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A network evaluation of human and animal movement data across multiple swine farm systems in North America

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ABSTRACT

Introduction: The U.S. swine industry is vulnerable to the rapid spread of disease due to systemic structural issues. While animal movement networks are used to identify disease spread risks and design response plans, human movement between farms were rarely accounted for. Human movements, when integrated with animal movement models, create a different, more inclusive, and accurate network structure when compared to animal movements alone.

Methods: One year of propriety farm visit data was analyzed and consisted of anonymized property IDs, location, and user/truck IDs, along with visit dates, property, vehicle, and entry types from three swine management companies. A static directed network was created using the igraph package in R for all movements, with separate sub-networks for each entry type (animal, human, and subsets of vehicle types). Network statistics for each sub-network were compared.

Results: The full network included 455 properties, 11 property types, 9 vehicle types, 12 entry types, and 320001 edges (trips between properties). The longest path length was 10 in the animal movement network but decreased to 5 for the full and human movement network, while the average path length decreased from 3.2 to 2.2. Edge density increased from 0.03 to 0.09 for the human network and 0.1 for the full network. For all network properties examined, the full and human movement networks demonstrated higher connectivity than the animal network. A heavy right skew in the degree distributions indicates a 'hub' structure (scale-free-like network) and the shorter path lengths indicates a small-world network topology.

Discussion: The full network is very well connected, more so than expected based on animal movement alone. Hubs may indicate points of disease susceptibility and 'super-spreader' properties. The high connectivity shows that swine farm networks may be more susceptible to spread of an introduced disease than expected from previous analyses.

Conclusions: Monitoring human, as well as animal movement, provides for a more complete and accurate understanding of swine farm biosecurity risks.

1. Introduction

The swine industry is a critical sector in agriculture, contributing significantly to the national and global economies and food supply. The United States is the 4th largest global swine producing nation (Statista, 2022), producing 12 % of the world's pork (Pork Checkoff, n.d) and contributing over $57 billion to the nation's GDP (National Pork Producers Council, n.d). It is essential for this industry to maintain robust biosecurity and health management practices to maintain disease-free status related to global trade and to prevent outbreaks of foreign animal diseases (FADs). Biosecurity measures stand between an infected farm and a non-infected farm. It determines if the pathogens are containable on site or if they might spread within the system (Manuja et al., 2014). Strict implementation of biosecurity protocols can

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determine whether a small outbreak evolves into a large epidemic.

Transportation plays an important role in the swine industry, serving various purposes such as moving animals between farms and processing facilities, feed transport, personnel, and services (Dutta et al., 2014; Konschake et al., 2013). While each of these elements contribute to the industry's functionality, they also increase the risk of farm-to-farm disease transmission. Human movements are shown to be an important transmission route in several important diseases, such as African Swine Fever virus (ASFv) and Porcine Endemic Diarrhea virus (PEDv). Risk assessments show that long range transmission of ASFv between countries are likely associated with human movement and importation of products (Montenegro and Manabat, 2023). USDA's risk assessment estimates that illegal entry of swine products and by-products via human-assisted movement pathways has a high likelihood of introducing ASFv into the U.S. (USDA APHIS, 2019). Hsu et al. (2023) found that the primary risk factor for ASFv transmission between commercial farms within the Philippines is contaminated vehicles and people. The initial outbreak mechanisms and subsequent spread patterns of PEDv through the U.S. swine system are widely considered to be indicators of the risk of ASFv spread and establishment (Linhares et al., 2023). It was determined that between-farm PEDv outbreaks spread via truck movement and personal vehicles. Other infectious diseases such as avian influenza and porcine reproductive and respiratory syndrome (PRRSv) were found on vehicle surfaces possibly contributing to disease transmission between farms in the United States (Galvis and Machado, 2024). Current swine response plans are insufficient to prevent transmission (Linhares et al., 2023). Including personal vehicles as modes of transmission (in this study, called human movement) in any analysis is essential for accurate model assessments.

In the last decade or so, network models gained attention in the livestock industry in areas like the European Union and the United Kingdom where animal movement records are routinely collected. Multiple studies evaluating livestock infectious diseases, including cattle and swine, using network analysis were developed in Italy, the United Kingdom, and Slovenia. Researchers used animal movement networks to model infection spread and determine high-risk farm properties (Bajardi et al., 2012; Knific et al., 2020; Lee et al., 2017; Smith et al., 2013; Thakur et al., 2016). In veterinary epidemiology, sentinel surveillance, informed by network analysis, represents a novel approach to early warning systems and utilizes the analysis of animal transport data (Andraud et al., 2022; Schirdewahn et al., 2021), also known as social network analysis (SNA) (Bajardi et al., 2012). SNA is used to improve resource allocation for surveillance, management, and control strategies in production settings (Kinsley et al., 2020; Passafaro et al., 2020; Rorres et al., 2018; Sykes et al., 2023; Thakur et al., 2016). Network analysis is also used to estimate disease transmission dynamics (such as new incursions of African Swine Fever (ASF) (Main et al., 2022) in naïve countries, such as the U.S. (Cardenas et al., 2022; Galvis et al., 2022a, 2022b; Sellman et al., 2022; Sykes et al., 2023).

Swine transport networks exhibit considerable heterogeneity (Nelson et al., 2020) between production sites. Various factors such as the different life stages of swine being transported, distances traveled, modes of transportation used, and the geographic layout of farms and processors all contribute to production differences (Knific et al., 2020; Nelson et al., 2020). Additionally, variations in regulations, infrastructure, and economic factors can also shape the complexity and structure of these networks (Knific et al., 2020; Schirdewahn et al., 2021). SNA aids in characterizing transport data with the potential to discern the influence of human movements (Gates and Woolhouse, 2015). It facilitates a systematic exploration of swine trade, enabling the assessment of the risk of disease transmission highlighting the role of human movement. In particular, local network measures or node centrality measures can effectively gauge the epidemiological significance of individual premises within the network (Andraud et al., 2022).

It was shown that optimal surveillance network models can significantly increase the accuracy of infectious disease transmission models (Convertino et al., 2014). Animal mobility data and transport networks are sufficient when transmission of disease depends generally on animal-to-animal contact (Rorres et al., 2018) but are insufficient when human mechanisms can transmit the disease, such as fomites on trucks, boots, or personal vehicles; other routes of infection should be considered (Passafaro et al., 2020). Hence, incorporating human movements between farms should be included in the network model to ensure better accuracy guaranteeing the most efficacious models (Kiang et al., 2021). Models not including all possible transmission routes are ultimately insufficient (Galvis et al., 2022a). This is especially true for ASF; professional visits to farms are a significant risk factor for transmission (USDA APHIS, 2019; Boklund et al., 2020; Hsu et al., 2023; Montenegro and Manabat, 2023; Oļševskis et al., 2016).

However, most studies of disease spread in swine and other livestock systems focus either on animal or human movements and are rarely integrated within the same network system. Particularly in the U.S., only one study examined human movement between swine farms (Black et al., 2022) and one known study to date included only crew movements in the network when determining network structure (Galvis and Machado, 2024). This limitation hinders our ability to characterize the complex networks of movements—including animals, products, vehicles, and workers—that can potentially influence disease spread. Currently there is a gap in the understanding of the role humans play in the connectivity structure. Understanding and addressing these risks are essential for controlling disease transmission within the swine industry and other sectors. National-level surveillance and control programs are essential to promptly detect and manage outbreaks of infectious diseases, ensuring early intervention and containment measures (Ferdousi et al., 2019; Guinat et al., 2016; Passafaro et al., 2020).

The main objective of this study is to understand how network structure might be affected by integrating the human movements with those of animal and truck movements on swine farm networks. These human movements include crew, service vehicles (such as maintenance calls), personal employee vehicles, farm visitors, veterinarians, and other personnel that arrive on farm. We hypothesize that adding the human movements to an animal movement network will alter the network statistics and will change the outcomes in a disease transmission model. To increase the accuracy of network disease models, it is crucial to include both human and animal movement data into the network.

2. Materials and methods

2.1. Study design

2.1.1. Data collection

Data were provided by Farm Health Guardian, LLC (FHG). FHG creates a geofence on all properties associated with a commercial system, including contract systems. Any vehicle associated with that system carries a device (with a device ID #) that notes the time of entry on and exit off these properties. Individuals associated with the system will log visits through a user ID on a separate device tablet called a kiosk located at the entryway and exit of the barns. Any individual not registered with the system (i.e a visitor to the farm), would be signed in without either a user or device ID. Data provided included anonymized location of properties, date, time, anonymized identity of vehicle (device ID) and user ID, entry type, and metadata for the property and vehicle types. Properties include ones with and without animal holdings, such as farms, truck washes, processing plants, and offices. The data included three co-located commercial swine systems encompassing all properties, company owned and contract trucks, and associated personnel between April 1st, 2022, to April 26th, 2023.

Visits were defined as any vehicle entering a property. For the purpose of this study, trucks were considered any entry where the driver does not exit the vehicle. Human movements are personal vehicles. The drivers park the vehicle and enter buildings. Any visits that were missing property identifications, a user ID or a device ID were removed. Any visit associated with a user or device ID that only appeared once was removed since it would not form a link between two properties. These links are necessary for network assembly and analysis. Missing values in the raw data for property type, vehicle type and property group ID were re-coded as “other” or “unknown”. Each property was assigned one or more property types, consisting of production type (Boar, Other/Boar, Farm, Farm/Sow/Nursery/Finisher, Sow/Finisher/Nursery, Boar/Finisher, Farrow to Finish, Nursery/Finisher, Nursery/Sow, Finisher Farm, Finisher, Finisher/Other, Office/Finisher, Nursery, Nursery/Office, Sow, Sow/Quarantine); management type (Farm/Livestock Broker, Other, Maintenance, Office); Dead Stock Storage; Distribution Center; Manure Storage; Transfer Dock; Feed Mill; Processing Plant/Processor; Quarantine; and Truck wash. For better visualization purposes and graph development only, properties assigned multiple property types were re-coded into a multi-site type, the production type being assigned as primary importance. Statistics were calculated on the originally named property type in FHG’s system.

2.2. Social network analysis

2.2.1. Network structure

The original data set had 503570 logged visits. Each visit had an ID, entry date and time, property ID, property group ID, user ID, device ID, entry type, property type, and vehicle type. All identifying data was anonymized. User IDs were individual users (named humans for the purpose of the study) and device IDs were individual vehicles. Nodes were defined as the individual geofenced properties, identified by property IDs. The variables “userID” and “deviceID” were combined into a single “edgeID” variable, representing individuals/trucks that moved between the nodes (properties). There were 1474 unique user IDs and 404 unique device IDs combined to form a total of 1878 unique edge IDs. Each trip was sorted in chronological order. An edge was considered a trip from one property to the next property by the same edge ID. There was a total of 320001 edges in the full network. The number of each vehicle type included were 110 car movements, 5120 deadstock movements, 103527 feed truck movements, 65423 livestock movements, 9 manure movements, 3431 service movements, 2847 truck movements, 1133 worker movements, and 138401 human type movements (these were made up of the user IDs). The network was then divided into three other sub-networks based on the assigned vehicle type attribute of the edge IDs: 1) animal movement only (livestock and deadstock trucks); 2) human movement only (workers, humans, and cars); and 3) truck movement only (feed, manure, truck, and service vehicles). Human movement assumed that individuals would exit their vehicles on a property. Truck movements assumed that individuals did not exit the vehicle while visiting the property. Animal movements assumed that there was an animal (live or carcass) on the truck. Network statistics were calculated for all four networks.

The trips for the whole year were aggregated into a static network. The full static network was a non-weighted, non-reflexive directed aggregated network graph created in RStudio (Posit team, 2024) using the R language (R Core Team, 2022) and the *igraph* package (Csárdi, Nepusz, 2006; Csárdi et al., 2024).

2.2.2. Metrics calculated

Metrics explain the network structure and are important because structure affects function (Kraemer, 2005), which then affects flow of information across the network. Our flow of interest is the spread of disease. Node, edge, and network centrality metrics were determined for each network. Nodal metrics included degree centrality (in, out, total), betweenness, local transitivity, local triangle count, and eigenvector centrality. Network metrics included average path length, graph diameter, longest path length, degree assortativity, reciprocity, transitivity, global transitivity (also known as cluster coefficient), edge count and edge density. Cliques and the largest giant strongly connected component (GSCC) were also explored. Table 1

Testing the full network fit to a scale-free topology was accomplished using the *powerLaw* package in R (Gillespie, 2015). Bootstrapping methods estimated the Xmin (the lower bound threshold for the degree distribution or cut-off value) and *gamma* (the estimated exponent parameter in the power law function, sometimes known as *alpha*). The Kolmogorov-Smirnov (KS) goodness-of-fit test statistic tested a truncated power-law fit of our data. It estimated D (the estimated largest difference between an empirical cumulative distribution function (cdf) (observed cdf) and the proposed theoretical cdf (simulated one)) and k-min (the network degree at which D is the smallest distance) (Clauset et al., 2009). Additional methods for determining if the degree distribution of the full network fits a power law distribution are explained in detail in the supplemental material section. Vuong’s log-likelihood ratio test for non-nested models was used to test the power-law distribution against the log-normal distribution in the full network (Gillespie, 2015; Vuong, 1989). The estimated Xmin from bootstrapping was used as the threshold for the log-normal distribution making the distributions comparable.

2.2.3. Important high degree properties

Properties in the top quartile (25 %) of the total degree distributions are potential super-spreaders of disease (in, out and total; properties with greater than 661 degrees). These were identified and characterized by property type and vehicles involved (see Table 4). The probability that a type of property or type of vehicle would be in the top quartile of highest degree was calculated by taking the number of that property/vehicle type in the top quartile and dividing it by the total number of that property/vehicle type present in the full network.

2.2.4. Shared edges

An edge is a vehicle trip connecting two properties together. Unique edges were identified by simplifying each network graph; in other words, all the multi-edges were removed so that there is only one trip present between two properties. These edges were then compared between the four networks and the results are shown in the Venn diagram in Fig. 4.

3. Results

3.1. Data description

The final dataset had 320001 edges among four property groups (the original three plus an added unknown group), twelve different entry types, thirty-three different property types, and nine different vehicle types. For the graphs only, the 33 property types were condensed into 11 by combining commonalities for better visualization. Table 2 describes the data underlying each of the different networks and Fig. 1 shows a graphical representation of each network with fixed property locations. The full and human networks included all 455 properties in the dataset. The animal and truck networks contained 416 and 414 properties respectively, indicating that not all the properties in the system had livestock present onsite. Both the full and human networks also had a large number of edge IDs (over 1500), corresponding to a higher number of users compared to the animal and truck networks, which only had approximately 100 different edge IDs.

3.2. Network metrics

The global and nodal network statistics for each of the four networks are presented in Table 3 and Figs. 2 and 3. We can directly compare each sub-network by its metrics since they have been normalized by the functions present in the R packages (Csárdi, Nepusz, 2006; Csárdi et al., 2024). As expected, when the human movements are included in a full network with animals and trucks, connectivity and density of the network structure both increase. The full and human networks have

Table 1
Description of Network Metric Terminology (based on the *igraph* package documentation (Csárdi, Nepusz, 2006).

Metric	Description
Node	Each property in the network
Edge	Each trip between two properties
Global Measures	Measures calculated at the level of the network.
Diameter	The length of the longest path across the network. This is the largest number of trips of any two properties are from each other. The shorter the diameter, the more connected the network of properties.
Edge Density	The ratio of actual number of edges (trips) to the largest possible number of edges (trips) in a network; assuming multiple edges are not present.
Edge Count	The number of total trips in that network. The larger the count, the denser the network is.
Average Path Length	The average path length calculates the shortest path between all possible pairs of properties and then takes the average. On average, you can get from any two properties in this number of trips. The shorter the average path length, the more connected the network of properties.
Transitivity	The number of closed triangles in the network. The higher the number, the more connected the network is. A closed triangle is an edge connecting any three properties.
Global Transitivity	The ratio of closed triangles to the number of triplets in the network. This is also sometimes called the cluster coefficient. The higher the number, the more connected the network is. The network was transformed into an undirected network to calculate this number. A triplet is a group of any three properties, whether they are connected or not.
Assortativity	This is how well a property of a type is connected to another property of the same type. A positive number means (in general) that properties of one type associate with other properties of the same type. A negative number means that properties of one type associate with properties of another type, forming hub structures. The larger the number, the stronger the association. This is measured by a Pearson Correlation Coefficient. The measure is already compared against a configuration model, so we don't need to run simulations and the values can be directly compared between the four networks.
Reciprocity	The probability that a property connected to another property in one direction is also connected in the other direction on a directed network.
Cliques	A clique is a sub-network within the network that is fully connected (every property within the clique is directly connected to each other).
Giant Strongly Connected Components	The largest subset of the directed network which any two nodes are connected and mutually reachable given the direction of the edges. In other words, the size is the number of farms within the network that can be directly linked to each other. A disease introduced to any property can potentially reach any other property in this component (Kiss et al., 2006).
Nodal Measures	Measures calculated for each property and shown as a distribution curve.
Degree Centrality Measures	The degree distribution for each of our 4 networks. Total degree is the total number of trips in and out of each node. In-degree is the total number of directed trips arriving on a property. Out-degree is the total number of directed trips leaving a property.
Betweenness (vertex)	The number of shortest paths going through a property. The higher the betweenness, the more these properties act as bridges during travel. Betweenness captures which properties are important in the flow of information, or in our case, the flow of disease spread. A connectivity measure.
Eigenvector Centrality	In general, properties with high eigenvector centralities are connected to many other properties, which are also connected to many other properties (and so on). This considers how central the other properties in the network are. A connectivity measure.

more similarity as compared to the animal and truck networks. The diameter, edge density, edge count, average path length, transitivity, global transitivity, degree assortativity, reciprocity, betweenness, degree distribution, eigenvalue centrality, and local transitivity are more similar between the full and human networks compared to the full and animal/truck networks. These are highlighted in Table 3. This may indicate that the human movements, which are more numerous than the animal and truck movements (Table 2 number of edge IDs), dominate the structure of the full network. Property group assortativity was high for all 4 networks, indicating that most movements stayed within the same property group. Property type assortativity was positive and close to zero, indicating movement between similar property types is close to no association.

Fig. 3a is a log-log complementary cumulative distribution plot for all nodal network metrics that were calculated. All the metrics deviate between the full, human, animal, and truck networks. Fig. 3b focuses on the degree distribution plots to better visualize their differences and Table 3 shows the median (range) differences between the four networks.

In all four networks, there were only one or two giant strongly connected components (GSCC). The full network had one GSCC and included all 455 properties. The animal network had two strongly connected components (SCC). The GSCC was made up of 411 properties, the second SCC only 5. The human network consisted of one GSCC including all 455 properties. The truck network consisted of two SCC. The GSCC was made up of 412 properties, the second SCC only 2.

3.3. Power-law testing

The results for power-law testing are shown in the supplemental material. The KS test suggested that the full network did not fit a power-law. Graphically, the power-law and log-normal distributions came closest to fitting the degree distributions. Vuong's test did not suggest a difference between the power-law and log-normal distributions. They both fit the observed cumulative distribution curve similarly.

3.4. Important high degree nodes

For both in- and out-degree distributions, any properties that had 661 or more degrees (number of contacts), were considered in the top 25 % and are identified in Table 4. The outcome was exactly the same in both, therefore the table is simplified to just showing in-degree results. Finisher, sow, and nursery barns comprised the most properties present in the upper quartile. Personnel, feed, and livestock vehicles comprised the most vehicle types present in the upper quartile.

3.5. Shared edges

The full network included a total of 22,531 unique trips between two properties. The human network had 18,958, the animal network had 4900, and the truck network had 4837. A visual is shown in Fig. 4. There were 2804 shared edges between the human and animal networks, 2908 shared edges between the human and truck networks, 1587 shared edges between the animal and truck networks, and 1135 shared edges between the human, animal, and truck networks.

4. Discussion

The main objective of this study was to analyze the structural effect of integrating human and animal movements together on swine farm networks. These human movements included crew, service vehicles (such as maintenance calls), personal employee vehicles, manure trucks, veterinarians, and other personnel that arrive on farm. We hypothesized that adding the movements of farm staff, service vehicles, management staff, and personal vehicles to an animal and truck movement network would alter the network statistics and change the parameters in a disease

Table 2
Description of data used to form each of the networks of three North American swine systems over one year.

Network Name	Number of Properties (n = 455)	Number of property groups (n = 4)	Number of Property types (n = 33)	Number of vehicle types (n = 9)	Number of vehicle entry types (n = 12)	Number of unique edge IDs (n = 1878)
Full	455	4	33	9	12	1771
Human	455	4	33	3	8	1555
Animal	416	3	31	2	4	114
Truck	414	3	29	4	5	102

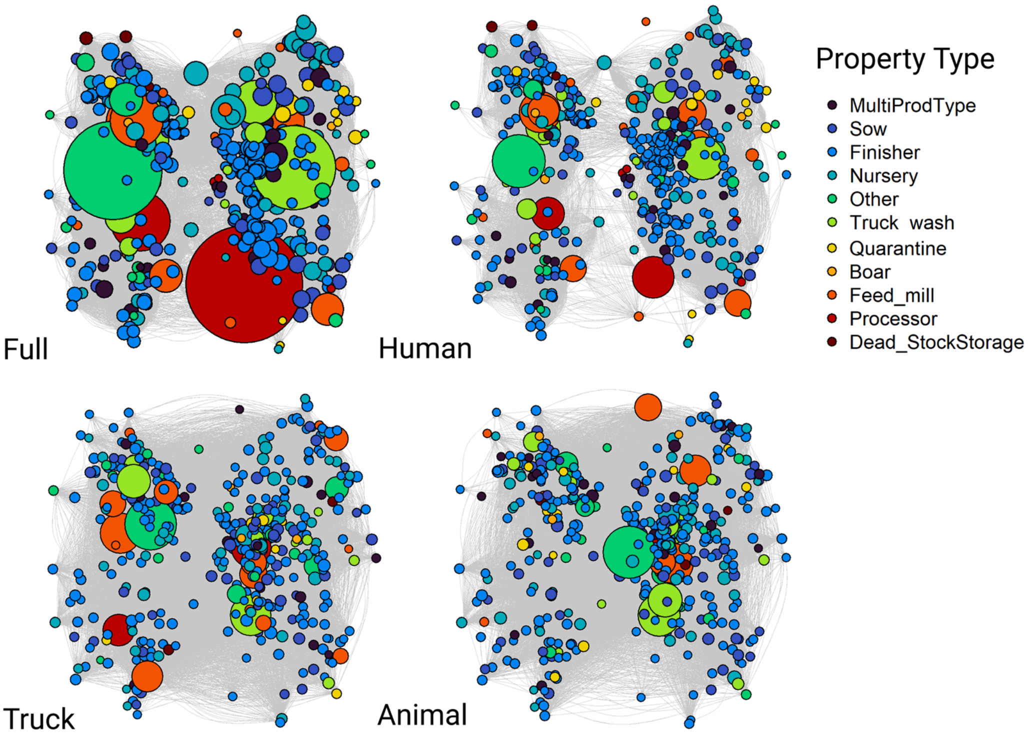

Fig. 1. Comparable graphical representations of each movement network among three co-located North American swine systems: weighted, directed graphs showing the top 25 % of edges (trips), using identical layouts for comparability. The nodes (properties) are colored by property type, with simplified groupings for better visualization. The size of the node indicates the total degree for that node.

transmission model. Four networks were created; a full network that included all movements, an animal network that included all animal movements, a truck network that included service, feed, and manure trucks, and a human network that included all personnel vehicles, veterinarians, and other associated farm workers. Network metrics were calculated for all four networks. We acknowledge that not each type of contact has the same risk of disease transmission. The aggregation of the different types of movement explains the difference in network metrics only. To evaluate transmission risks, each type of movement can be assigned a different transmission parameter during risk assessments in modeling studies.

We found that including the human movements altered the network statistics, and that the full network more closely resembled the human network than it did the animal or truck networks. We concluded that to increase the accuracy of network disease models, it is crucial to include all elements of the full network, including human, animal, and truck movement data.

4.1. Network metrics

The diameter, edge density, edge count, average path length, transitivity, global transitivity (clustering coefficient), degree assortativity, reciprocity, betweenness, degree distribution, eigenvalue centrality, and local transitivity are more similar between the full and human networks compared to the full and animal/truck networks. The addition of the human movements with the animal and truck movements changed the structure of the network, and therefore, will most likely change disease spread if the disease of interest can be transmitted indirectly. These metrics indicate an increase in connectivity and density, and potentially change the properties indicated for surveillance and control measures.

Strongly connected components play a crucial role in disease transmission. All four networks have a very large giant strongly connected component (GSCC) and many cliques. GSCC can be an indication of final epidemic size. The properties included in the GSCC are all connected in various ways and have a chance of being infected during an epidemic (Kiss et al., 2006; Marquetoux et al., 2016). The largest GSCC tends to increase in real-world social networks as the number of nodes and the average degree increases. Therefore, it is not surprising that we have very few numbers of strongly connected components in our networks (M, Jiaqi, personal communication, February 28th, 2024).

The high centrality measures (betweenness, eigenvector) and shorter average path lengths are more indicative of a small-world network topology (Marquetoux et al., 2016). Small-world networks are described as having shorter average path lengths and a 6x greater clustering coefficient compared to a random graph (Lee et al., 2017; Relun et al., 2016). Our full network had an average path length of 2.125 and a global transitivity of 0.4363, which is almost twice the average of a randomly generated graph with the same number of edges and vertices (1.895 and 0.2062, respectively, based on 1000 simulations; data shown in supplemental). Shorter average path lengths and diameter means that

Table 3
Global and Median Nodal Centrality Measures for each sub-network of three co-located North American swine systems over one year.

	Full	Animal	Human	Truck
Global Statistics				
Number of nodes	455	416	455	414
Longest path length (Diameter)	5	10	5	15
Edge density	0.1091	0.02838	0.09178	0.02829
Edge count	92800	24740	52040	16030
Average path length	2.125	3.225	2.194	3.139
Transitivity	215800	16090	157500	10830
Global transitivity	0.4363	0.3189	0.4051	0.2541
Property type assortativity	0.07544	0.004057	0.04693	0.03692
Property System assortativity	0.9152	0.9757	0.8684	0.9434
Degree assortativity	-0.1912	-0.269	-0.147	-0.3438
Reciprocity	0.6077	0.35	0.6442	0.7159
Largest Cliques: Number (size)	3 (24)	4 (15)	10 (21)	7 (11)
Giant Strongly Connected Component: Number (size of GSCC)	1 (455)	2 (411)	1 (455)	2 (412)
Median (range) Nodal Statistics				
Betweenness	88.79 (0, 35670)	26.35 (0, 85730)	108.8 (0, 41930)	37.87 (0, 52500)
Betweenness (normalized)	0.0004317 (0, 0.1735)	0.0001533 (0, 0.499)	0.0005289 (0, 0.2039)	0.0002226 (0, 0.3085)
Total degrees	295 (2, 6664)	68 (2, 3706)	162 (2, 6655)	46 (2, 2400)
Degree in	146 (1, 3341)	32 (1, 1948)	81 (1, 3337)	22 (1, 1279)
Degree out	149 (1, 3323)	35 (1, 1890)	83 (1, 3318)	24 (1, 1121)
Eigenvalue centrality	0.001575 (1.156e-07, 1)	0.00002768 (0, 1)	0.000476 (2.074e-07, 1)	0.0001931 (0, 1)
Local transitivity	0.5142 (0.2016, 1)	0.6056 (0, 1)	0.4649 (0.178, 1)	0.6 (0, 1)
Local triangle count	1051 (1, 9487)	37.5 (0, 1875)	619 (1, 8722)	46.5 (0, 1248)

infection is more likely to spread between properties (Kiss et al., 2006). Small-world networks can have faster disease spread reaching more distant properties from the central properties but tend to have a smaller epidemic size due to the increase in clustering (Newman, 2003; Thakur et al., 2016). However, the increase in clustering can decrease the epidemic threshold (Newman, 2003), making an outbreak more likely. If the network has a very high betweenness score, as we found here, this can actually increase the epidemic size (Marquetoux et al., 2016).

Reciprocity was high for the full, human, and truck networks, and half as much for the animal network. Reciprocity indicates bidirectional movements and a deeper look into which properties in the animal network have reciprocal movement is warranted. Reciprocal movement may indicate that although animals do not move up the hierarchical pyramid (which directs animal movement from source to production properties), people and trucks do. The reciprocity for the animal network was 0.35. We would expect a reciprocity of 0 if all the animals were moving in one direction. This movement may result in biosecurity breaks at source farms that can then be propagated through the system. Identifying reciprocal movements may help identify potential biosecurity breaches.

4.2. Network structure

Network topology is not mutually exclusive. An empirical network might have structural aspects typical of multiple network models (i.e. scale-free, small word, etc) (Langendorf and Burgess, 2021). We see that

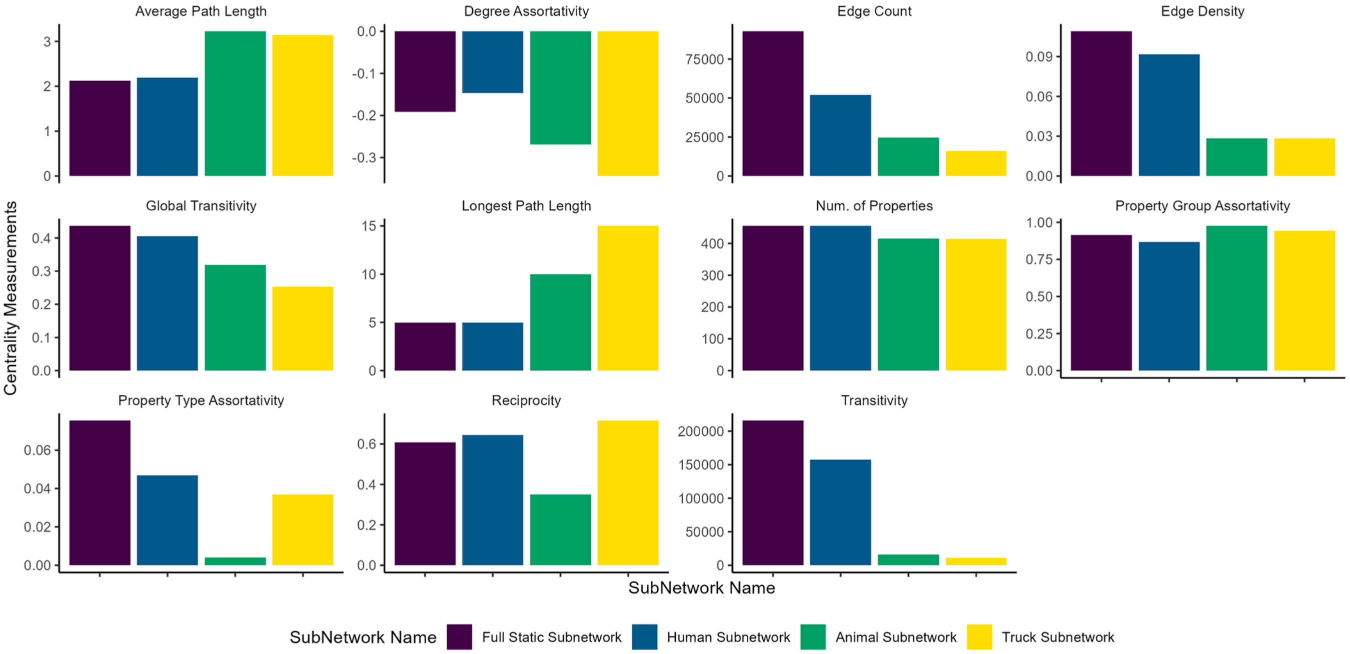

Fig. 2. Global centrality measures for each sub-network of vehicle movement among three co-located North American swine systems. From left to right (top to bottom): average path length, degree assortativity, edge count, edge density, global transitivity, longest path length, number of properties, property group assortativity, property type assortativity, reciprocity, transitivity. The differences in diameter, edge density, edge count, average path length, transitivity, global transitivity, degree assortativity, reciprocity, can be visualized in these bar charts.

our full network has aspects of both small-world (shown by average path length and global transitivity) and scale-free topology (based on the power-law testing) present. The full network does not strongly resemble a scale-free network. This is not surprising as true strong scale-free networks are not as common as the scientific literature portends, and most social networks can exhibit scale-free like structures. Even though the network is not strongly scale-free, the power-law distribution can still be used to model epidemics (Relun et al., 2016). In our analysis, we found that the KS test failed to reject the null and showed that there was not enough evidence to say we had a true scale-free structure. Broido et al. showed that the log-normal distribution usually fits just as well as the power-law (Broido and Clauset, 2019). Vuong's test on our full network did not indicate a difference between the power-law and log-normal distributions, agreeing with Brodio's research. However, the best fit theoretical distribution should be used as the approximation of the underlying distribution in epidemic models (Marquetoux et al., 2016). Topology can also differ within the same livestock production type. For example, Relun et al. (2016) found that the swine industry networks in Europe differed by production system in network structure and properties. Direct comparison with systems outside North America is ineffectual because of their difference in regulations, farm layouts, and practicing guidelines.

We found all of the subnetworks, as well as the full network, have scale-free-like attributes. Compared to random graphs, scale-free networks usually have larger epidemic sizes due to the formation of central hubs in the structure. The larger the estimated exponent in the power-law (2.40 in our estimate), the larger the estimate of the epidemic size (Lee et al., 2017; Passafaro et al., 2020). A negative degree assortativity can also lead to a larger epidemic size (Lee et al., 2017) and is seen in all four of our networks. Disease spread is also faster on scale-free networks but can slow down once it reaches secondary and tertiary contacts (Thakur et al., 2016). Disease spread is highly likely on a scale-free network, regardless of the estimated disease transmissibility. However, it is not affected by clustering (Newman, 2003). Scale-free networks are resistant to random introduction of disease but highly susceptible to targeted disease introduction (such as in agro-terrorism) (Nair and Vidal, 2011; Thakur et al., 2016). The hubs in a scale free network are highly connected and can act as super-spreaders during a disease outbreak (Kraemer, 2005). These hubs, as identified in our network, would be important to include in surveillance programs.

One way we have identified potential hubs is through analysis of degree distributions. A high correlation between the in- and out-degree distributions in directed graphs indicates that properties are more likely to become infected and transmit disease. The covariance of these distributions determines the epidemic outbreak threshold (Kiss et al., 2006). Highly connected nodes (nodes with high degrees and high betweenness, as seen in our networks and listed in Table 4) are also more likely to increase disease spread (Marquetoux et al., 2016; Passafaro et al., 2020). Increased connections between high and low degree nodes, or increases in the clustering, may slow down spread, even with an $R_0 > 1$ (Kiss et al., 2006; Marquetoux et al., 2016; Newman, 2003). However, as connectivity increases, such as with the high betweenness and increasing density we found in our full network, disease may begin to spread faster (Newman, 2003). We found the full network to have a very high betweenness, especially compared to the animal sub-network, indicating that diseases that can be transmitted through fomites have the potential to spread faster through this system than those transmitted only directly. On a positive note, our full network has a heavy-tailed degree distribution and negative degree assortativity. According to Passafaro et al. (2020), networks that exhibit these structural properties are more responsive to targeted interventions due to the ability to cause network fragmentation.

The potential hubs in the network are those with the highest in- and out-degrees (Table 4). Finishing barns are expected to have high in-degrees, since they are at the bottom of the production pyramid. Sow and nursery barns, however, are expected to be at the top of the production pyramid, with low in-degree due to their need for high biosecurity; they may have higher out-degree due to shipment of piglets to finishing sites, which is a risk for propagating infection after introduction. When including human movements, our full network found that 38 % of sow farms had both high in- and out-degree contacts. This indicates that the production pyramid biosecurity structure may be disrupted by human movement, which should be considered when facing an outbreak involving spread via fomites or human carriage.

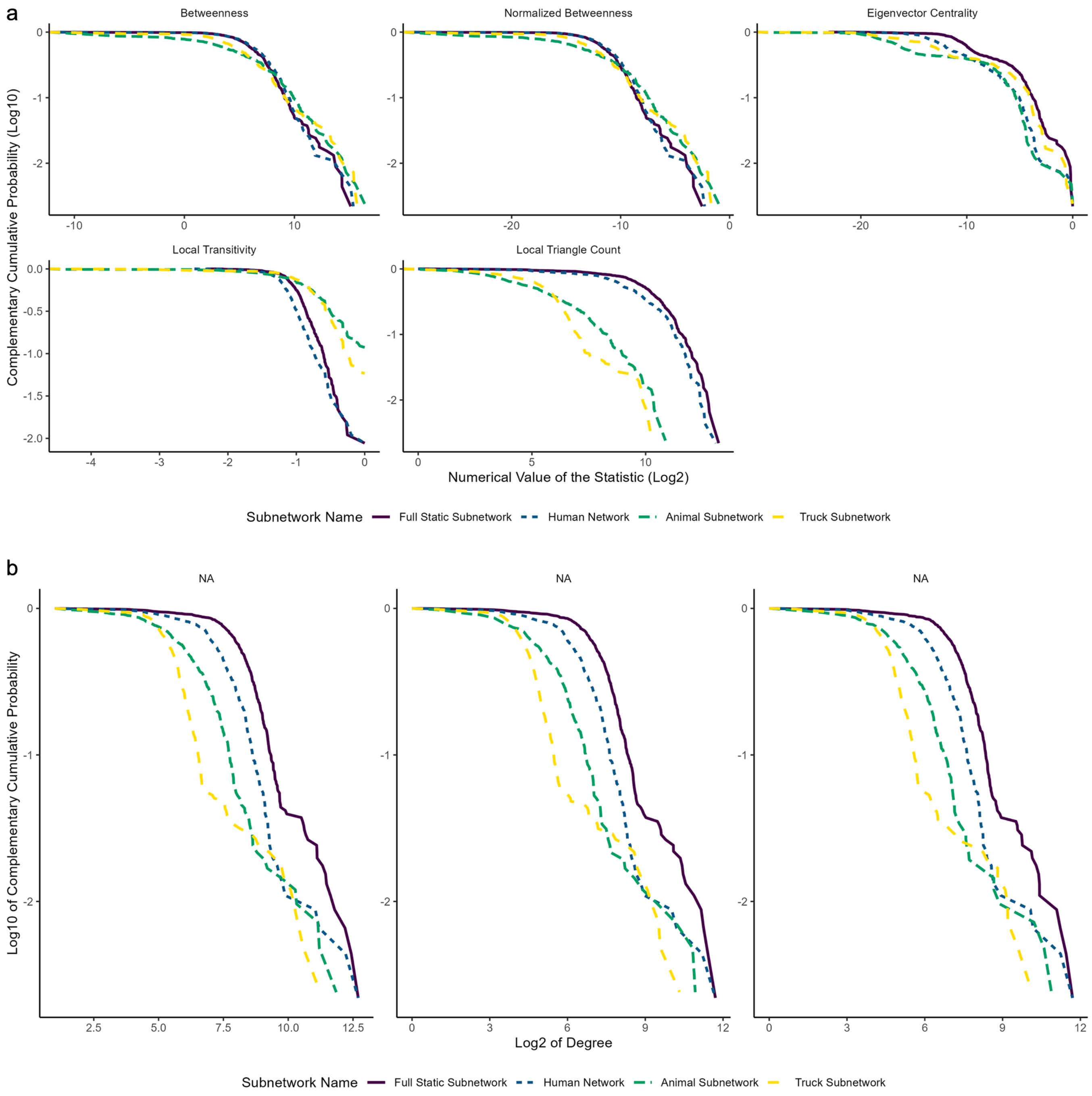

Fig. 3. Complementary Cumulative Distribution Plots for: a) each sub-network nodal centrality measures (in log10-log2 scale for visualization) From left to right (top to bottom): betweenness, normalized betweenness, eigenvector centrality, local transitivity, local triangle count. b) degree distributions only (in log10-log2 scale for visualization). From left to right: Total degree, In-degree, Out-degree. The differences in betweenness, degree distributions, eigenvalue centrality, local transitivity, and local triangle count can be visualized.

An edge represents a connection between two properties in the system that can transmit disease. The edges that are shared among our different sub-networks (Fig. 4) do not add any additional connections between properties, although they may increase the number of potentially infectious contacts between those properties. The edges unique to each subnetwork, however, are additional contacts added to the system because of incorporation of that transmission type. The human network has a total of 18,958 connections between properties. Only 5712 of them are shared with other subnetworks, leaving 13,246 connections added to the network by incorporating human movements. Thus, the number of potential transmission pathways via human movement is 2.3 times those possible through all other pathways.

The network presented here is a static network, aggregated over one year. Static networks approximate annual farm to farm transmission rates, although they may overestimate those rates given the shorter time frame of many outbreaks (Passafaro et al., 2020). Galvis et al. (2022a) demonstrated that, in some cases, static networks can closely approximate dynamic or temporal networks; their vehicle static network approximated their temporal network well, with causal fidelity values greater than 89 %. A static network model also provides cumulative statistics of the aggregated networks evaluated, although the comparability of static and dynamic networks in this regard has been inconsistent (Marquetoux et al., 2016; Passafaro et al., 2020).

The current study found that human movements dominated the

Table 4
The number and type of properties and vehicles found in the top quartile of the in- and out-degree distributions. For both in- and out-degree, the top 25 % of properties were those with degrees higher than 661. Percent represents the percent of that property type in the top quartile. The vehicle types were those present in the edges associated with each high degree property.

Property Type	Number (%) of nodes of this type in top 25 % by degree	Percent of type compared to total of that type % (total n in graph)	Vehicle Type	Number (%) of vehicles of this type in top 25 % by degree	Percent of type compared to total of that type % (total n in graph)
Finisher	34 (29.82 %)	15 % (225)	Personnel	90957 (41.82 %)	33 % (273274)
Sow	24 (21.05 %)	38 % (63)	Feed	72239 (33.22 %)	57 % (125870)
Nursery	17 (14.91 %)	27 % (63)	Livestock	45298 (20.83 %)	55 % (82756)
Feed Mill	9 (7.89 %)	53 % (17)	Deadstock	3713 (1.71 %)	65 % (5656)
Truck Wash	8 (7.02 %)	73 % (11)	Service	2243 (1.03 %)	28 % (7952)
Quarantine	3 (2.63 %)	25 % (12)	Truck	2202 (1.01 %)	35 % (6132)
Distribution Center	2 (1.75 %)	67 % (3)	Workers	725 (0.33 %)	44 % (1660)
Nursery, Finisher	2 (1.75 %)	18 % (11)	Car	106 (0.05 %)	76 % (139)
Nursery, Sow	2 (1.75 %)	67 % (3)	Manure	5 (< 0.01 %)	19 % (26)
Office	2 (1.75 %)	67 % (3)			
Processing Plant	2 (1.75 %)	40 % (5)			
Dead Stock Storage	1 (0.88 %)	50 % (2)			
Farm, Other	1 (0.88 %)	50 % (2)			
Finisher, Other	1 (0.88 %)	100 % (1)			
Maintenance	1 (0.88 %)	100 % (1)			
Manure Storage	1 (0.88 %)	100 % (1)			
Other	1 (0.88 %)	12.5 % (8)			
Other, Dead Stock Storage	1 (0.88 %)	100 % (1)			
Other, Transfer Dock	1 (0.88 %)	100 % (1)			
Sow, Finisher, Nursery	1 (0.88 %)	100 % (1)			

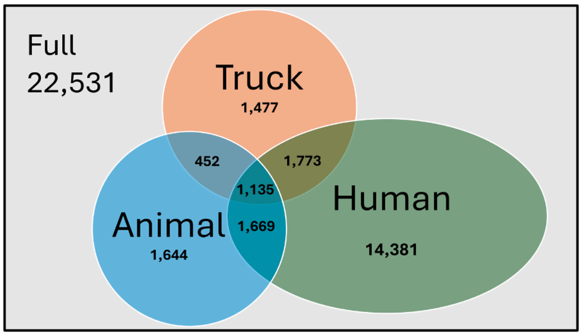

Fig. 4. Venn diagram of shared edges between the four networks. The full network is represented by the entire outer rectangle. Each colored circle represents a different sub-network. The overlap in the diagram represents the number of shared unique edges between those networks.

contact network of a group of commercial swine farms in North America. Most of the previous livestock industry network modeling including human movement were performed outside North America, and previous U.S. studies generally include either only human movements (Black et al., 2022), or only animal movements (Lee et al., 2017; Passafaro et al., 2020; Thakur et al., 2016). The sole exception is one study describing network statistics of a single swine company in the United States (Galvis and Machado, 2024); this network differed from that described in this study in production system, region, number of nodes, different types of vehicles making up the sub-networks, visit definition, and different proportions of those vehicles within each sub-network. One main difference between these networks was the number of human vehicles included. About 88 % (1555/1771) of our total vehicles (edge IDs) were comprised of human movements, whereas only 32 out of a total of 398 (8 %) vehicles represented human movements in Galvis' network. However, despite the differences, both models found a more highly connected network when trucks and human vehicles were included with animal movement, as shown by higher network densities, betweenness measurements, and lower path lengths.

Our animal sub-network is comparable to previously published movement networks based on animal movement only in North American swine systems. For instance, a static network of a multi-site swine production system in Iowa over 36 months found an average path length of 6.56 and a diameter of 24 (Passafaro et al., 2020) after excluding animal shipments delivered to abattoirs, cull stations, boar studs, and any animal movement that lacked certain information or were in directions opposite to the expected hierarchical structure. Our 12-month animal network included all animal movements, resulting in an average path length of 3.225 and a diameter of 10. However, a 12-month aggregated time network in the same study matched more closely with ours, with an average path length of 3.7 and a diameter of 12. Similarly, another study found an average path length of 3.20 and a diameter of 9 when aggregating monthly over a 12-month time frame (Lee et al., 2017). Both networks found a negative degree assortativity and heavy right tail degree distribution, suggesting a scale-free like structure (Lee et al., 2017; Passafaro et al., 2020), as did ours, although Lee et al. did find a positive degree assortativity, indicating possibly less hub structure. These data, and therefore the network structure appreciated, is specific for the swine systems used in this study. However, the structural outcomes were similar to other US studies and indicate that the overall findings may be applied generally within the country. Because of the varied structure of swine production networks in other geographical locations, such as Europe, means that these results may not be globally generalizable. This approach can be generalized to any swine system, given the data are prepared similarly.

4.3. Limitations

Our network analysis was constrained by the finite number of farms (nodes) included and limited (one year) time scale. This limited our ability to check assumptions, fully evaluate the scale-free nature, or evaluate seasonality in the network topology. However, the data is from a large multi-scale production system that is not expected to have seasonality in production (Relun et al., 2016). The small sample size may have limited our statistical power in fitting our network to the scale-free topology (Marquetoux et al., 2016); however, human systems frequently fail to fit exact topologies, so this lack of fit could represent the actual network structure. This study primarily focused on network structures and the effect of different movement types on those structures. We did not assess the effects of specific bio-security protocols and determined that it is not feasible at this time to develop specific recommendations. Ongoing research will include examining effects of specific interventions on disease spread within this network. Because we aggregated a years' worth of data into a single network, we are not able to comment on the temporal variability of the network structure nor the impact on the analysis.

Despite its limitations, this work is novel in North America since we incorporated all known movements in and out of properties within three production sites, including living and deceased animals, various truck types, farm personnel, service vehicles, and contract workers.

5. Conclusion

The full network representing three co-located North American swine systems shows topology similar to both small-world networks, due to the shorter path lengths and higher centrality measures, and heavy-tailed degree distributions, from which we could identify potential super-spreader premises. This is in accordance with other livestock networks. There are potential super-spreader properties that can disseminate infection to less connected properties. Even though these hubs can be locations targeted for control measures, the increased connectivity allows other pathways for disease to spread around these centers, allowing continuation of epidemics and potential failure of targeted interventions. We may see higher epidemic sizes, lower epidemic thresholds, faster disease spread, and less resistance to randomly introduced infection compared to random graphs.

We show that network structure changes when additional transmission pathways are added to the model. Changes in structure will affect function and therefore transmission of infectious diseases. These results indicate that biosecurity protocols should involve human flow in addition to animal flow in a hierarchical direction. If disease transmission routes include indirect contacts, such as fomites and physical transmission, then human movements need to be included in biosecurity protocols as well as disease transmission models. Recommendations for biosecurity protocols based on animal and truck movements alone may be insufficient.

CRediT authorship contribution statement

Rebecca Lee Smith: Writing – review & editing, Supervision, Resources, Methodology, Conceptualization. **Tara Prezioso:** Writing – review & editing, Writing – original draft, Visualization, Software, Resources, Project administration, Methodology, Formal analysis, Data curation, Conceptualization. **Jeff Wrathall:** Writing – original draft, Data curation. **Alicia Boakes:** Resources, Conceptualization. **Suman Bhowmick:** Writing – review & editing, Supervision, Methodology. **Jonas Reger:** Software.

Declaration of Competing Interest

Tara Prezioso, Rebecca Smith, Suman Bhowman, and Jonas Reger declare that they have no conflicts of interest. Alicia Boakes and Jeff Wrathall are both employees of Farm Health Guardian, LLC.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.prevetmed.2024.106370.

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