRS control programs must incorporate control of both local spread and movement related disease risks. Currently there is little documentation or description of point-to-point pig transportation in the US and the implicit disease risks.

Social network analysis has previously been used to study relationships between farm premises. Social network analysis has its origins in graph theory[119], using data arranged in matrices to provide structural insight into node-node relationships. Webb considered geographic distance and exhibit participation as relationship networks connecting sheep farmers in the United Kingdom[133], and identified potential mechanisms for inter-farm disease transmission. In Denmark, where swine movements are captured in a central spatial database, movement patterns were shown to be heterogeneous, and analysis indicated that actual farm-farm movement information is necessary for creating valid disease transmission models[140]. The 2001 UK FMD epidemic allowed for retrospective analysis of network movement, which revealed the likely influence of network characteristics on FMD virus transmission risk[132].

The movement of livestock into and amongst Midwestern states has been described using data from health certificates required to move animals between states in the USA[220]. However, farm to farm movements at a local scale have not been previously assessed, nor have network analysis techniques been applied to actual animal movement data in the USA.

The goal of this project was to analyze interstate and intrastate pig movements between farms to assess the potential disease risks for geographic dissemination of PRRS virus.

Materials and Methods:

The specific objectives of this study were to:

- Use social network analysis (SNA) to describe and analyze pig movement patterns in two Minnesota counties.
- Use SNA to describe and analyze Interstate Pig Movement in the US
- Describe Interstate Movement patterns to and from Minnesota at a local level to define regional patterns of potential risk for pathogen introduction

Pig movement in two Minnesota Counties

For several years, University of Minnesota has led regional PRRS management programs in two Minnesota counties (Rice County in south-central Minnesota; and Stevens County in west-central Minnesota). One-hundred and twenty-four active farms (47 in Rice County and 77 in Stevens County) and three local markets (one in Rice County and three in Stevens County) were used in this study. The PRRS status of many of these farms had been documented by serum testing (either ELISA 2XR or virus PCR). Farms receiving pigs from a source of known status were ascribed the PRRS status of their source.

A standard survey instrument was administered to collect information about pig movement patterns for these enterprises. Farmer owners, managers, or their veterinarians were surveyed to collect relevant information for the survey. The survey (Figure-22) gathered the following information about pig movements: the geographic location of origin and destination farms; frequency of shipments between respective locations (number of deliveries per time period); size of shipment (number of pigs per load); and age group of pigs being transported (weaned pigs; feeder pigs; slaughter hogs; replacement stock; cull animals).

A relational database (Microsoft Access) was created to warehouse these data, allowing for one-to-many data relationships to capture the complexity of multiple relationships among farms. The database was incorporated into a geographic database (ESRI ArcGIS Personal Geographic Database) already in use for managing diagnostic and location information of Rice County and Stevens County (Figure-23). Certain farm characteristics were summarized and described from this database, including type of production, involvement in multi-site production, and PRRS status. Multisite production was defined as a commercial entity in which incorporated regular movement of pigs to non-market locations at distant sites for completion of their growth. The PRRS status of site was defined as negative, positive, or unknown. As mentioned before, this status was derived either by diagnostic testing or by assuming the status of source population with all-in-all-out pig movement. No central database of diagnostic test results was kept. The tested or assumed status of sites was communicated by the herd veterinarian involved with the site or animal flow. Changes of PRRS status were not recorded in this dataset.

Spatial (geographic) visualization of pig movement flow was generated using Flowdata Model Tools[221], an ArcGIS extension developed by Allan Glennon. This mapping application presents point-to-point relationships as weighted arrows and allows for specific characteristic filtering (i.e. only market shipments). Standard cartographic techniques were also applied to point specific network characteristics to reflect varying levels of connectivity and potential risk. Non-geographic network structure was also depicted using Netdraw network visualization software.[222]

Social network analysis of the relationship data was performed using UCINET social network analysis software.[123] Raw data were imported in Edgelist1 Data Language file format[223] derived from a relational database query. Within UCINET, network centrality statistics were generated. In particular, DegreeCentrality, ReachCentrality, and FlowBetweenness were derived for all network components. Descriptive and inferential statistics were calculated using these values, alone and in combination with other related farm specific data, to understand potential influences within the relationship network. A value for geographic proximity to other farms was calculated by summing the inverse of the squared distance to each neighbor within the county [Σ (1 / kilometers squared)]. Farm sites outside the respective counties were not well documented and not used in the proximity calculation. Wilcoxon Rank Sum Test was used to compare the centrality statistics between the two counties, and a logistic regression model was built to assess possible associations of centrality measures and geographic proximity to other farms with herd PRRS status. To construct the model, five social network analysis centrality statistics (InDegree, OutDegree, InReach, OutReach, and Flowbetweenness), county, and the inverse distance squared value were considered. These were processed using the stepwise logistic regression technique with the forced inclusions of inverse distance squared (Statistix).

Interstate pig movement across the United States

Data of recorded interstate pig movements 2001available from the USDA Economic Research Service (www.ers.usda.gov/Data/InterstateLivestockMovements/) were incorporated into a relationship database (MS Access), compiled as a point-to-point transaction table, and converted to an Edgelist1 Data Language file. These network data were imported into UCINET for social network analysis. Network centrality characteristics (DegreeCentrality, ReachCentrality, and FlowBetweenness) were generated for comparison of states and Canada. Spatial and non-spatial visualizations of the movement network were created using Flowdata Model Tools and Netdraw to illustrate the patterns of interstate pig movement.

Interstate pig movement to and from points within Minnesota

Paper copies of interstate pig shipments into and out Minnesota are held at the Minnesota Board of Animal Health office in St. Paul, MN. Information from 11,759 individual health paper submissions (year 2006) was captured in a relationship database (Microsoft Access). Movements represented included shipments to and from Minnesota and other states as well as Canada. Data captured included type of swine (breeding or feeding), shipment date, number of animals shipped, origin Zip code, and destination Zip code.

The number of pig farms per county or census division was obtained from the USDA's NASS website (www.nass.usda.gov) and the Canadian census of agriculture (www.statcan.ca). These data were imported into ArcGIS where Zip code centroids were identified by their encompassing county, giving a county designation to every pig movement record's origin and destination. This was done because data from the 2002 US Agriculture Census and the 2001 Canadian Agriculture Census was available at the county and census division level.

County centroids were then used to calculate approximate travel distances between sites and to represent animal flow between counties (using Flowdata Model Tools) differentiating between breeding and feeding swine moving into and out of Minnesota. Linear directional means were calculated using ArcGIS for each of the four types of pig movements- 1) "Breeding Swine Moving Into Minnesota", 2) "Breeding Swine Moving Out Of Minnesota", 3) "Feeder Swine Moving Into Minnesota", and 4) "Feeder Swine Moving Out Of Minnesota". Risk approximations were created by multiplying the count or size of pig shipments and calculated pig farm density of county of origin (pig farms per 100 square kilometers). Individual counties' movement characteristics were summarized and differences analyzed using Kruskal-Wallis One-Way Nonparametric AOV (Statistix). Calculated values were displayed using standard ArcGIS cartographic techniques to visualize the relative degree of pig movements and potential for transportation-associated epidemic spread. A geographic data file ("shapefile" or .shp) was exported to GeoDA for statistical analysis of spatial correlation of movement characteristics between counties (using a queen’s contiguity weighting matrix[201] to define the neighborhood of all areas sharing a common border).

Results:

Pig movement in two Minnesota Counties

Farm locations were documented and specified at precise locations (Figure-24), being either the center of a single building or the centroid of the farm site. Of the 124 commercial farms considered, 112 (90%) were involved in multi-site production (Table-15). The proportion of multisite production differed significantly between counties (Fisher’s Exact test p-value = 0.03) with a greater proportion of multi-site production in Rice County. Overall, 30% of farms were categorized to be PRRS positive (Table-16), and the proportion of PRRS positive farms was significantly higher in Rice County than Stevens County (Fisher’s Exact test p-value = 0.01).

Spatial visualization of animal movement patterns (Figure-25) revealed that farms in the movement networks of the two study counties spanned a large geographic area from Alberta to Quebec in Canada and as far south as Kentucky. Also notable is that Stevens County-associated movements frequently geographically overlapped the Rice County-associated movements, although no movements of pigs were recorded between the two counties. Movements of pigs (fat hogs or culls) to markets (either intermediary or terminal), illuminate the limited number of destination premises involved (Figure-26). In contrast, non-market movements (those involving growing pigs and replacement breeding stock) were much more dispersed (Figure-27), with most movement destinations being breeding stock customers or grow-out facilities in multi-site production systems. County-level views for Stevens and Rice Counties (Figure-28 and Figure-29) show that local-level pig movements frequently overlap each other. At the county level scale, the intermediary markets (livestock buying stations) within the counties are more obvious.

The mean distances of pig movement events differed between counties. Whether considering ‘all pig movements’, ‘outward pig movements’, ‘outward pig movements (non-slaughter), or inward pig movements, the mean distance of movements involving Stevens county sites were consistently greater than for Rice County (Table-17). With respect to the frequency of pig shipments, the two counties differed only with respect to outward pig movements with Rice County farms having greater frequency of annual outward pig movements than Stevens County (Table-18). Stevens county had statistically greater total annual shipment distance (shipments/yr * km/shipment) for inward pig movements, but no other significant differences were observed (Table-19).

Table-20 and Table-21 display the measures of centrality calculated using UCINET (InDegree, OutDegree, InReach, OutReach, and FlowBetweenness) for farms in the two counties. The mean centrality measures did not differ significantly between counties, although there was a trend that Rice County farms had higher values for every measure except OutReach (Table-22). The five measures of centrality were positively correlated, but not significantly for OutDegree-InReach or InReach-OutReach (Table-23). Odds Ratios for PRRS positive status, using County, each of the five centrality measures, and InvDistSq was derived in seven single-term logistic regression models (Table-24). Of the terms analyzed, only County and InReach were found to be significantly related to the outcome of PRRS positive status. InvDistSq was presented an odds ratio of 1.18, but this was not statistically significant ($P=0.06$). When a step-wise logistic regression model was created (Table-25), only the County term resulted in a $P<0.05$, with Rice County being approximately 200% more likely to be PRRS positive than Stevens County. Other terms were retained in the model (InvDistSq, OutDegree, and InReach) but were not found to be statistically significant ($p > 0.05$).

Interstate pig movement across the United States

When visualized with the Flow Data Model Tool, interstate movement of pigs in 2001 is dramatic (Figure-30). The highest value states were Iowa (InDegree Centrality), North Carolina (OutDegree Centrality), Illinois (InReach Centrality and OutReach Centrality), and Kansas (Flowbetweenness Centrality) – see Table-26. These rankings, reflected graphically (Figure-31 – Figure-35), show Minnesota, Iowa, Missouri, and Illinois to be consistently in the top quartile of all centrality measurements, with highest values for centrality measurements being located primarily in the Midwestern states.

Interstate pig movement to and from points in Minnesota

Four sets of point-to-point lines were generated in ArcGIS using Flowdata Model Tools (Figure-36), showing movements of breeding swine and feeder swine to and from Minnesota. A linear directional mean was generated each of the four movement types. The linear directional mean graphics show movement to be along a North-South axis for all four datasets. Minnesota received both breeding swine and feeder swine from Canada during the year, but did not reciprocate with any shipments to Canada. Breeding swine came from several outlying points in Canada, Idaho, Georgia, Texas, and North Carolina at the furthest distances.

Travel distances, number of shipments, sum of pigs moved, and pig farm density for county of origin are shown in Table-27. Kruskal-Wallis one-way non-parametric AOV reveals that statistically significant differences exist among the four types of pig movements. Feeding swine traveling from MN travel shorter distances (267.5 km mean) than for other types of pig movement. Feeding swine movements were significantly larger than breeding swine movements, considering the number of shipments, average size of shipment, and sum of pigs moved during the period. The pig farm density for county of origin was different among all four categories of movement, with breeding swine coming from lower density counties and feeder swine coming from higher density counties.

Risk of transportation spread epidemics was estimated by calculating the product of movement data (number of shipments or sum of pigs moved) and pig farm density in the origination county. Maps displaying data for pigs shipped from Minnesota (Figure-37), show that the heaviest concentration of pigs originating from Minnesota were destined for Northern Iowa. Maps of risk estimation differ slightly, but most notable are two counties in Southern Iowa that had received many smaller shipments over the course of the year. In general, the patterns were the same for both risk maps. Figure-38 shows pig movements and risk estimates for shipments into Minnesota. All views confirm that most pigs entering the state are destined for the Southern tier of counties. Risk maps were similar and support this observation.

Pig movement data was analyzed in GeoDA to assess spatial clustering. The resultant maps demonstrate patterns of spatial clustering for sum of pigs shipped x origination county pig farm density, for pigs shipped out of Minnesota and into Minnesota. Pigs shipped out of Minnesota to other states demonstrated high-high clustering (Moran's I = 0.50) throughout the Northern half of Iowa and the Southeastern corner of South Dakota (Figure-39). For pig shipped into Minnesota, there was significant spatial clustering (Moran's I = .23) in five source areas- 1) Southern Ontario, 2) Southern Manitoba, 3) Northeastern Nebraska/Southeastern South Dakota/Northern Iowa, 4) West-central Illinois, and 5) Samson/Duplin/Bladen Counties of North Carolina (Figure-40). Minnesota counties receiving pigs from other states demonstrated significant spatial clustering (Moran's I = 0.68) in the Southwestern portion of the state (Figure-41). Minnesota counties sending pigs to other states showed significant spatial clustering (Moran's I = 0.35) of source counties in the Southcentral portion of the state (Figure-42).

Discussion:

The current US swine industry relies heavily upon the movement of swine between locations. These movements present a special risk – pigs transported into an area bypass the slower, local area spread, which would normally limit the speed of an epidemic disease event. Multisite production is very prevalent. The majority of sites in the two Minnesota counties evaluated (Rice and Stevens) were part of multisite production systems. The predominance of this is similarly reflected in interstate pig movements. The average pig movement distances for Rice and Stevens counties were 68.6 kilometers and 132.0 kilometers, respectively. Interstate pig movements to and from Minnesota had an average travel distance of 493 kilometers. Map illustration of these movement patterns shows significant overlap of swine movements. With a high degree of animal movement, there cease to be discretely contained geographic areas, as one area readily bleeds across to another distant area via transportation. Social network analysis of a national survey of interstate pig movements showed states to differ with regards to their network characteristics. In particular, North Carolina has a high InReach centrality statistic, illustrating their influence on other states via a large net pig export to the Midwest.

Social network analysis has been used to describe infection risk for swine diseases in countries other than the US. In these efforts, very large network datasets were available for analysis (using national movement-level datasets), and the authors were able to demonstrate that animal movement patterns were highly heterogeneous, making traditional modeling very less valid. In some cases, the calculated network analysis statistics have been demonstrated as valuable in identifying sites at a higher risk for infection[132]. Modeling exercises which specifically restricted those sites identified by higher centrality values, showed significant reduction in size of a disease epidemic[136, 137]. The current study was limited by the size and completeness of its network. Of the sites considered, only half were within the county (93 or 158 sites in Stevens County and 63 or 129 sites in Rice County). PRRS status for sites outside the county was not known. Therefore half of the potential network components were not included in the logistic regression analysis. Aside from this, the complexity of disease transmission over time and the persistence of PRRS on a farm are not well addressed by such a cross-sectional view. For example, PRRS may have been introduced years before by to any number of routes, persisting until today, regardless of the size or nature of the farm network described here.

Compared with other developed nations, the US lacks detailed livestock premise and movement. The data analyzed here (pig movements in two Minnesota counties, a detailed account of one year's interstate pig movements into and out of Minnesota, and a summary of annual interstate pig movements) offer insight into the degree of pig movement occurring regularly throughout the year. Social network analysis offers the possibility of identifying high risk entities and focusing resources for diagnostic monitoring, preventive action, and intervention during an epidemic. These observations further illustrate the need for a comprehensive national system to identify farm location and track animal movements.

Figures

Figure-1 (Reprinted from Southeastern Cooperative Wildlife Disease Study). Pages 13 and 33.

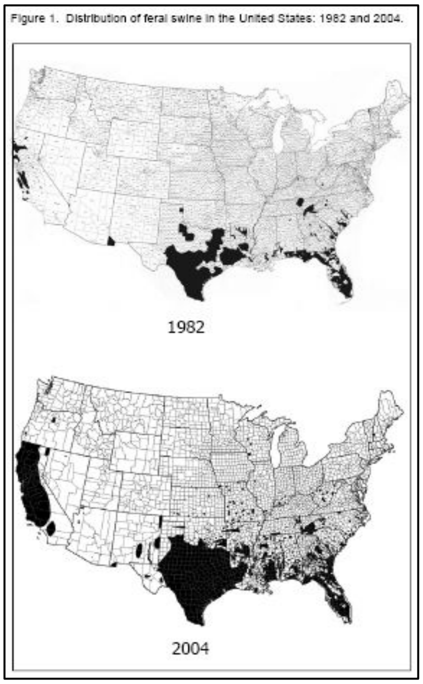


Figure-2 (Reprinted from Google Earth). Page 34.

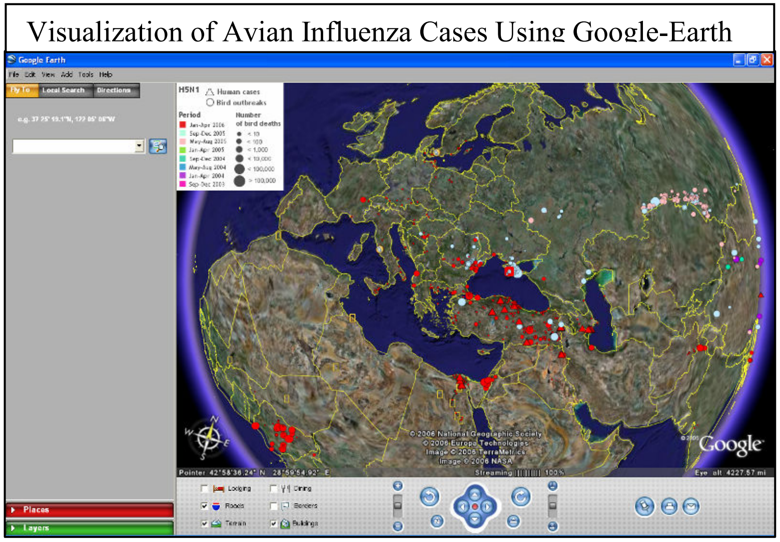


Figure-3 (Reprinted from MN Cooperative Disease Mapping Website. Page 34

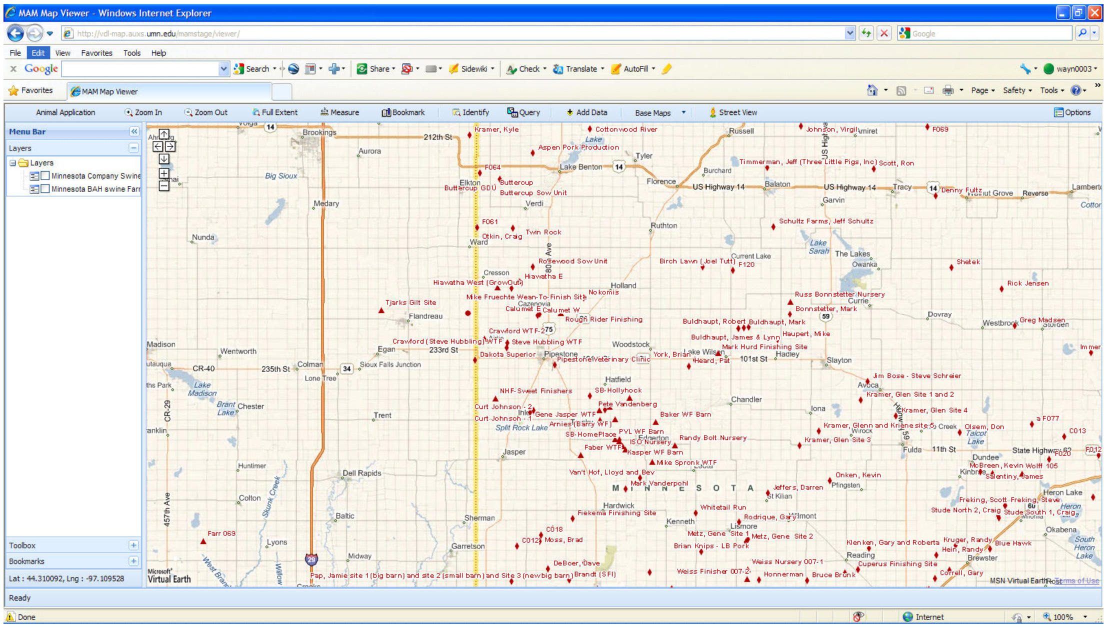


Figure-4. Page 41.

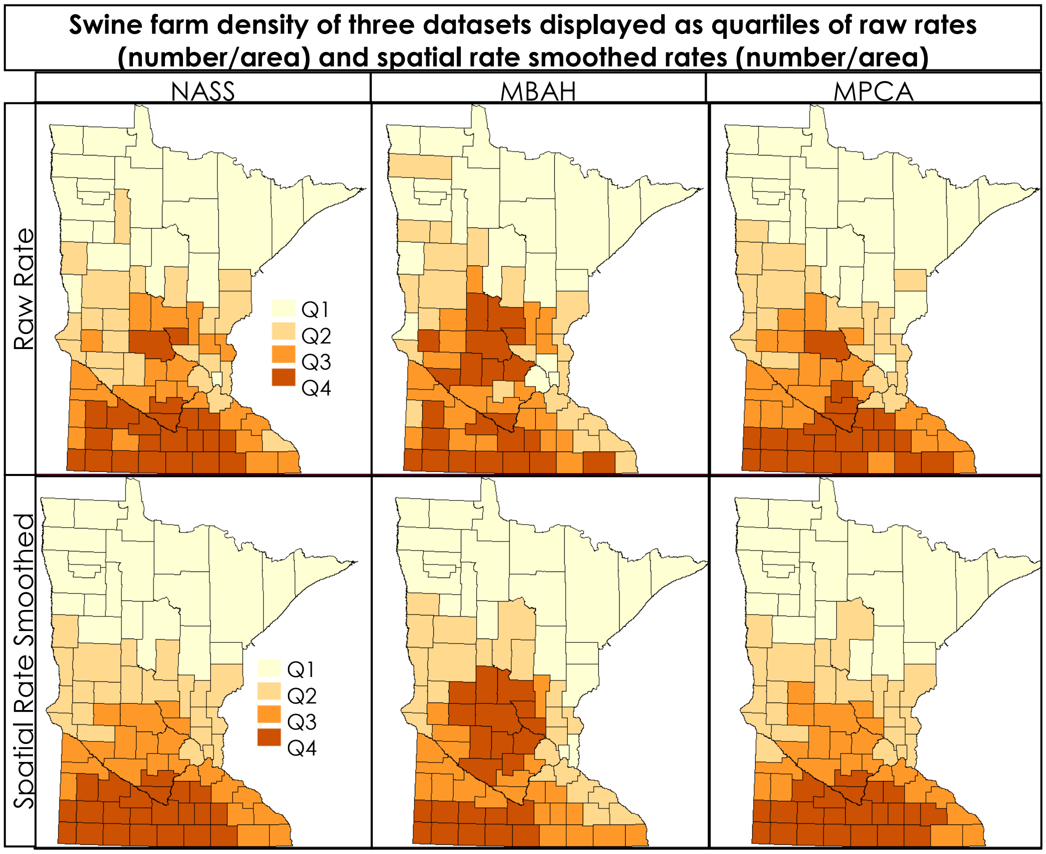
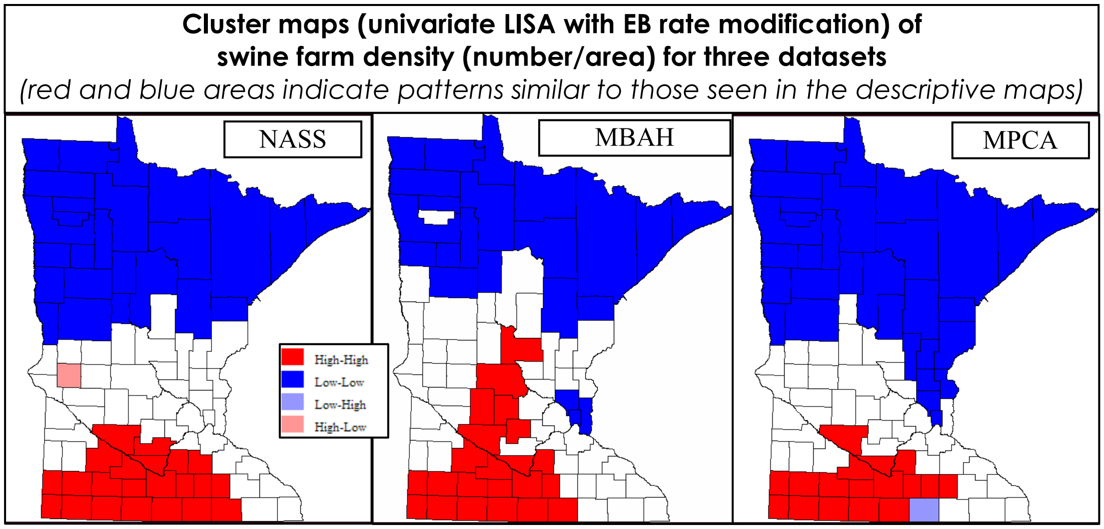

Swine farm density of three datasets displayed as quartiles of raw rates (number/area) and spatial rate smoothed rates (number/area)

Figure-5. Page 41.


Cluster maps (univariate LISA with EB rate modification) of swine farm density (number/area) for three datasets

(red and blue areas indicate patterns similar to those seen in the descriptive maps)

Figure-6. Page 42.

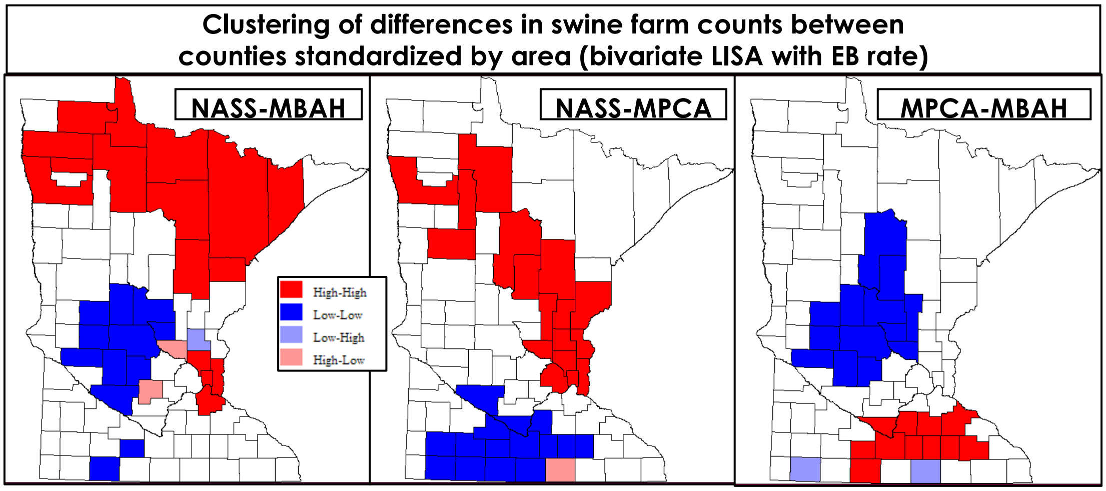

Clustering of differences in swine farm counts between counties standardized by area (bivariate LISA with EB rate)

Figure-7. Pages 42, 44, and 45.

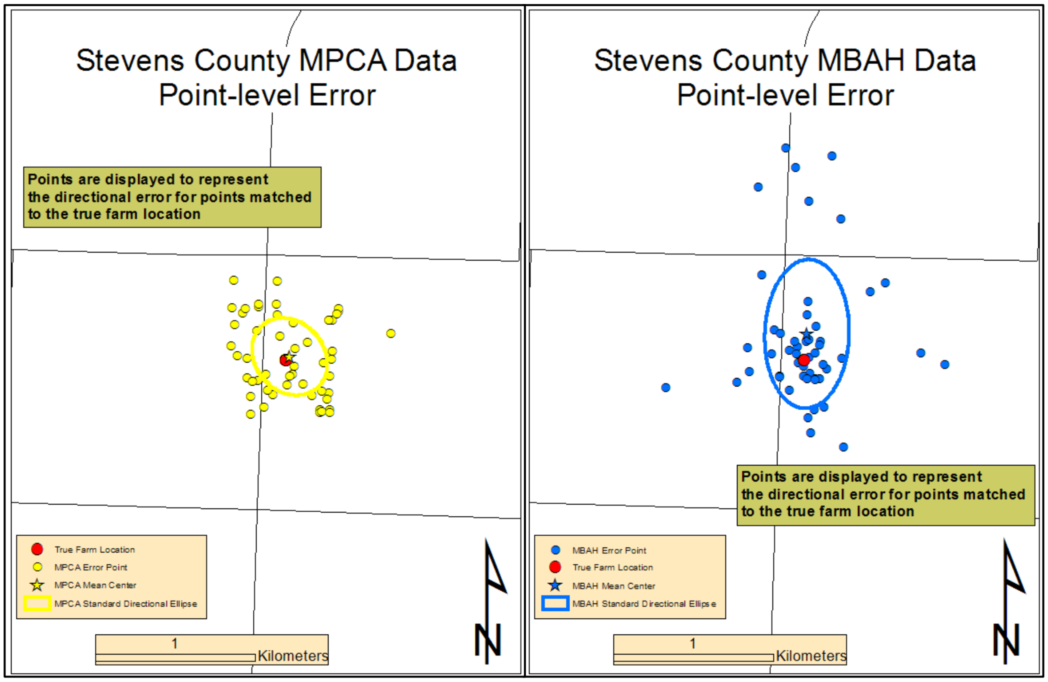


Figure-8. Pages 42, 44, and 45.

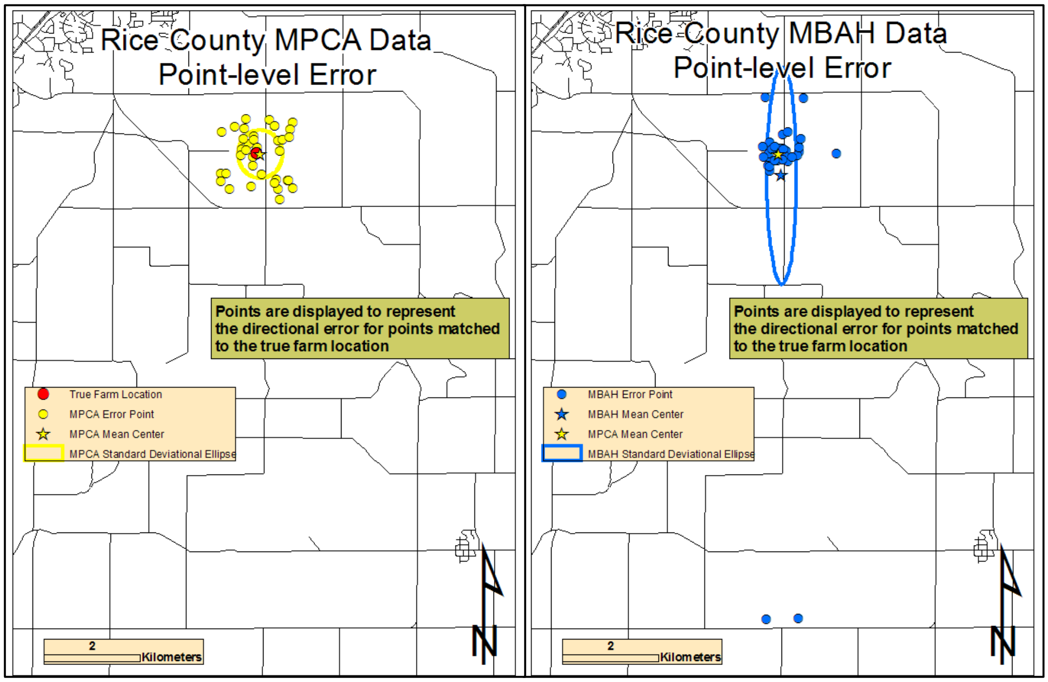


Figure-9. Page 43.

Histograms of point-level error (distance from presumed location to verified true location) for two datasets in Stevens County and Rice County

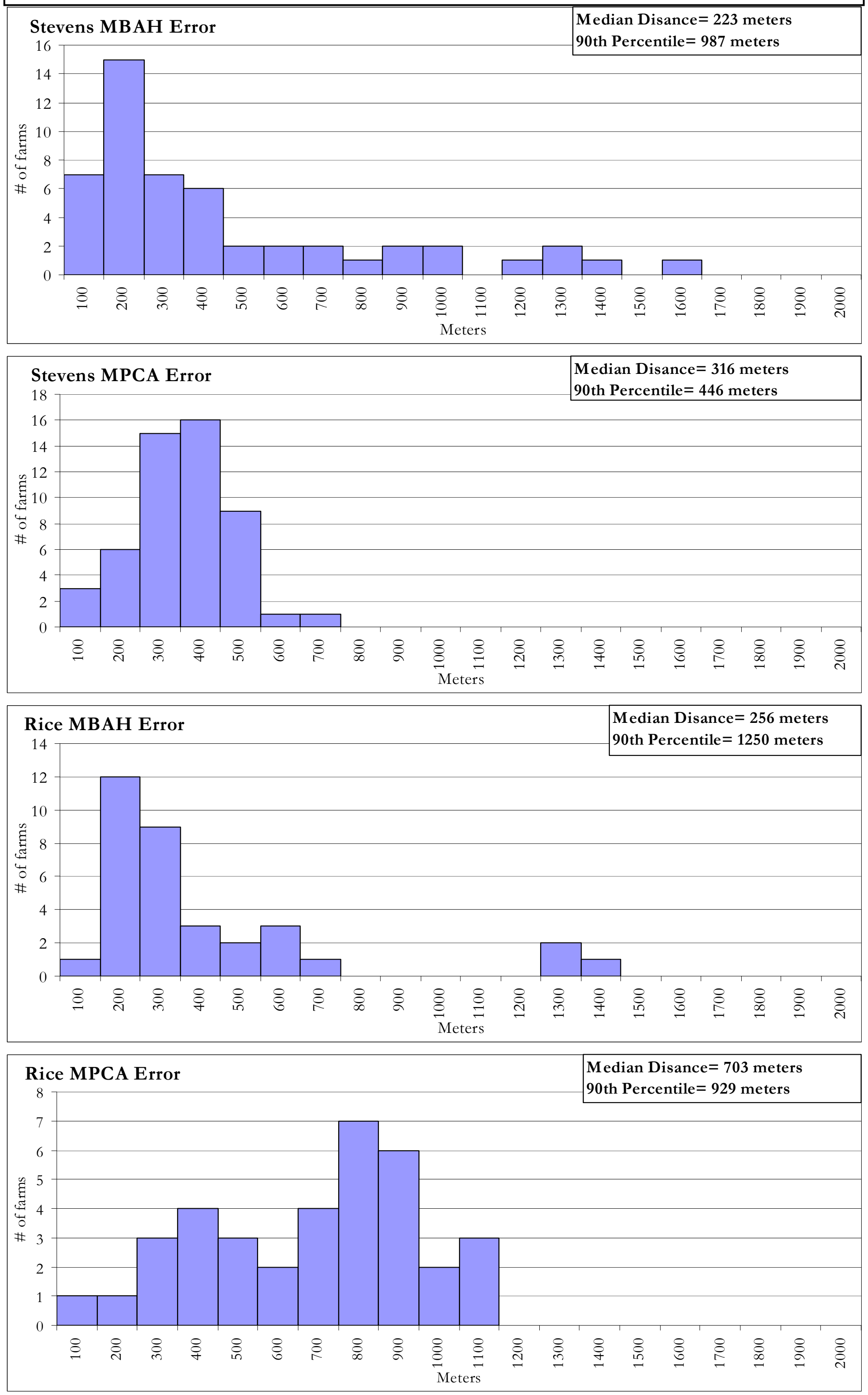
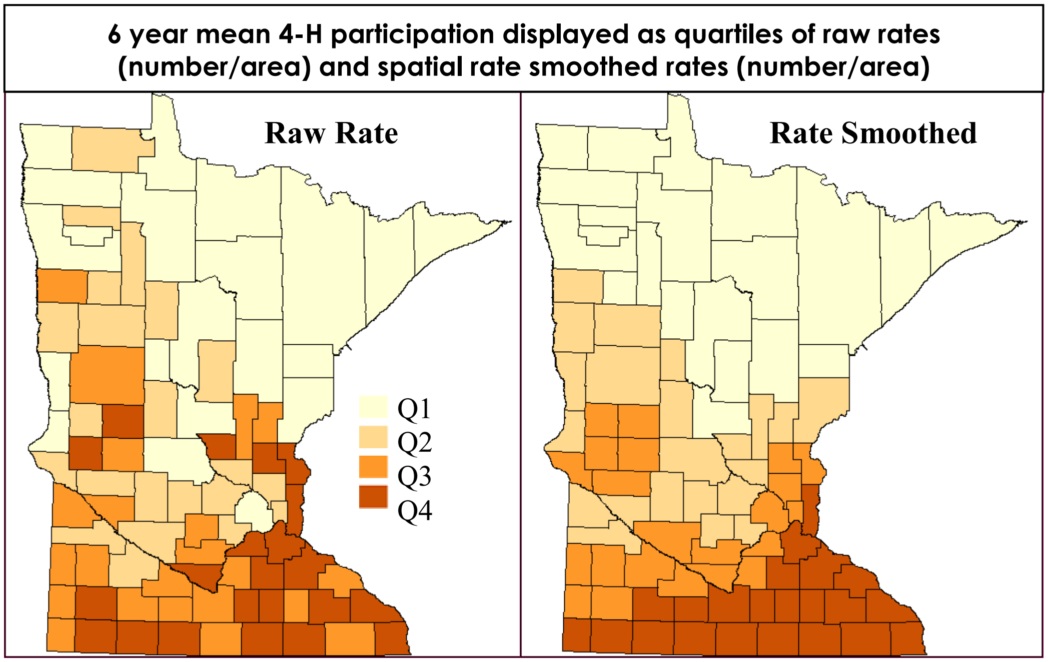
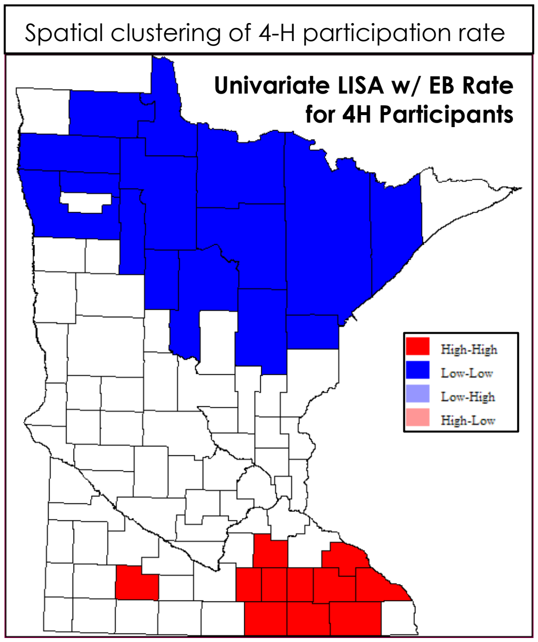


Figure-10. Page 43.



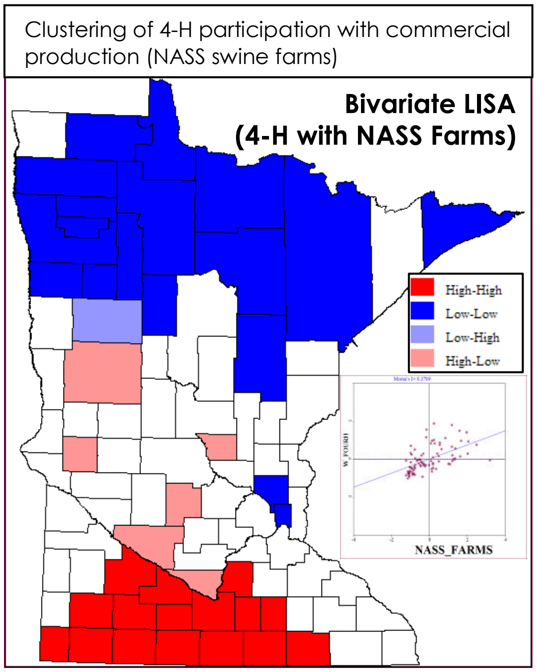
6 year mean 4-H participation displayed as quartiles of raw rates (number/area) and spatial rate smoothed rates (number/area)

Figure-11. Page 43.



Spatial clustering of 4-H participation rate

Figure-12. Page 43.



Clustering of 4-H participation with commercial production (NASS swine farms)

Figure-13. Page 49.

Orthophotograph with overlay of temperature grid given as an example of different data scales

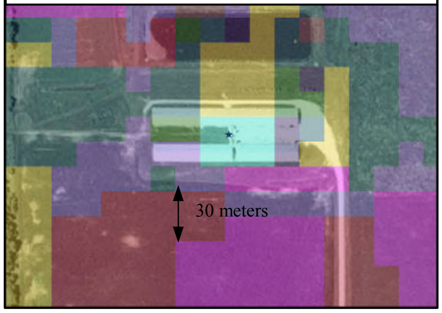


Figure-14. Page 50.

Geographic distributions of three different point datasets

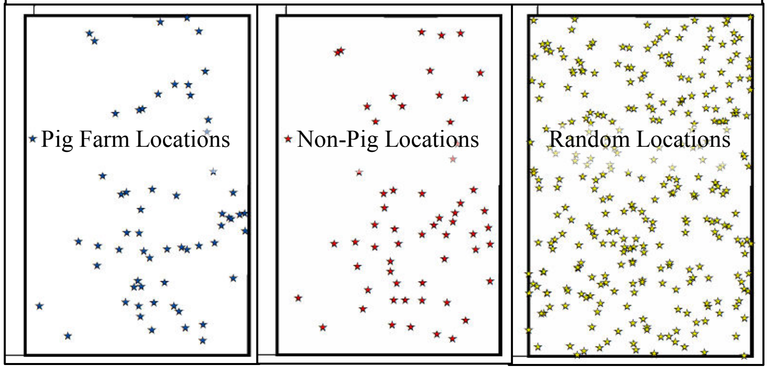


Figure-15. Page 50.

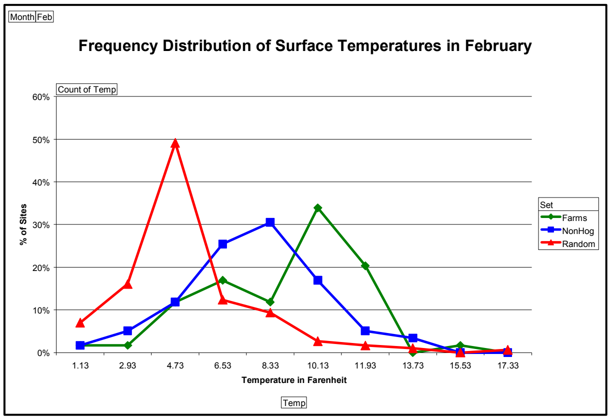


Figure-16. Pages 50 and 51.

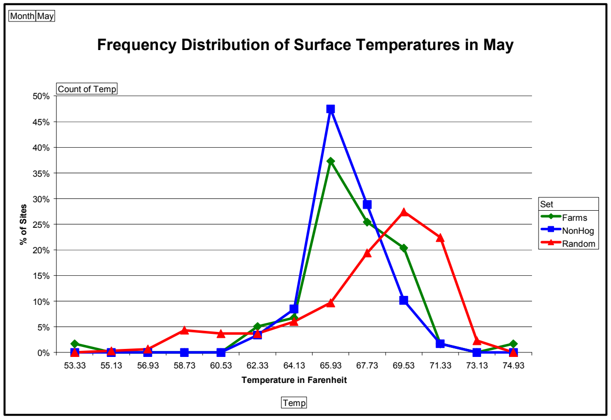


Figure-17. Page 51.

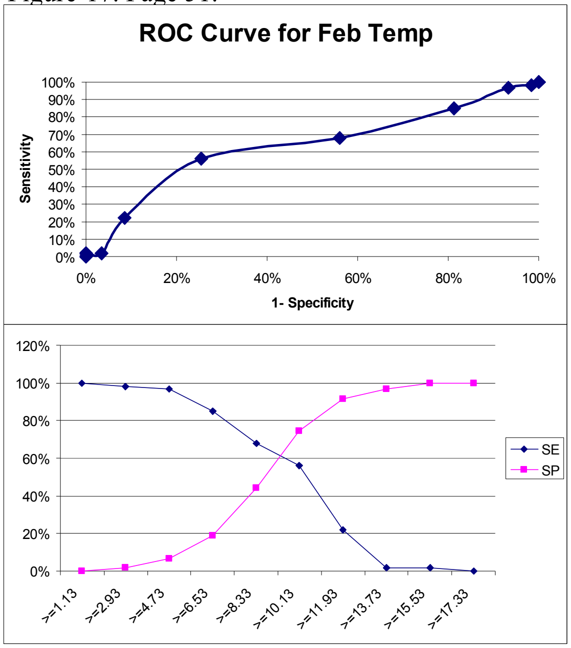


Figure-18. Page 51.

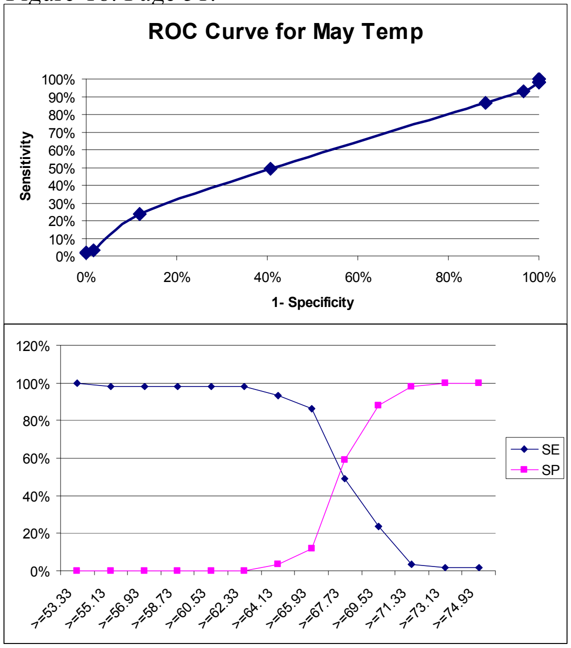
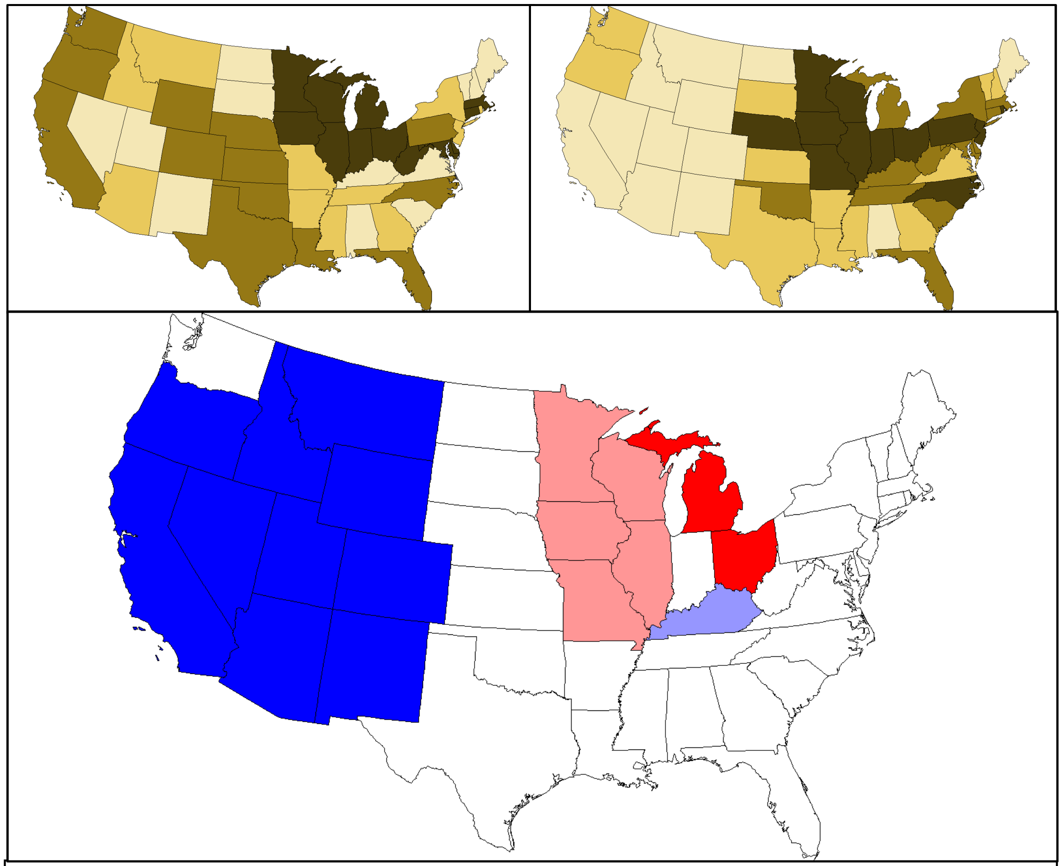
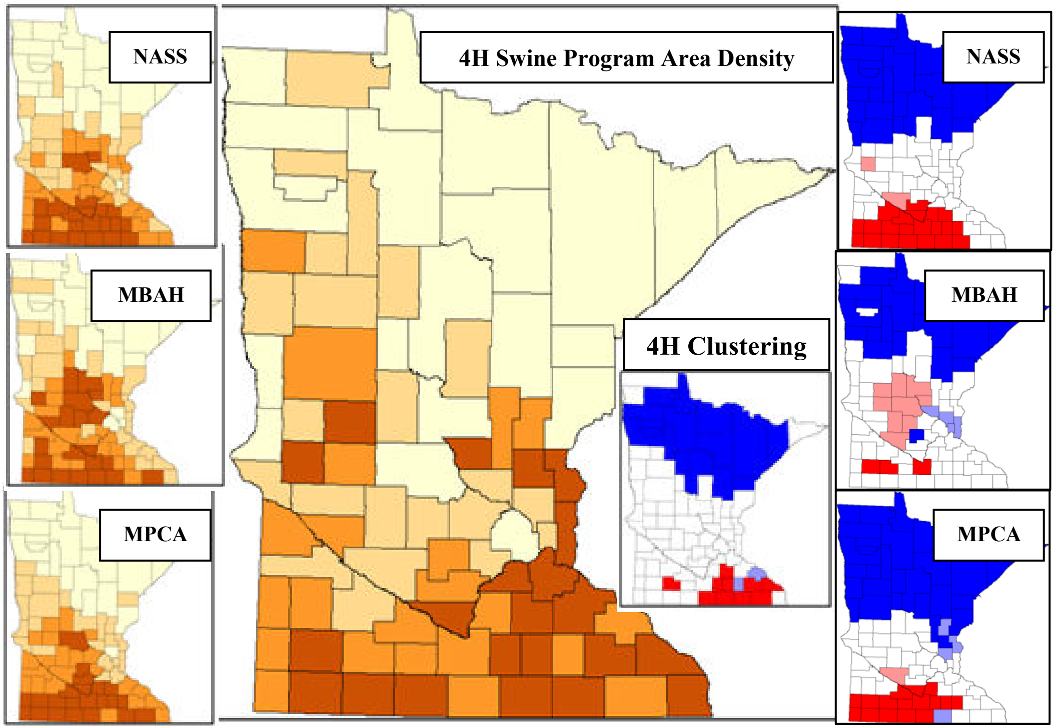


Figure-19. Page 59.



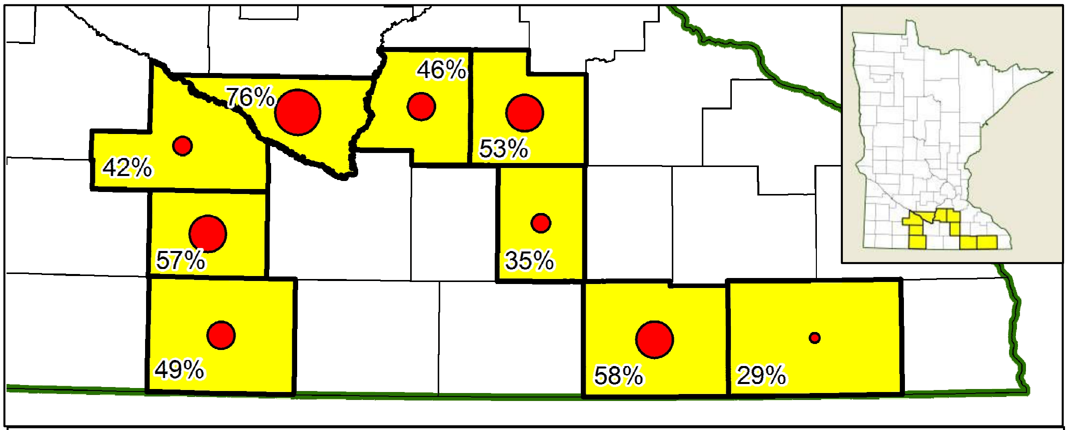
Spatial correlation (state level) between 4-H swine program participation density and commercial swine production (NASS 2002). Quartile map of 4H swine program participation area density (upper left) Quartile map of commercial swine production area density (upper right). Light to dark shading indicates low to high density. Bivariate LISA map showing spatial correlation of 4H swine program participation area density with commercial swine production area density. Dark Red = “High-High” spatial autocorrelation; Dark-blue “Low-Low” autocorrelation; Light-red = “High commercial-Low 4-H” autocorrelation; Light-blue = “Low commercial-High 4-H” autocorrelation; White = no significant spatial autocorrelation.

Figure-20. Page 59.



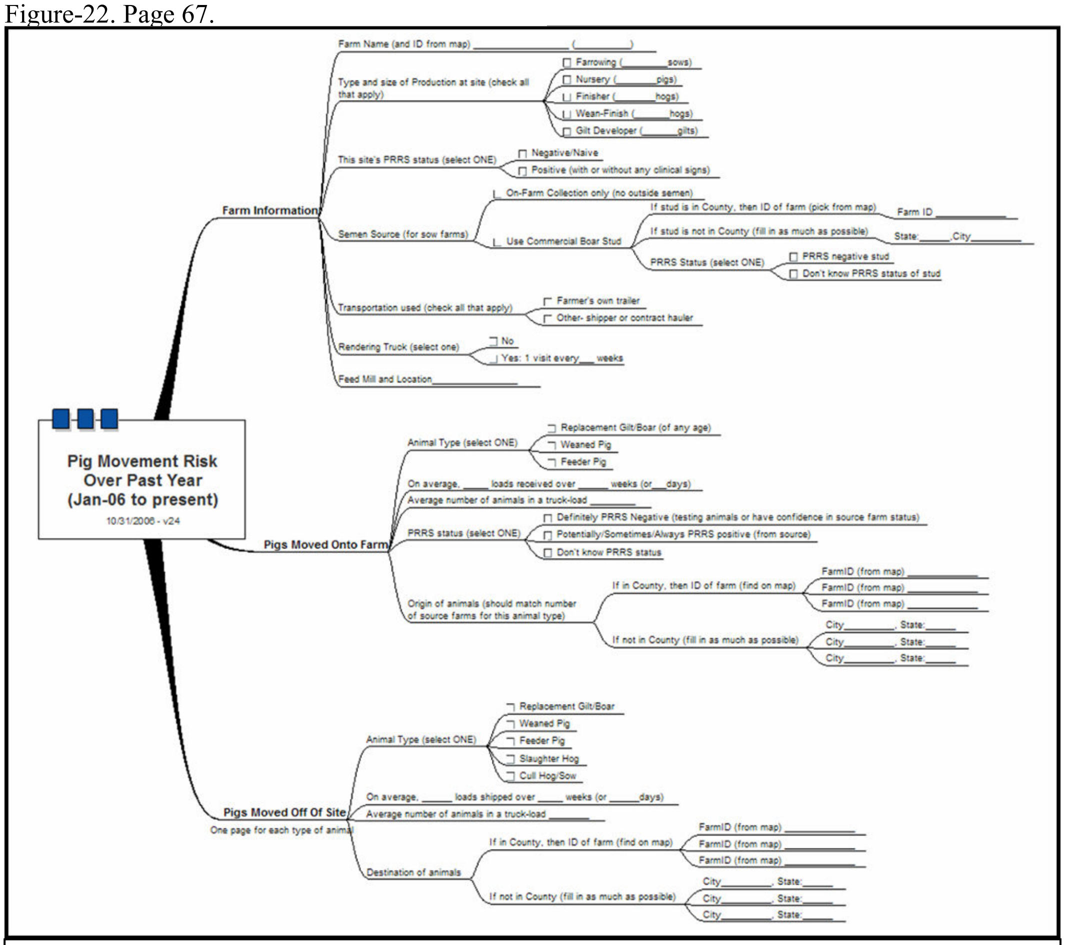
Spatial correlation (county level) between 4-H swine program participation density and commercial swine farm area density based on NASS (A) MBAH (B), and MPCA databases(C). Quartile maps of Commercial Swine production area density from three databases (left). Quartile map of 4H swine program participation area density (center). Univariate LISA map of spatial autocorrelation of 4H swine program participation area density (center inset). Bivariate LISA maps of spatial correlation of 4H swine program participation area density with three databases of commercial swine production area density (right). Dark Red = "High-High" spatial autocorrelation; Dark-blue "Low-Low" autocorrelation; Light-red = "High commercial-Low 4-H" autocorrelation; Light-blue = "Low commercial-High 4-H" autocorrelation; White = no significant spatial autocorellation.

Figure-21. Page 61.



Seroprevalence of PRRS virus in nine Minnesota counties with pigs sampled at slaughter following the respective county fairs (inset shows locations in Minnesota)

Figure-22. Page 67.



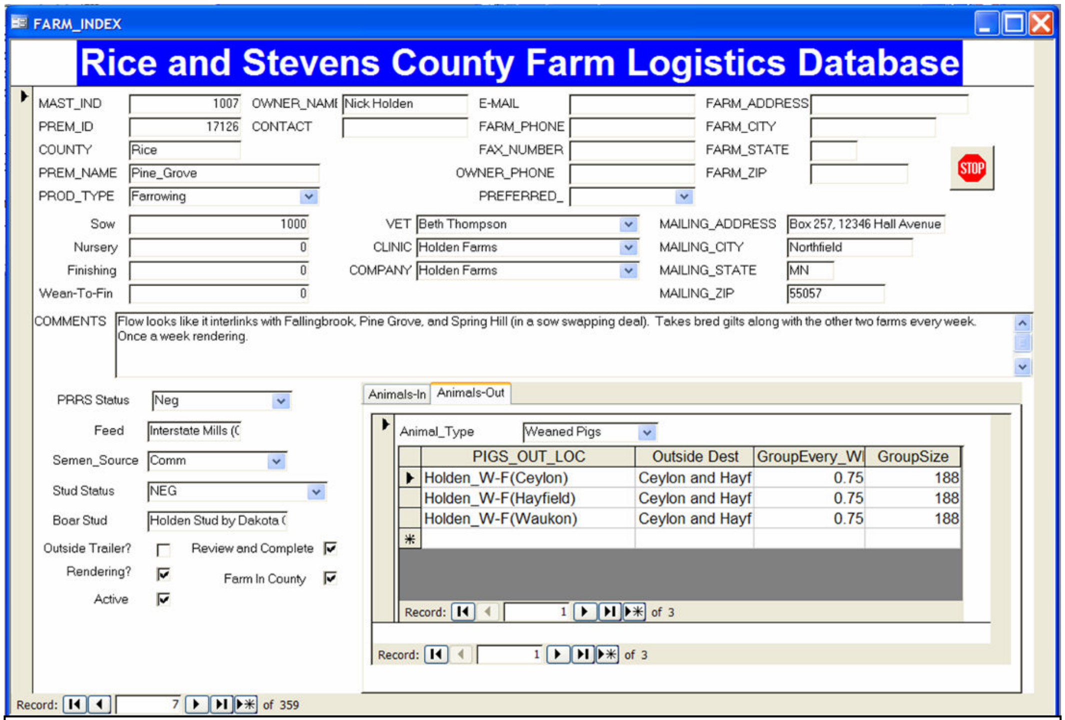
Pig Movement Risk Over Past Year (Jan-06 to present)

10/31/2006 - v24

- **Farm Information**
  - Farm Name (and ID from map) ______________ (__________)
  - Type and size of Production at site (check all that apply)
    - ☐ Farrowing (________sows)
    - ☐ Nursery (_______pigs)
    - ☐ Finisher (_______hogs)
    - ☐ Wean-Finish (______hogs)
    - ☐ Gilt Developer (______gilts)
  - This site's PRRS status (select ONE)
    - ☐ Negative/Naive
    - ☐ Positive (with or without any clinical signs)
  - Semen Source (for sow farms)
    - ☐ On-Farm Collection only (no outside semen)
    - ☐ Use Commercial Boar Stud
      - If stud is in County, then ID of farm (pick from map)
        - Farm ID ____________
      - If stud is not in County (fill in as much as possible)
        - State:______,City__________
      - PRRS Status (select ONE)
        - ☐ PRRS negative stud
        - ☐ Don't know PRRS status of stud
  - Transportation used (check all that apply)
    - ☐ Farmer's own trailer
    - ☐ Other- shipper or contract hauler
  - Rendering Truck (select one)
    - ☐ No
    - ☐ Yes: 1 visit every___ weeks
  - Feed Mill and Location_______________
- **Pigs Moved Onto Farm**
  - Animal Type (select ONE)
    - ☐ Replacement Gilt/Boar (of any age)
    - ☐ Weaned Pig
    - ☐ Feeder Pig
  - On average, _____ loads received over ______ weeks (or___days)
  - Average number of animals in a truck-load _________
  - PRRS status (select ONE)
    - ☐ Definitely PRRS Negative (testing animals or have confidence in source farm status)
    - ☐ Potentially/Sometimes/Always PRRS positive (from source)
    - ☐ Don't know PRRS status
  - Origin of animals (should match number of source farms for this animal type)
    - If in County, then ID of farm (find on map)
      - FarmID (from map) ____________
      - FarmID (from map) ____________
      - FarmID (from map) ____________
    - If not in County (fill in as much as possible)
      - City__________, State:______
      - City__________, State:______
      - City__________, State:______
- **Pigs Moved Off Of Site**
  One page for each type of animal
  - Animal Type (select ONE)
    - ☐ Replacement Gilt/Boar
    - ☐ Weaned Pig
    - ☐ Feeder Pig
    - ☐ Slaughter Hog
    - ☐ Cull Hog/Sow
  - On average, ______ loads shipped over _____ weeks (or ______days)
  - Average number of animals in a truck-load ________
  - Destination of animals
    - If in County, then ID of farm (find on map)
      - FarmID (from map) ____________
      - FarmID (from map) ____________
      - FarmID (from map) ____________
    - If not in County (fill in as much as possible)
      - City__________, State:______
      - City__________, State:______
      - City__________, State:______

Survey administered to farmers, managers, and veterinarians associated with swine farms and markets within the Rice County and Stevens County study area.

Figure-23. Page 67.



Rice and Stevens County Farm Logistics Database

MAST_IND	1007	OWNER_NAMI	Nick Holden
PREM_ID	17126	CONTACT	
COUNTY	Rice		
PREM_NAME	Pine_Grove		
PROD_TYPE	Farrowing		

E-MAIL		FARM_ADDRESS	
FARM_PHONE		FARM_CITY	
FAX_NUMBER		FARM_STATE	
OWNER_PHONE		FARM_ZIP	
PREFERRED_			

Sow	1000	VET	Beth Thompson	MAILING_ADDRESS	Box 257, 12346 Hall Avenue
Nursery	0	CLINIC	Holden Farms	MAILING_CITY	Northfield
Finishing	0	COMPANY	Holden Farms	MAILING_STATE	MN
Wean-To-Fin	0			MAILING_ZIP	55057

COMMENTS Flow looks like it interlinks with Fallingbrook, Pine Grove, and Spring Hill (in a sow swapping deal). Takes bred gilts along with the other two farms every week. Once a week rendering.

PRRS Status	Neg
Feed	Interstate Mills ((
Semen_Source	Comm
Stud Status	NEG
Boar Stud	Holden Stud by Dakota (

Outside Trailer? ☐ Review and Complete ☑
Rendering? ☑ Farm In County ☑
Active ☑

Animals-In | Animals-Out

Animal_Type Weaned Pigs

PIGS_OUT_LOC	Outside Dest	GroupEvery_WI	GroupSize
Holden_W-F(Ceylon)	Ceylon and Hayf	0.75	188
Holden_W-F(Hayfield)	Ceylon and Hayf	0.75	188
Holden_W-F(Waukon)	Ceylon and Hayf	0.75	188

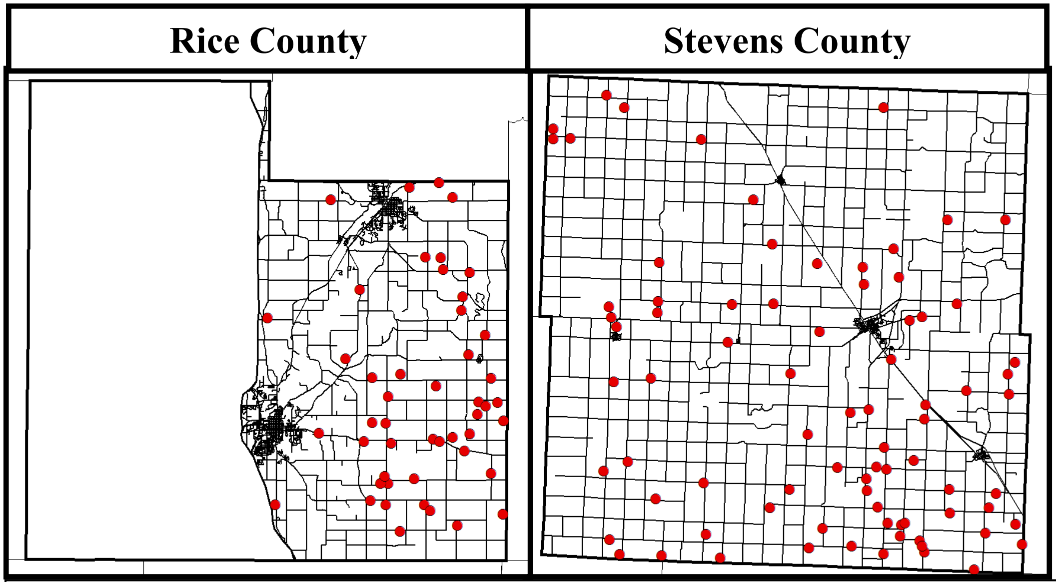
Record: 1 of 3

Record: 1 of 3

Record: 7 of 359

Screenshot of data entry form in Microsoft Access database used for collecting pig movement information.

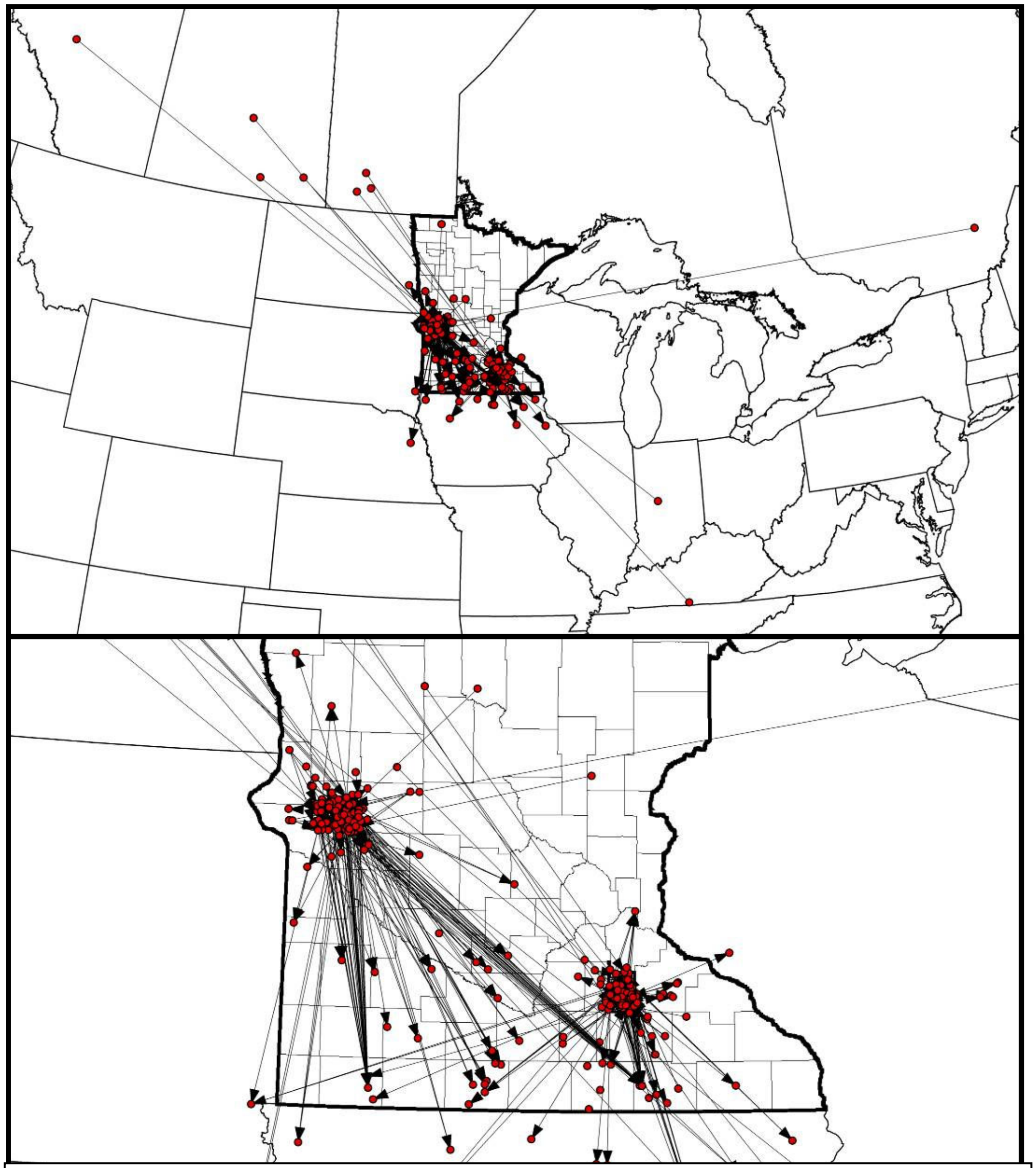
Figure-24. Page 70.


Rice County

Stevens County

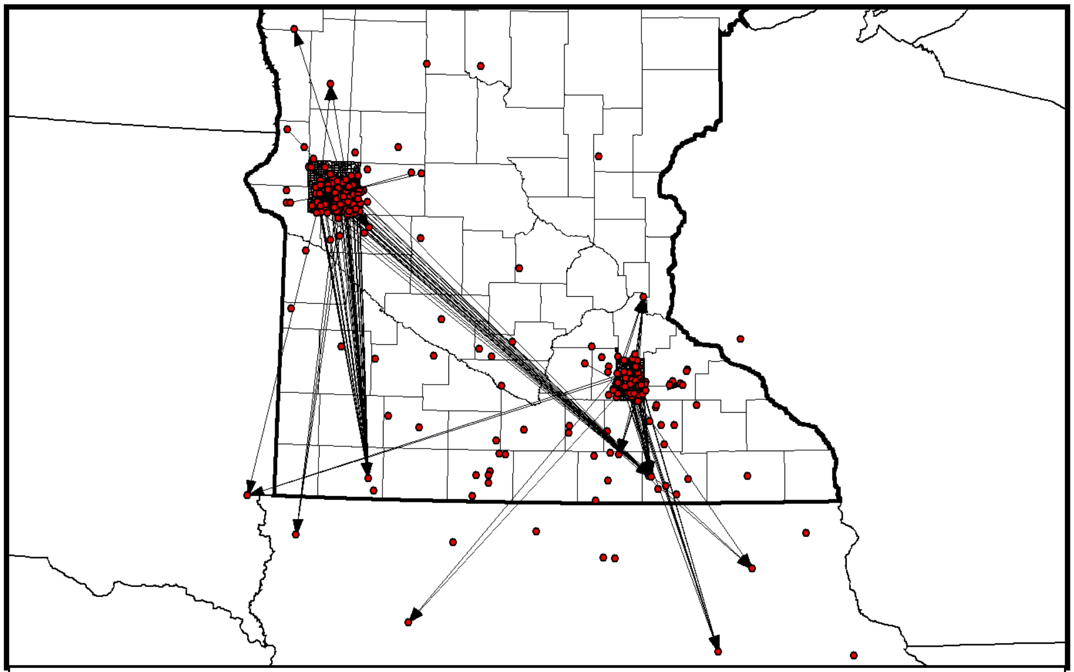
Map Rice and Stevens counties, showing 128 farm or market locations (red dots), with county boundaries and public roads. Only the eastern portion of Rice County was included in the study.

Figure-25. Page 70.



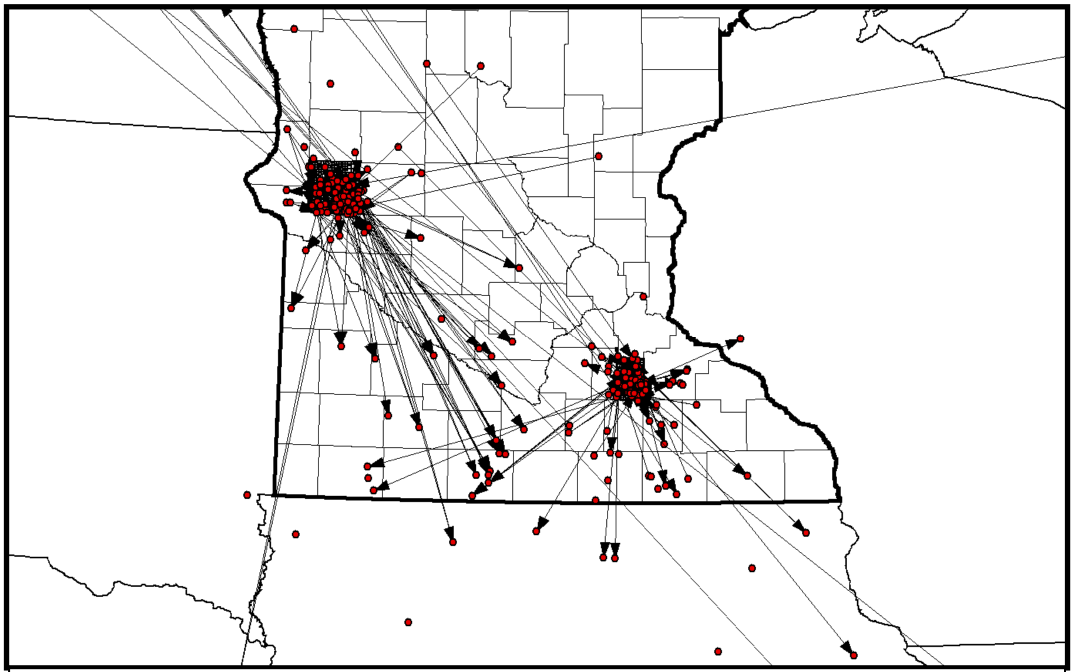
Flow representation of movements into, out of, and within Stevens County and Eastern Rice County, displayed at different scales- Central North America (top) and Southern Minnesota (bottom). Red dots represent farm locations. Black arrow lines represent pig movements.

Figure-26. Page 70.



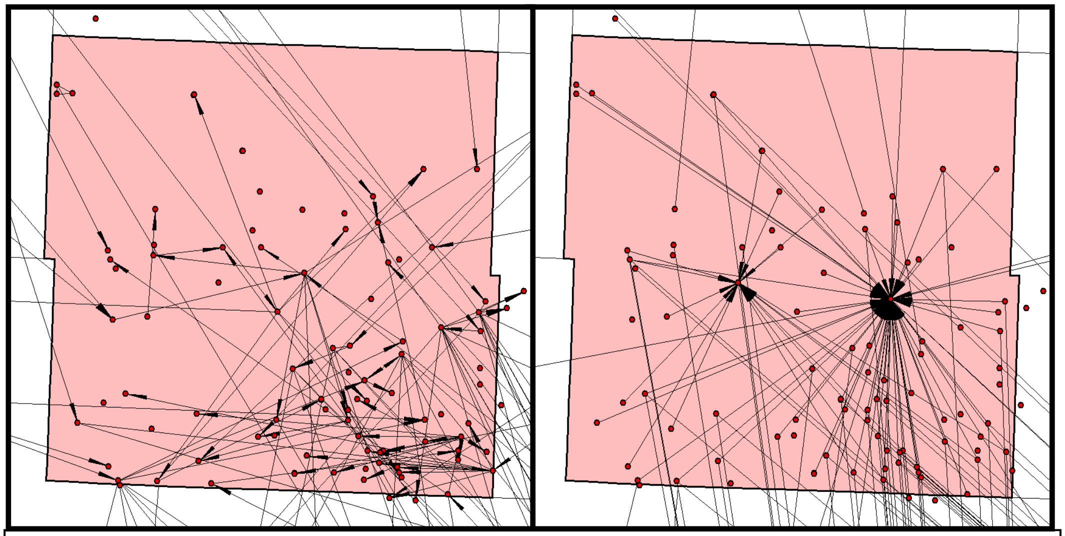
Flow of pigs moving to market destinations, either commercial slaughter or cull animals. Markets are either intermediary or terminal.

Figure-27. Page 70.



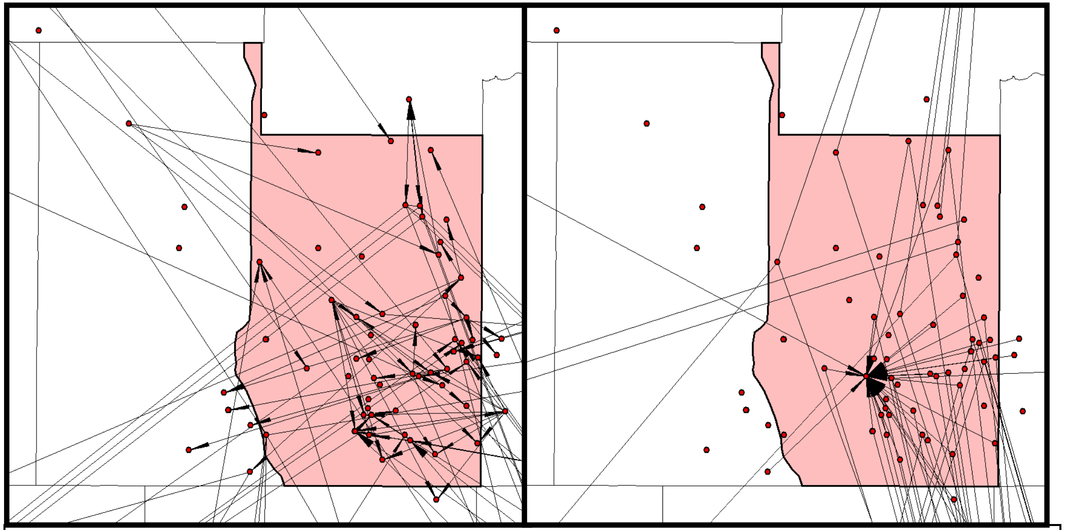
Flow of pigs moving to non-market destinations, either as weaned pigs, feeder pigs, or replacement breeding stock.

Figure-28. Page 70.



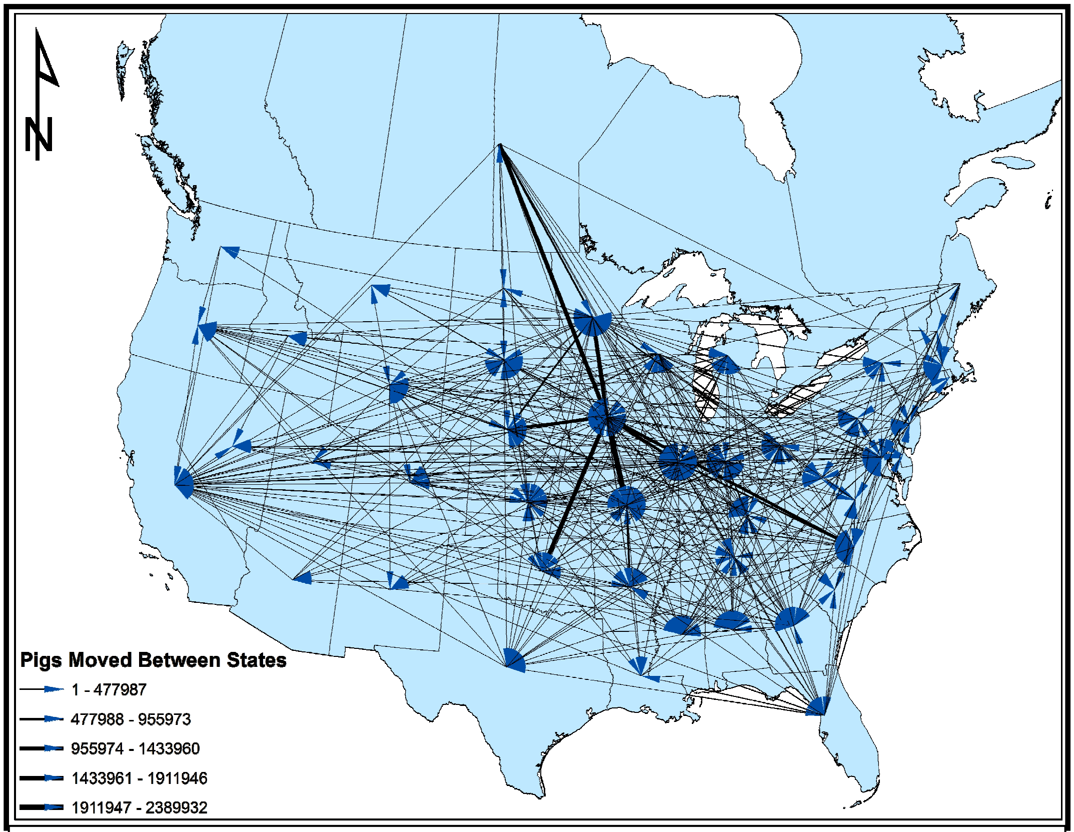
County-level view of non-market pig flow (left) and market-directed pig flow (right) in Stevens County

Figure-29. Page 70.



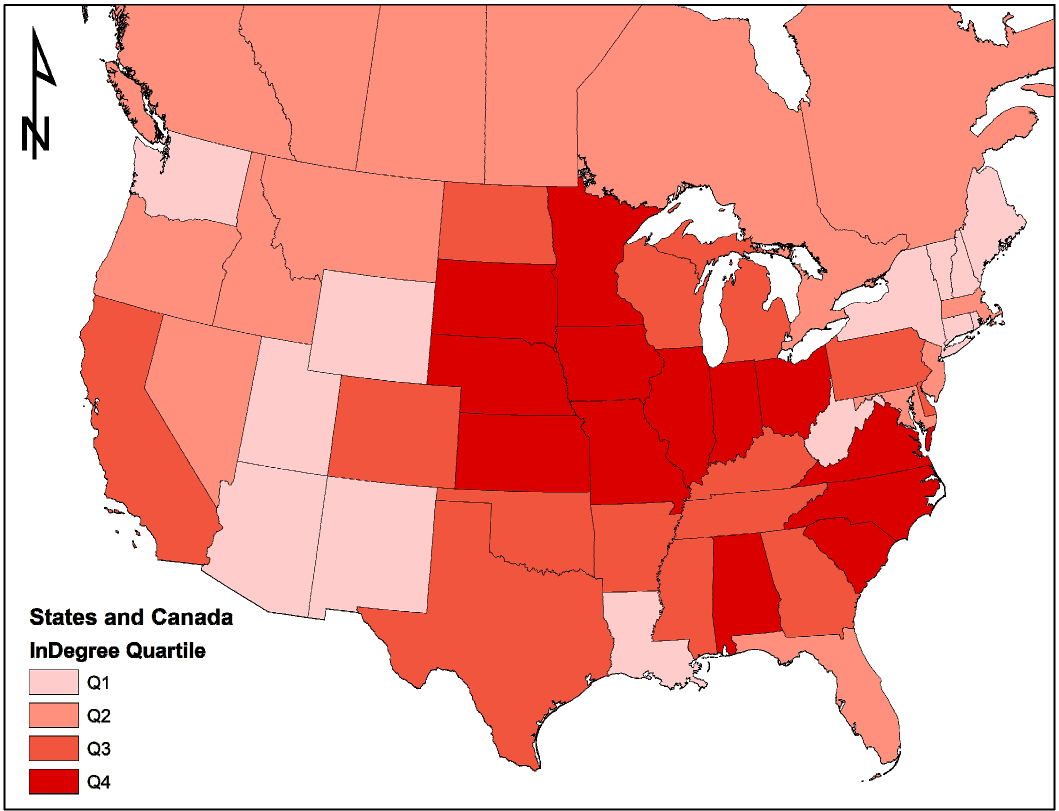
County-level view of non-market pig flow (left) and market-directed pig flow (right) in Rice County

Figure-30. Page 71.



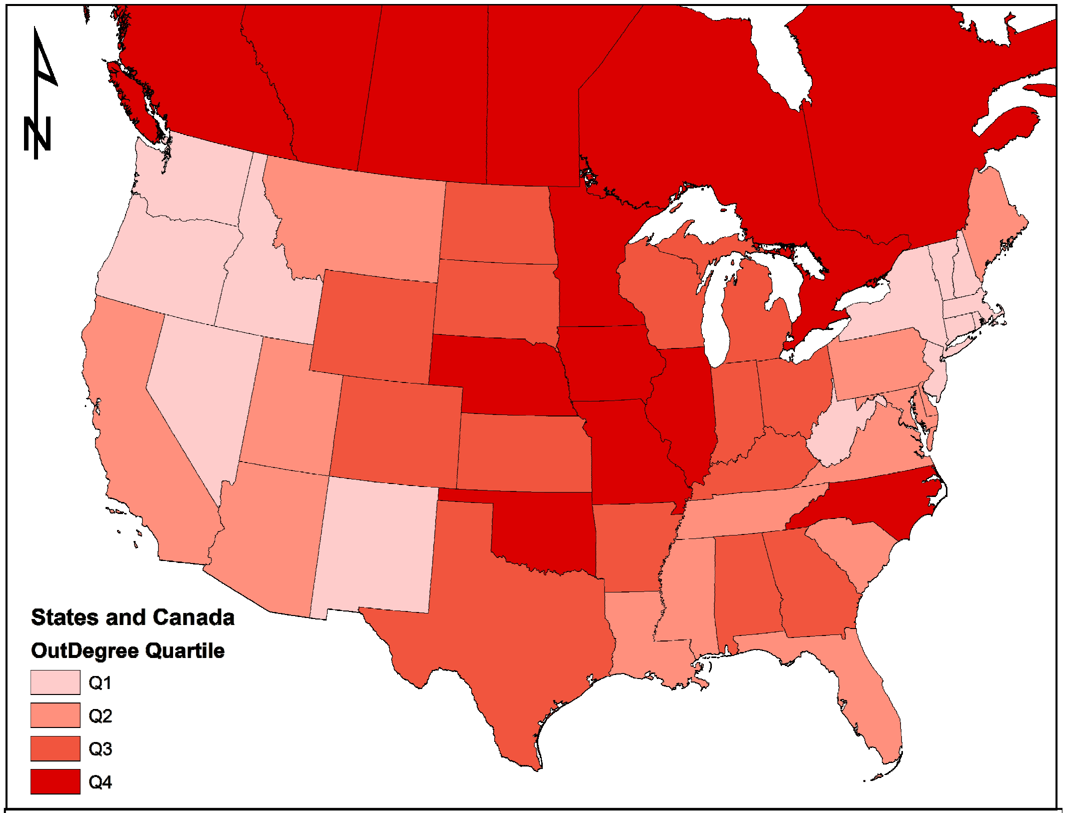
Interstate movement of pigs between all states and Canada. Canada is represented as a single point. Black flow lines are weighted to represent number of pigs moved.

Figure-31. Page 71.



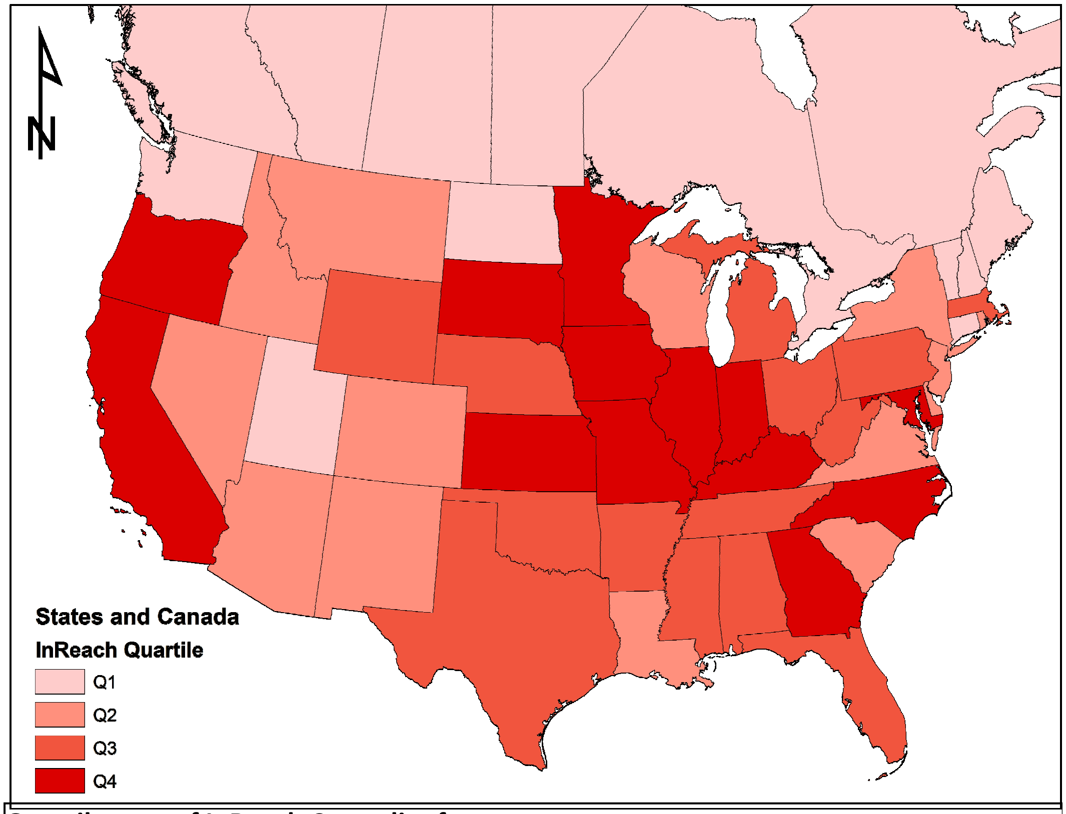
Quartile map of InDegree Centrality for states.

Figure-32. Page 71.



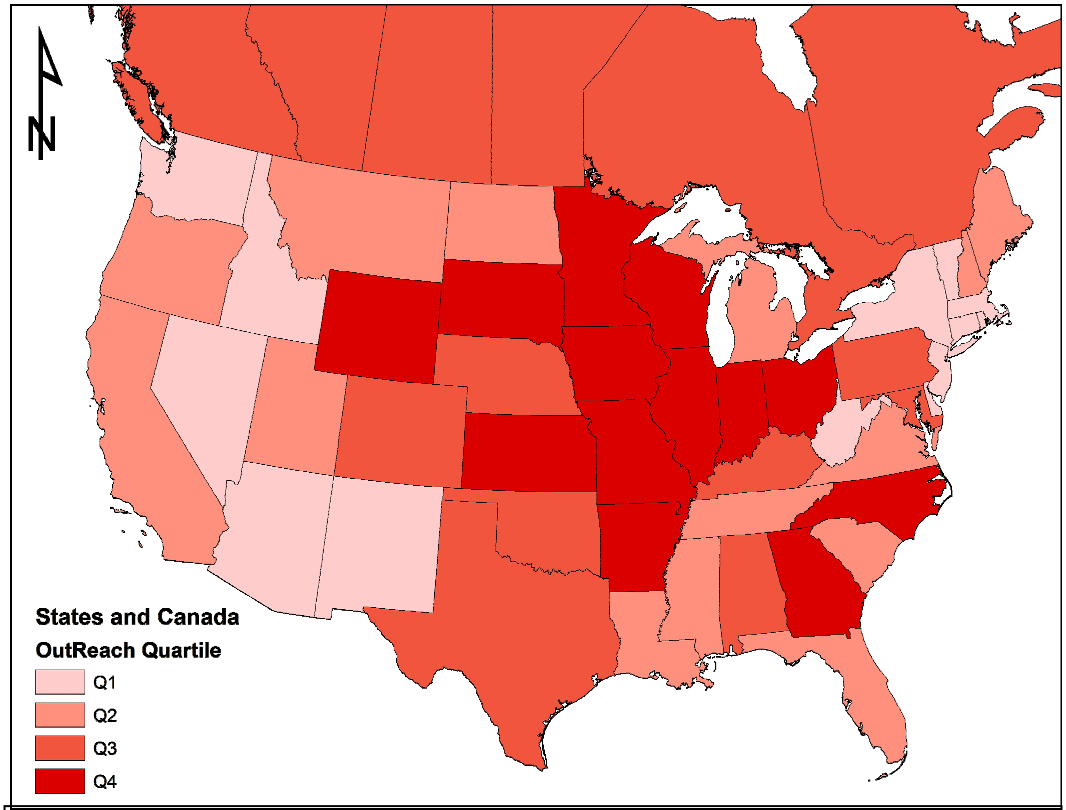
Quartile map of OutDegree Centrality for states.

Figure-33. Page 71.



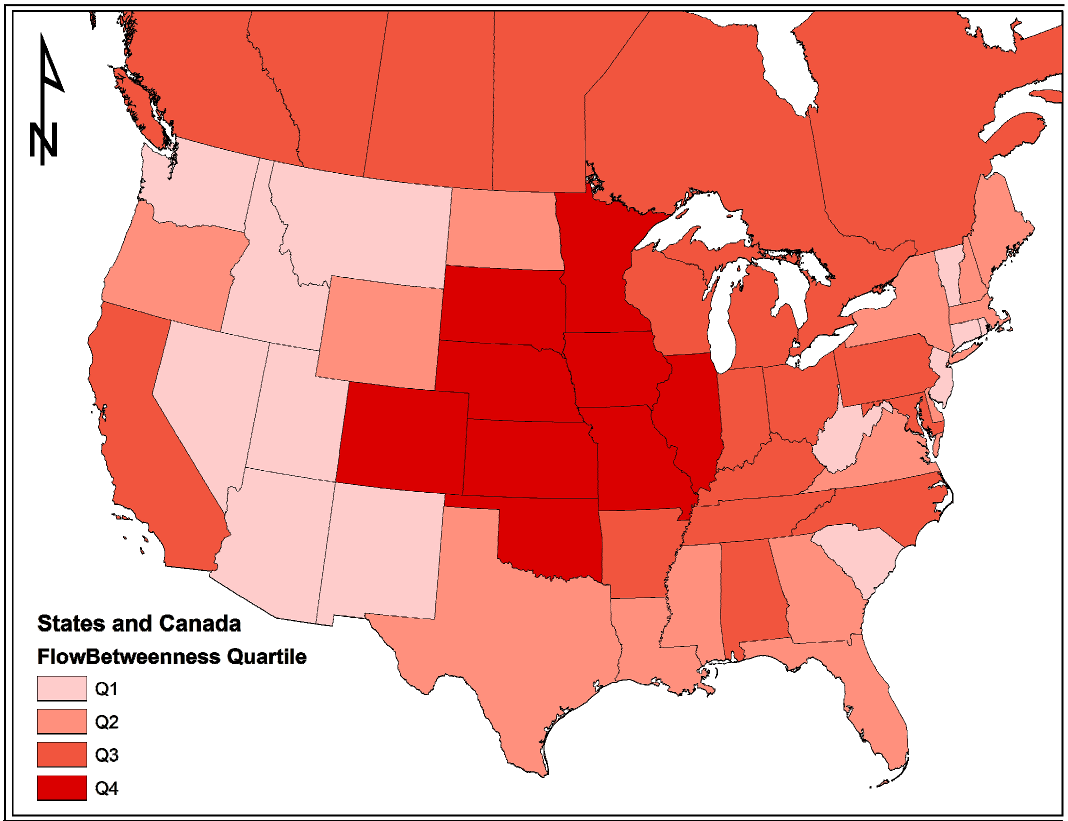
Quartile map of InReach Centrality for states.

Figure-34. Page 71.



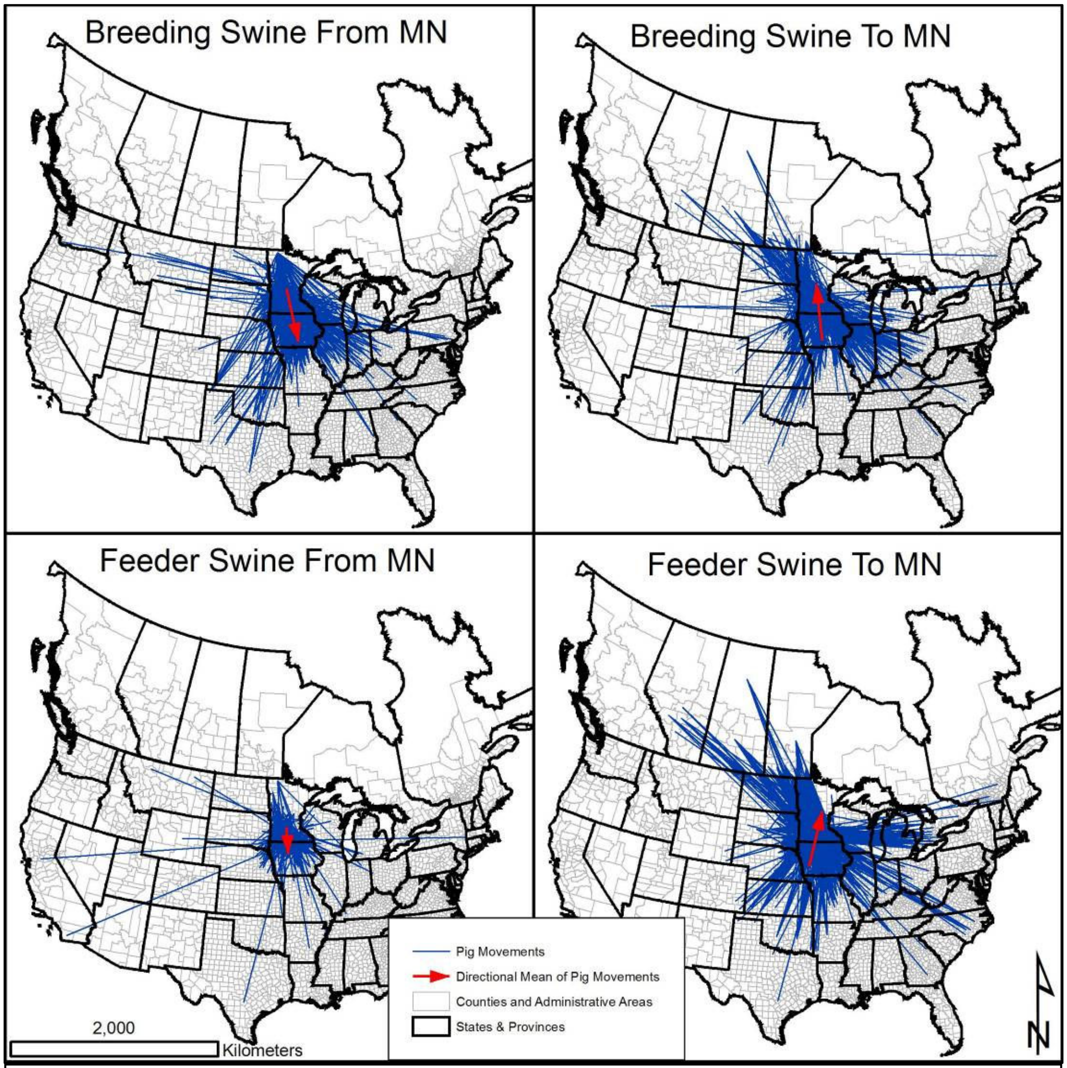
Quartile map of OutReach Centrality for states.

Figure-35. Page 71.



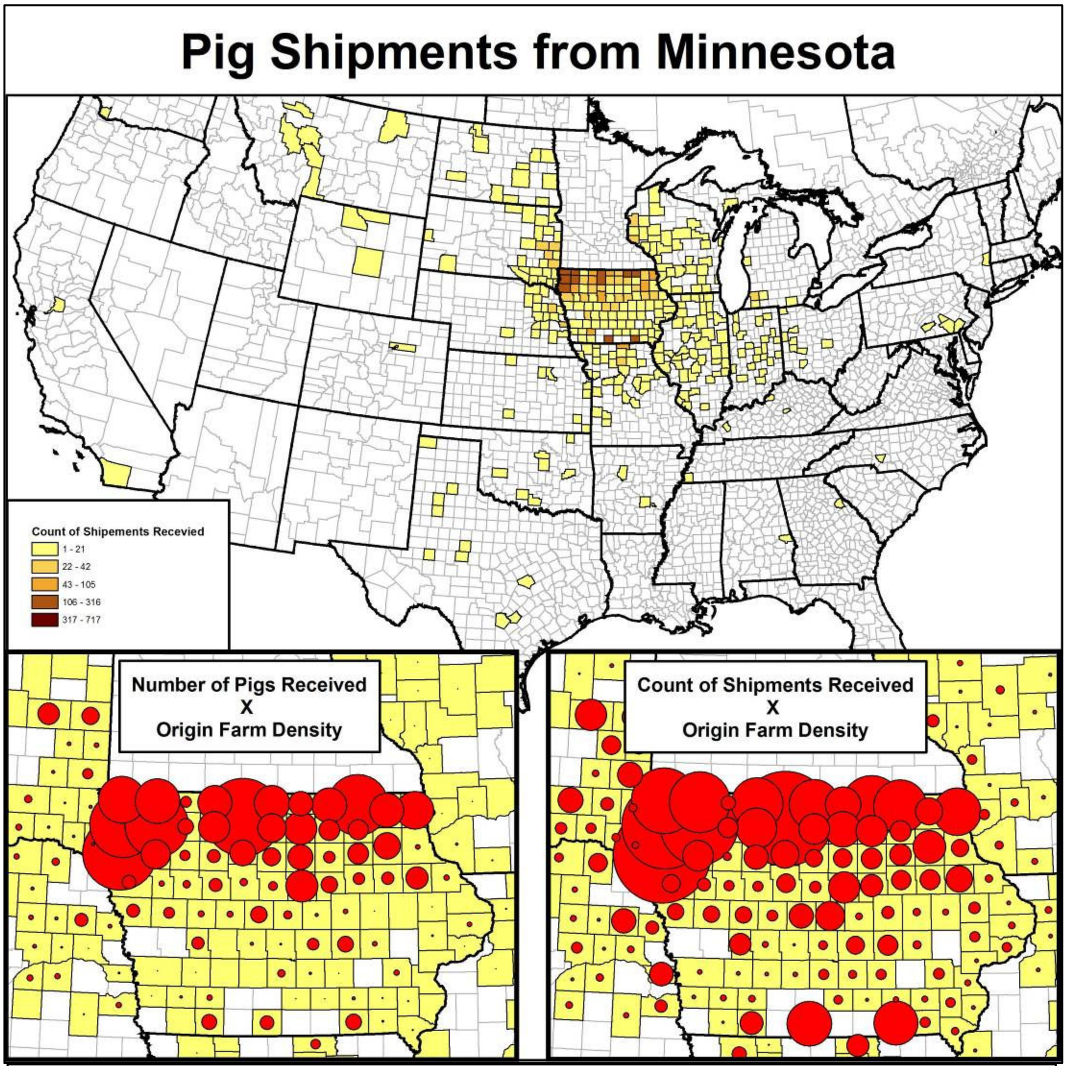
Quartile map of FlowBetweenness Centrality for states.

Figure-36. Page 72.



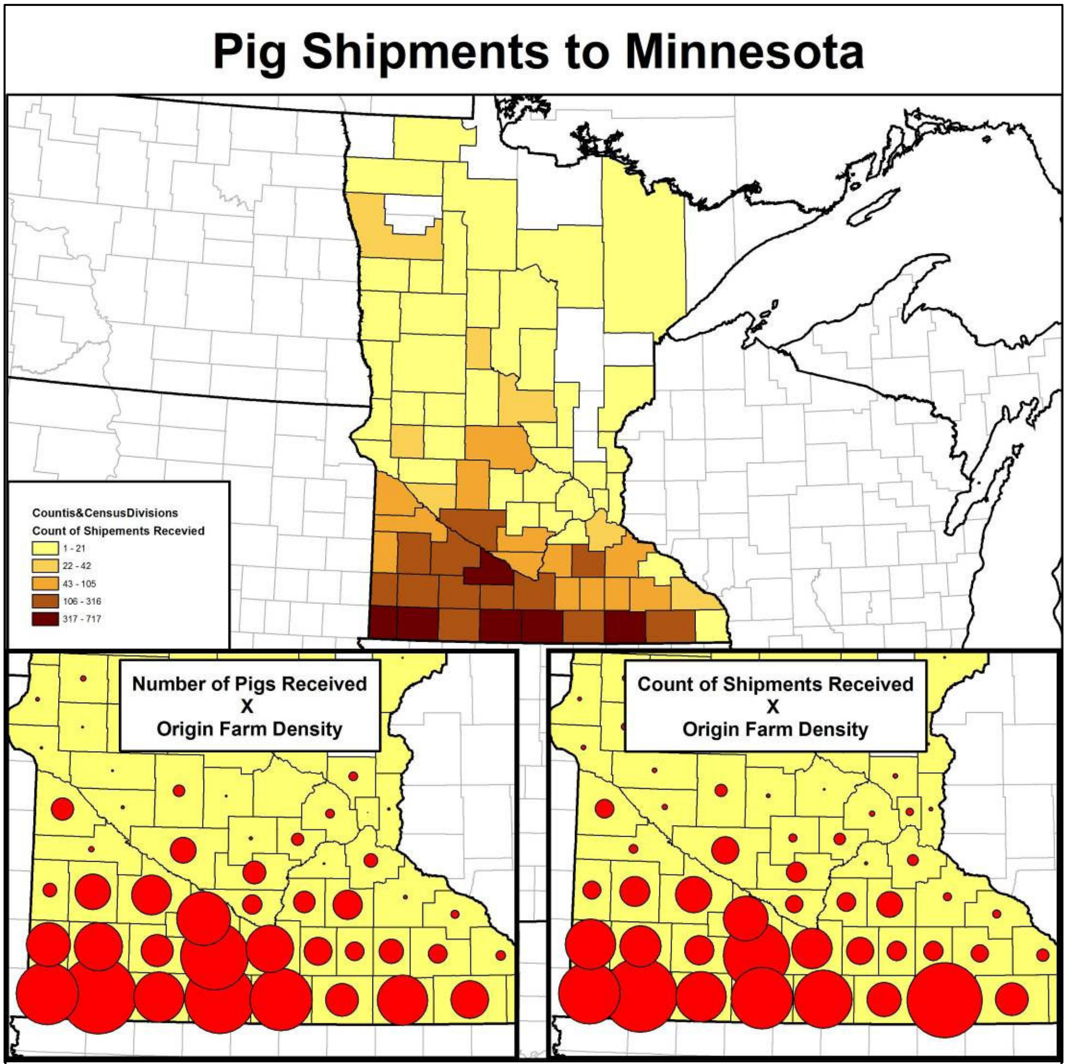
Four views showing movement patterns of Breeding Swine and Feeder Swine, to and from the state of Minnesota. Data are taken from Interstate Health Papers written in 2006 and kept at Minnesota Board of Animal Health.

Figure-37. Page 72.



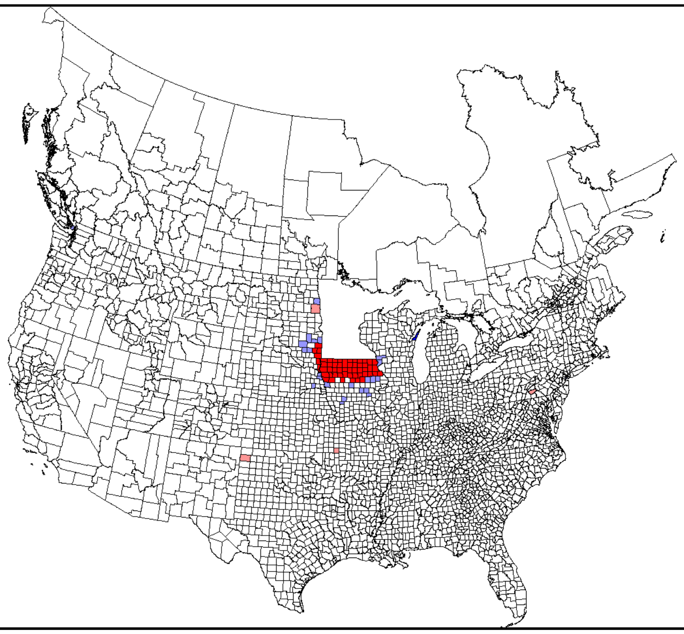
Map showing pig movement patterns for swine traveling from Minnesota to other states. Top map displays counties receiving pigs from Minnesota with increasing number of shipments indicated with darker shading. Two bottom maps show risk estimation for receiving counties, calculated as the product of pig movement data and density (pig farms per 100 square kilometers) in origination county.

Figure-38. Page 72.



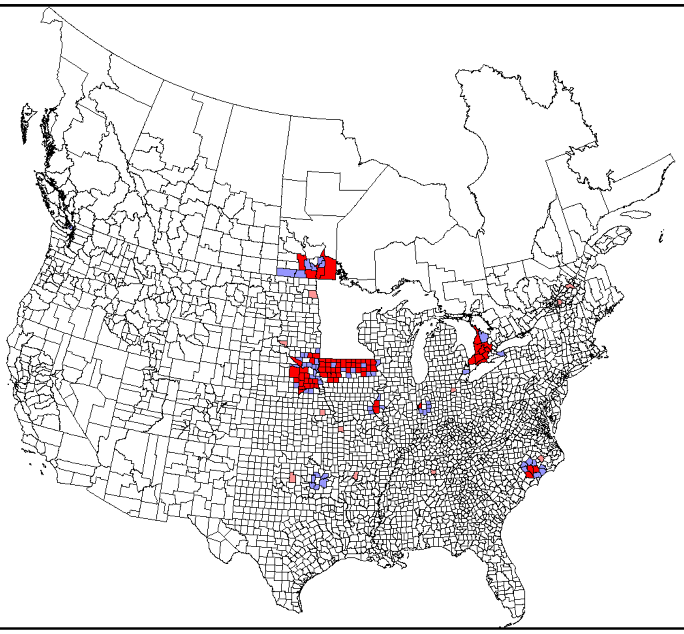
Map showing pig movement patterns for swine traveling into Minnesota from other states or administrative areas. Top map displays counties receiving pigs, with increasing number of shipments indicated with darker shading. Two bottom maps show risk estimation for receiving counties, calculated as the product of pig movement data and density (pig farms per 100 square kilometers) in origination county.

Figure-39. Page 73.



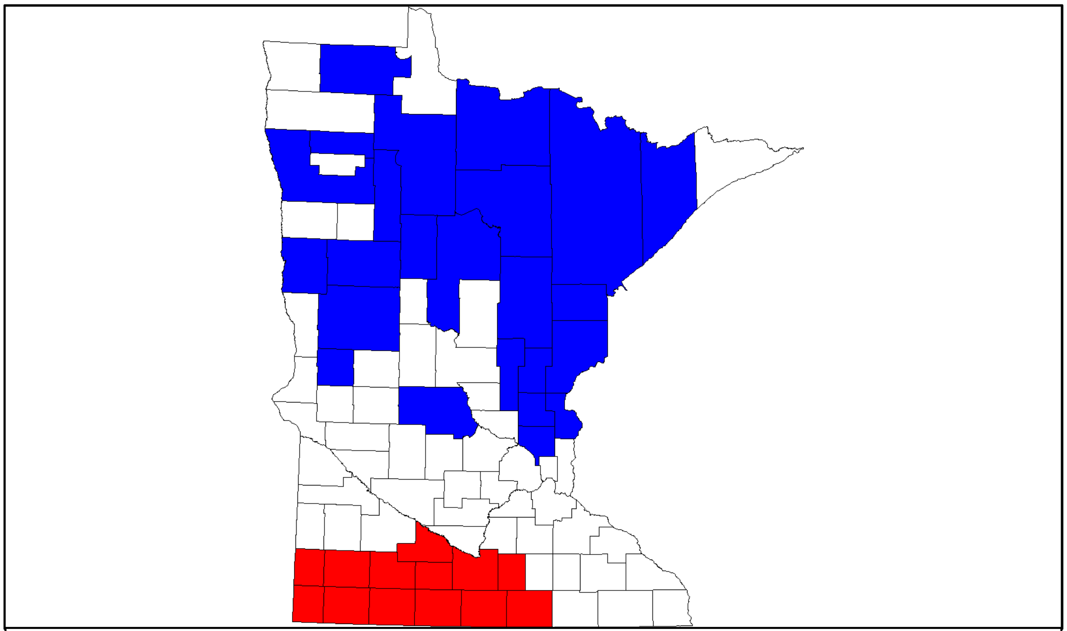
LISA map showing spatial correlation for Movement Risk (sum of pigs shipped between counties x pig farm density of origination county) for pigs originating in Minnesota, shipped out of state.

Figure-40. Page 73.



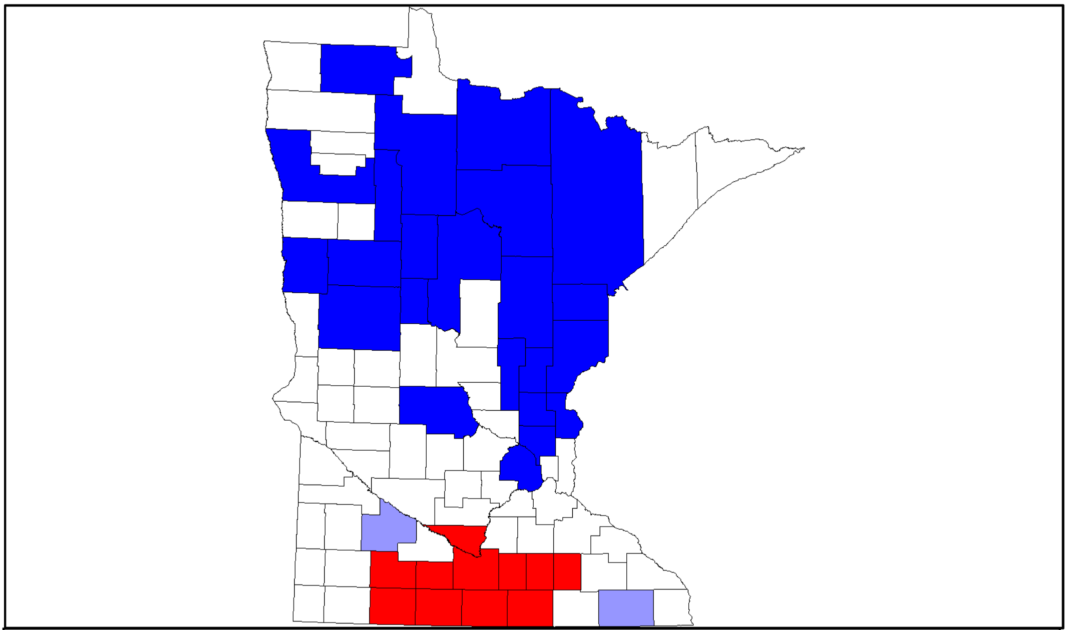
LISA map showing spatial correlation for Movement Risk (sum of pigs shipped between counties x pig farm density of origination county) for pigs destined for Minnesota, shipped from other states or administrative areas.

Figure-41. Page 73.



LISA map showing spatial correlation for Movement Risk (sum of pigs shipped between counties x pig farm density of origination county) for pigs destined for Minnesota, shipped from other states or administrative areas.

Figure-42. Page 73.



LISA map showing spatial correlation for Movement Risk (sum of pigs shipped between counties x pig farm density of origination county) for pigs originating in Minnesota, shipped out of state.

Tables

Table-1. Page 41.

Minnesota Swine Farm Counts

	State Total	County Average	County StdDev
NASS	5626	65	53
MBAH	10768	124	111
MPCA	8331	96	115

Table-2. Page 41.

Spearman's Rank Correlation of County Swine Farm Counts From Different Datasets

Data Pair	R
MBAH-NASS	0.87
MPCA-NASS	0.92
MBAH-MPCA	0.86

*all correlations had p<0.0001

Table-3. Page 42.

Stevens County data accuracy for two datasets of farm locations matched to a verified farm location

		Verified Farms		Probability	Probability
		Present	Absent	Estimate 1[a]	Estimate 2[b]
MBAH Farms	Present	68	96	84%	41%
	Absent	13	0		
MPCA Farms	Present	60	21	74%	74%
	Absent	21	0		

a probability that a dataset includes an actual, existent farm site

b probability that a farm listed in either the MBAH or the MPCA dataset was actually a current swine operation

Table-4. Page 42.

Rice County data accuracy for two datasets of farm locations matched to a verified farm location

		Verified Farms		Probability	Probability
		Present	Absent	Estimate 1[a]	Estimate 2[b]
MBAH Farms	Present	45	20	85%	69%
	Absent	8	0		
MPCA Farms	Present	40	72	75%	36%
	Absent	13	0		

a probability that a dataset includes an actual, existent farm site

b probability that a farm listed in either the MBAH or the MPCA dataset was actually a current swine operation

Table-5. Page 43.

Nearest Neighbor Analysis

County	Dataset	Cluster Z-score	
Stevens	MBAH	-3.65	Clustered
	MPCA	-0.17	Random
Rice	MBAH	-5.86	Clustered
	MPCA	1.00	Random

Table-6. Page 43.

Year-To-Year Spearman Correlation for 4-H Swine Participation by County

Year-Year	R
2000-2001	0.83
2001-2002	0.93
2002-2003	0.97
2003-2004	0.97
2004-2005	0.97

*All correlations significant (P<0.0001)

Table-7. Page 43.

Spearman Rank Correlation of 4-H Participants vs. Commercial Production

	R
NASS Farms	0.663
MBAH Farms	0.595
MPCA Farms	0.673

*all P-values <0.0001

Table-8. Page 51.

ANOVA analysis of location type and season

ANOVA table for Temp

Source	DF	SS	MS	F	P
Month	1	432653	432653	48422.5	0.000
Location Type	2	202	101	11.33	0.000
Month*LocType	2	743	371	41.55	0.000
Error	828	7398	9		
Total	833				

Table-9. Page 51.

Means and statistical differences in °F for location type and season

	Winter	Summer
Hog Farms	8.8 ^{a}	66.8 ^{ab}
Non-Hog Farms	7.7 ^{b}	66.6 ^{a}
Random Points	5.2 ^{c}	67.8 ^{b}

One-Way ANOVA

Tukey HSD All-Pairwise Comparisons

Table-10. Page 51.

Means and statistical differences in °F for hog farm type and season

	n	Winter	Summer
Farrowing	12	9.2 ^{a}	66.4 ^{a}
Nursery	6	10.4 ^{a}	67.4 ^{a}
Finishing	41	8.5 ^{a}	66.9 ^{a}
	ANOVA-p	0.261	0.755

One-Way ANOVA

Table-11. Page 51.

February Cut-Off of 10.13°F

Variables	Coefficient	Std Error	Coef/SE	P
Constant	-0.52609	0.24732	-2.13	0.0334
Cutoff10	1.31455	0.39752	3.31	0.0009

	OR
Lower 95CI	1.71
Odds Ratio	3.72
Upper 95CI	8.11

Table-12. Page 51.

May Cut-Off of 67.73°F

Variables	Coefficient	Std Error	Coef/SE	P
Constant	-0.15415	0.24881	-0.62	0.536
Cutoff68	0.34339	0.37156	0.92	0.3554

	OR
Lower 95CI	0.68
Odds Ratio	1.41
Upper 95CI	2.92

Table-13. Page 60.

Biosecurity measure	Important	Unimportant	Unfamiliar
Transport sanitation	95	2	3
Pig Source Health	94	2	4
Segregation of pigs	85	11	4
Pest control	85	13	3
Washing hands/equipment	84	12	4
Quarantine and testing	82	9	8
Farm specific clothing	69	27	4
Restricting visitors	66	29	5
Boot baths	61	24	15
Shower in/out	58	35	7
Bird proofing	54	31	15
Visitor log	39	53	8
Wearing mask/gloves	38	57	6

Perceived importance of various biosecurity measures for swine health (% of responses)

Table-14. Page 60.

	% Important	% Unfamiliar	Ratio[a]
Influenza	71	25	2.84
E. coli scours	65	28	2.32
Salmonella	63	28	2.25
Mycoplasma	62	37	1.68
PRRS	58	41	1.41
Pseudorabies	55	41	1.34
Mange	43	48	0.90
Epidemic diarrhea[b]	43	51	0.84
Erysipelas	44	54	0.81
Parvovirus	39	58	0.67
Leptospirosis	31	67	0.46
Ileitis	31	67	0.46
Streptococcus suis	30	67	0.45
Teschen/Talfan[b]	28	68	0.41

[a] Ratio of proportion ranking a disease important and proportion unfamiliar

[b] exotic diseases thought likely to be unfamiliar to participants

Proportion of 4-H respondents indicating specific diseases to be important and proportion unfamiliar with the disease (n = 133)

Table-15. Page 70.

Farm Type	Rice County Single-Site Production	Rice County Multi-Site Production	Stevens County Single-Site Production	Stevens County Multi-Site Production
BoarStud	0 (0%)	0 (0%)	1 (1%)	0 (0%
Farrowing	1 (2%)	7 (15%)	10 (13%)	10 (13%)
Nursery	0 (0%	8 (17%)	0 (0%	6 (8%)
Finishing	0 (0%	31 (66%)	0 (0%	50 (65%)
Total	1 (2%)	46 (98%)	11 (14%)	66 (86%)

Breakdown of 124 pig farm locations, by farm type and multisite production, in two Minnesota Counties (Rice and Stevens)

Table-16. Page 70.

PRRS Status	**Rice County**	**Stevens County**
Negative	25 (53%)	56 (73%)
Positive	21 (45%)	16 (21%)
Unknown	1 (2%)	5 (6%)
Total	47 (100%)	77 (100%)

Breakdown of 124 pig farm locations, by PRRS infection status.

Table-17. Page 70.

Travel Distance (Km)

	County	N	Mean	Median	P-value
All Pig Movements	Rice	183	74	28	0.00
	Stevens	277	137	36	
Outward Pig Movements	Rice	83	96	66	0.00
	Stevens	125	206	207	
Outward Pig Movements (Non-Slaughter)	Rice	39	73	41	0.00
	Stevens	55	155	164	
Inward Pig Movements	Rice	46	113	30	0.00
	Stevens	31	337	58	

Pig movement distances for Rice and Stevens County

Table-18. Page 71.

Shipments Per Year

	County	N	Mean	Median	P-value
All Pig Movements	Rice	183	21	10	0.07
	Stevens	277	15	7	
Outward Pig Movements	Rice	83	29	13	0.00
	Stevens	125	15	7	
Outward Pig Movements (Non-Slaughter)	Rice	39	32	13	0.00
	Stevens	55	10	7	
Inward Pig Movements	Rice	46	15	6	0.07
	Stevens	31	19	13	

Pig movement frequencies for Rice and Stevens County

Table-19. Page 71.

Annual Distance (Shpmt/Yr * Km/Shpmt)

	County	N	Mean	Median	P-value
All Pig Movements	Rice	183	1881	183	0.07
	Stevens	277	2050	351	
Outward Pig Movements	Rice	83	3075	1043	0.26
	Stevens	125	3628	1230	
Outward Pig Movements (Non-Slaughter)	Rice	39	2872	963	0.82
	Stevens	55	1764	1083	
Inward Pig Movements	Rice	46	1850	255	0.00
	Stevens	31	2939	824	

Pig movement annual shipment distances for Rice and Stevens County

Table-20. Page 71.

Centrality Measures for farms in Stevens County

Farm	PRRS Status	Production Type	OutDegree Centrality	InDegree Centrality	OutReach Centrality	InReach Centrality	FlowBetweenness
1	Neg	BoarStud	26	26	4	5	0
2	Neg	Finishing	19	26	5	4	3
3	Unknown	Farrowing	13	0	3	1	0
4	Neg	Finishing	13	10	4	2	0
5	Neg	Finishing	29	12	5	3	0
6	Neg	Finishing	11	6	3	3	0
7	Pos	Finishing	8	6	6	3	0
8	Neg	Finishing	22	12	7	3	0
9	Pos	Finishing	2	21	3	3	0
10	Neg	Finishing	0	13	1	2	0
11	Neg	Finishing	15	6	5	3	1
12	Neg	Finishing	22	17	5	3	2
13	Pos	Finishing	2	3	3	3	0
14	Neg	Nursery	24	23	3	4	2
15	Neg	Finishing	12	6	5	5	0
16	Neg	Finishing	13	14	9	3	1
17	Neg	Finishing	40	26	4	2	0
18	Neg	Finishing	17	6	5	3	0
19	Neg	Finishing	5	6	5	3	0
20	Neg	Finishing	5	3	5	3	0
21	Neg	Finishing	17	6	5	3	0
22	Neg	Finishing	22	4	5	2	1
23	Neg	Finishing	52	52	2	4	0
24	Neg	Finishing	13	3	5	3	0
25	Neg	Finishing	9	3	5	3	0
26	Neg	Finishing	17	6	5	3	0
27	Neg	Finishing	17	6	5	3	0
28	Neg	Farrowing	29	15	9	4	1
29	Neg	Finishing	81	13	11	3	6
30	Pos	Finishing	30	12	6	3	0
31	Pos	Finishing	4	6	6	3	0
32	Pos	Finishing	30	12	6	3	0
33	Neg	Finishing	77	35	6	3	0
34	Neg	Nursery	53	104	7	2	0
35	Pos	Finishing	46	17	6	3	0
36	Pos	Finishing	8	3	6	3	0
37	Neg	Finishing	11	9	5	4	0
38	Neg	Finishing	35	13	6	3	1
39	Neg	Finishing	17	6	5	3	0
40	Neg	Finishing	39	12	3	2	0
41	Neg	Nursery	104	35	4	4	2
42	Neg	Nursery	55	208	13	4	14
43	Neg	Finishing	107	52	15	3	0
44	Neg	Nursery	60	52	13	3	0
45	Neg	Farrowing	26	0	3	1	0
46	Pos	Farrowing	52	0	3	1	0
47	Neg	Farrowing	58	2	6	3	0
48	Neg	Finishing	6	17	2	2	0
49	Unknown	Farrowing	13	1	2	2	0
50	Pos	Farrowing	188	1	13	2	0
51	Neg	Farrowing	26	0	2	1	0
52	Neg	Farrowing	147	26	6	3	1
53	Neg	Finishing	12	6	5	5	0
54	Neg	Finishing	30	23	9	4	1
55	Neg	Farrowing	158	14	13	4	12
56	Unknown	Farrowing	29	0	6	1	0
57	Pos	Farrowing	26	6	3	2	0
58	Neg	Farrowing	74	13	14	2	0
59	Pos	Finishing	16	6	6	3	0
60	Neg	Farrowing	156	2	11	2	1
61	Neg	Farrowing	175	2	13	2	2
62	Neg	Farrowing	27	0	4	1	0
63	Neg	Farrowing	26	0	4	1	0
64	Neg	Farrowing	29	5	4	2	0
65	Neg	Finishing	163	58	17	3	1
66	Unknown	Nursery	0	6	1	3	0
67	Neg	Finishing	52	55	2	5	0
68	Neg	Finishing	5	3	5	3	0
69	Unknown	Farrowing	13	0	3	1	0
70	Neg	Finishing	17	6	5	3	0
71	Neg	Finishing	37	11	5	4	0

Stevens County social network analysis statistics

Table-21. Page 71.

Centrality Measures for farms in Rice County

Farm	PRRS Status	Production Type	OutDegree Centrality	InDegree Centrality	OutReach Centrality	InReach Centrality	FlowBetweenness
1	Neg	Farrowing	45	0	8	1	0
2	Pos	Farrowing	36	12	6	6	5
3	Neg	Farrowing	126	12	12	6	32
4	Pos	Nursery	78	13	3	3	2
5	Neg	Farrowing	467	208	8	5	6
6	Neg	Farrowing	467	208	8	5	14
7	Neg	Farrowing	467	208	8	5	6
8	Pos	Farrowing	50	2	11	2	6
9	Pos	Finishing	14	6	4	5	0
10	Neg	Farrowing	33	0	3	1	0
11	Pos	Finishing	11	5	4	5	0
12	Neg	Finishing	61	6	4	2	0
13	Neg	Finishing	68	9	2	2	0
14	Neg	Finishing	46	15	3	3	0
15	Pos	Finishing	27	11	11	7	23
16	Pos	Finishing	9	4	4	5	0
17	Pos	Finishing	19	9	4	5	0
18	Pos	Finishing	19	10	4	5	0
19	Pos	Finishing	10	10	4	5	0
20	Pos	Finishing	6	3	4	5	0
21	Neg	Finishing	7	3	2	3	0
22	Pos	Finishing	20	6	2	3	0
23	Neg	Finishing	40	12	3	3	0
24	Neg	Finishing	30	10	4	2	0
25	Neg	Finishing	16	2	3	2	0
26	Neg	Finishing	43	18	4	4	1
27	Neg	Finishing	80	26	3	2	0
28	Neg	Finishing	16	5	8	2	0
29	Pos	Finishing	12	5	3	3	0
30	Pos	Finishing	40	13	4	2	0
31	Neg	Finishing	18	6	11	4	0
32	Neg	Finishing	32	12	6	3	2
33	Pos	Nursery	48	91	14	4	18
34	Neg	Nursery	52	13	9	2	0
35	Neg	Nursery	1	0	3	1	0
36	Neg	Nursery	26	13	2	2	0
37	Pos	Nursery	30	12	8	2	6
38	Neg	Nursery	50	52	6	2	0
39	Pos	Finishing	19	9	4	5	0
40	Neg	Finishing	58	20	3	3	0
41	Neg	Finishing	13	4	3	3	0
42	Pos	Finishing	12	3	4	2	0
43	Neg	Finishing	58	20	3	3	0
44	Neg	Finishing	27	16	4	3	0
45	Pos	Nursery	80	59	10	2	2
46	Pos	Finishing	19	9	4	5	0
	Rice County Averages		**63.2**	**25.9**	**5.1**	**3.2**	**2.6**

Rice County social network analysis statistics

Table-22. Page 70.

Mean Statistics for Centrality Measures

Centrality Measure	Stevens	Rice	P-value
InDegree	17.5	25.9	0.59
OutDegree	40.8	63.2	0.19
InReach	2.7	3.2	0.23
OutReach	5.8	5.1	0.16
Flowbetweenness	0.7	2.6	0.30

Mean values for social network analysis statistics comparing two Minnesota counties (Rice and Stevens). Statistical differences determined using Wilcoxon Rank Sum Test p-value. Stevens (n=76) and Rice (n=46)

Table-23. Page 71.

Pearson Correlation Of Centrality Measures

	InDegree	**OutDegree**	**InReach**	**OutReach**
OutDegree	**0.75***			
InReach	**0.25***	0.17		
OutReach	**0.35***	**0.39***	0.11	
FlowBetweenness	**0.36***	**0.34***	**0.43***	**0.46***

Correlation between different social network analysis measures for two Minnesota counties (Rice and Stevens). * $p<0.05$

Table-24. Page 71.

Logistic Regression Values for PRRS Positive Status

	Coefficient	**Std Error**	**P-value**	**Odds Ratio [95%CI]**
County(Rice)	**1.124**	**0.421**	**0.01**	**3.08 [1.35, 7.03]**
InDegree	-0.009	0.008	0.25	0.99 [0.98, 1.01]
OutDegree	-0.009	0.006	0.13	0.99 [0.98, 1.00]
InReach	**0.395**	**0.177**	**0.03**	**1.48 [1.05, 2.10]**
OutReach	-0.003	0.061	0.96	1.00 [0.89, 1.12]
FlowBetweenness	0.021	0.042	0.62	1.02 [0.94, 1.11]
InvDistSq	0.167	0.090	0.06	1.18 [0.99, 1.41]

Logistic regression statistics from seven different, single-term models.

Table-25. Page 71.

Stepwise Logistic Regression

Variable	Coefficient	Std Error	P-Value	Odds Ratio [95%CI]
Constant	-2.395	0.694	0.00	
County(Rice)	1.125	0.448	0.01	3.08 [1.28, 7.41]
InvDistSq	0.121	0.090	0.18	1.13 [0.95, 1.35]
OutDegree	-0.009	0.005	0.10	0.99 [0.98, 1.00]
InReach	0.362	0.193	0.06	1.44 [0.98, 2.09]

Logistic regression statistics. Model P-value 0.227 and Deviance = 122 (out of 140 for model without terms).

Table-26. Page 71.

Rank	InDegree	OutDegree	InReach	OutReach	FlowBet
1	Iowa	North Carolina	Illinois	Illinois	Kansas
2	Minnesota	Missouri	Minnesota	Missouri	Missouri
3	Illinois	Canada	California	Wisconsin	Illinois
4	Missouri	Oklahoma	Iowa	Kansas	Colorado
5	Indiana	Nebraska	North Carolina	Minnesota	Minnesota
6	South Dakota	Illinois	Missouri	Iowa	South Dakota
7	Kansas	Minnesota	Georgia	North Carolina	Nebraska
8	Nebraska	Iowa	Maryland	Arkansas	Iowa
9	North Carolina	Colorado	Indiana	Georgia	Oklahoma
10	Ohio	Arkansas	South Dakota	Ohio	Canada

Social Network Analysis values for US interstate pig movements.

Table-27. Page 72.

		Travel Distance (Km)				
	N	Mean	Minimum	Maximum	Median	StdDev
Breeding Swine From MN ^{a}	651	526.2	35	2109	437	354.1
Feeder Swine From MN ^{b}	486	267.5	33	2573	205	258.7
Breeding Swine To MN ^{a}	535	551.4	34	1859	465	358.1
Feeder Swine To MN ^{a}	976	551.0	33	1967	462	396.7

		Count of Pig Shipments				
	N	Mean	Minimum	Maximum	Median	StdDev
Breeding Swine From MN ^{a}	651	2.7	1	72	1	4.9
Feeder Swine From MN ^{b}	486	5.5	1	80	2	9.0
Breeding Swine To MN ^{a}	535	2.0	1	22	1	2.2
Feeder Swine To MN ^{b}	976	5.5	1	89	2	9.0

		Sum Total of Pigs Moved				
	N	Mean	Minimum	Maximum	Median	StdDev
Breeding Swine From MN ^{a}	651	249.9	1	12107	20	783.1
Feeder Swine From MN ^{b}	486	3482.2	1	89807	1255	6795.3
Breeding Swine To MN ^{a}	535	206.4	1	6500	9	582.6
Feeder Swine To MN ^{b}	976	3827.7	1	61450	1520	6466.8

		Average Shipment Size				
	N	Mean	Minimum	Maximum	Median	StdDev
Breeding Swine From MN ^{a}	651	78.6	1	3120	12	187.9
Feeder Swine From MN ^{b}	486	684.1	1	5300	500	640.5
Breeding Swine To MN ^{a}	535	84.6	1	2400	5.5	229.8
Feeder Swine To MN ^{c}	976	744.4	1	7000	624.31	569.6

		Pig Farm Density (#/100sqkm) of Origin County				
	N	Mean	Minimum	Maximum	Median	StdDev
Breeding Swine From MN ^{a}	651	5.0	0	11.331	4.6294	2.9
Feeder Swine From MN ^{b}	486	6.7	0.2703	19.048	7.0371	2.8
Breeding Swine To MN ^{c}	533	3.7	0.1045	26.501	2.9828	3.2
Feeder Swine To MN ^{d}	971	5.4	0.001168	28.611	3.6009	5.7

Comparison of travel distances, count of shipments, sum of pigs moved, average size of shipment, and pig farm density of origination county. Statistical differences using Kruskal-Wallis One-Way Nonparametric AOV are denoted by different letters.

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Appendix

Terms Defined and Abbreviations:

Diseases:

AI	Avian Influenza
BSE	Bovine Spongiform Encephalopathy (aka ‘Mad Cow’ Disease)
CSF	Classical Swine Fever (aka Hog Cholera)
FLV	Feline Leukemia Virus
FMD	Foot and Mouth Disease
PCV2	Porcine Circovirus type-2 (etiologic agent of PMWS)
PMWS	Postweaning Multisystemic Wasting Syndrome
PRRS	Porcine Reproductive and Respiratory Syndrome
PRV	Pseudorabies Virus (aka Aujesky’s Disease)
SIV	Swine Influenza Virus
TB	Tuberculosis (usually bovine tuberculosis- Mycobacterium bovis)
VSV	Vesciculo Stomatitis Virus

Other:

FAO	Food and Agriculture Organization
GIS	Geographic Information System(s)
NAIS	National Animal Identification System
OIE	Office International des Epizooties (World Organisation for Animal Health)
SNA	Social Network Analysis
USDA	United States Department of Agriculture