Quantifying the dynamics of pig movements improves targeted disease surveillance and control plans

Running title: Networks to improve surveillance in pigs

Gustavo Machado[1*], Jason Ardila Galvis[1], Francisco Paulo Nunes Lopes [2], Joana Voges[2], Antônio Augusto Rosa Medeiros [2], Nicolas Cespedes Cárdenas[3]

[1]Department of Population Health and Pathobiology, College of Veterinary Medicine, Raleigh, North Carolina, NC, USA

[2] Secretary of Agriculture, Livestock and Agribusiness of State of Rio Grande do Sul (SEAPI-RS), Porto Alegre, Brazil.

[3]Department of Preventive Veterinary Medicine and Animal Health, School of Veterinary Medicine and Animal Science, University of São Paulo, São Paulo, Brazil.

Corresponding author: Dr. Gustavo Machado, gmachad@ncsu.edu

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Summary

Tracking animal movements over time may fundamentally determine the success of disease control interventions. In commercial pig production growth stages determine animal transportation schedule, thus it generates time-varying contact networks showed to influence the dynamics of disease spread. In this study, we reconstructed pig networks of one Brazilian state from 2017 to 2018, comprising 351,519 movements and 48 million transported pigs. The static networks view did not capture time-respecting movement pathways. For this reason, we propose a time-dependent network approach. A susceptible-infected model was used to spread an epidemic over the pig network globally through the temporal between-farm networks, and locally by a stochastic model to account for within-farm dynamics. We propagated disease to calculate the cumulative contacts as a proxy of epidemic sizes and evaluate the impact of network-based disease control strategies in the absence of other intervention alternatives. The results show that targeting 1,000 farms ranked by degree would be sufficient and feasible to diminish disease spread considerably. Our modeling results indicated that independently from where initial infections were seeded (i.e., independent, commercial farms), the epidemic sizes and the number of farms needed to be targeted to effectively control disease spread were quite similar, indeed this finding can be explained by the presence of contact among all pig operation types The proposed strategy limited the transmission the total number of secondarily infected farms to 29, over two simulated years. The identified 1,000 farms would benefit from enhanced biosecurity plans and improved targeted surveillance. Overall, the modeling framework provides a parsimonious solution for targeted disease surveillance when temporal movement data is available.

KEYWORDS: swine movement data, dynamic contact networks, disease surveillance, SI models.

Introduction

Between-farm animal movement has historically been associated with disease spread (Ortiz-Pelaez et al., 2006; Smith et al., 2013). Animal movement data has allowed for the initial development of network-based approaches, which are dominated by the use of static network, which are representations of animal movements of many months as one snapshot, from which metrics are calculated and used to ranked farms providing targeted locations for surveillance and risk mitigation (Martínez-López et al., 2009; Bastard et al., 2020). Indeed, disease transmission events have proven not to restricted to the historical record of movement (Firestone et al., 2019; K. Schulz et al., 2019; Qi et al., 2019; Sterchi et al., 2019), therefore, it is recognized that the current neglected temporality of real-world animal movements has been a constant roadblock to the advancement of network epidemiology, especially in the development of new methodologies (Pellis et al., 2015; Chaters et al., 2019), and the design of applied surveillance and control measures. Ultimately, the use of network-based metrics to select farms for isolation or surveillance schemes has shown great value (Mohr et al., 2018; Firestone et al., 2019; Payen et al., 2019). This is a direct consequence of the availability of animal movement data (Büttner et al., 2016; Firestone et al., 2019).

Stochastic simulations have been used extensively to measure the impact of disease control strategies in future disease spread scenarios (Smith et al., 2017; Funk et al., 2018; Kim et al., 2019; Lanzas et al., 2020). Mathematical models have also been used to experimentally spread disease over contact networks and reveal important dynamic characteristics of epidemics (Miller, 2017; P. Kim and Lee, 2018; Darbon et al., 2019). For example, mathematical models have been used to describe the epidemic spreading in temporal contact networks, which provides an opportunity for tracing outbreaks and contact among nodes over time (Guinat et al., 2016; Colman et al., 2019; Ferdousi et al., 2019; Sterchi et al., 2019). Some examples of software readily available to model epidemic on networks include EMULSION (Picault et al., 2019) GEMFsim (Sahneh et al., 2017) EpiModel (Jenness et al., 2018), and SimInf (Widgren et al., 2019), computationally and algorithm used are diverse, which make some more efficient or flexible than other. We chose to use SimInf, mainly because it was design to accommodate large networks, thus feasible to be use over national or sub-national networks. Indeed, has been successfully used to select sentinel nodes in cattle networks (Chaters et al., 2019; Engblom et al., 2020).

Here, we used two years of pig movement data from one Brazilian state to estimate the optimal number of farms for target surveillance by tracking between-farm contact pathways and inferring epidemic sizes throughout disease propagation. We first described the complete pig movements and then challenged the use of static networks against dynamic networks. We proposed a stochastic compartmental model to simulate disease spread in a two-year empirical network while accounting for the daily order of the movements. Our model formulation allowed the calculation of the minimum number of farms needed to be targeted and undergo for example, lockdown or stamping out, in a scenarios when foreign animal diseases (FAD) are detected in the territory. Finally, we applied the proposed model, ultimately to identify the farms that during peacetime would constitute a list of farms to where active surveillance activities should be prioritized (i.e., sampling, periodic visits), which were then mapped and described in regard to their biosecurity and infrastructure.

Material and methods

Data collection and entry

The record of pig shipments among all registered farms from the state of Rio Grande do Sul which holds 14,6% of the total swine population in the county (third largest pork-producing state in Brazil), was used to reconstruct contact networks from 2017 until 2018 (SEAPI-RS, 2018). Information about each swine farm included farm identification, production types (breeding, certified-swine-breeder, sow, nursery, wean-to-finisher, finisher, subsistence and others), farms infrastructure (e.g., presence of a fence, presence of a cleaning and disinfection station, see table 2 for the full list), geolocation and farms population capacity. Each pig shipment included date(s), farm of origin and destination, number of animals transported and purpose of movement (weaning, finishing, slaughter or other). Movement data with missing information of farm location, production type, farm of origin or destination were excluded prior to the analysis. Additionally, farms declared inactive (no pigs raised in the past two years or out of business) were not considered in the analysis. Movements from or to other states were also excluded from any analysis. Based in information reported to the local authorities in June 2018 all farms were classified as i) “commercial” farm with active contracts with integrated swine companies, ii) “independent” farm that declared to be commercial but did not have active contract with integrated swine companies and small farm holders and iii) “not reported” farms that did not report to local authorities their pig operation type (e.g., commercial or independent). The identification of 1,911 (21.4%) not reported farms, resulted in regional policy in which the state authorities issued a request to all farms report pig operation status, within one year, farms that do not report will have all pig movements blocked until information is shared. Finally, farms with missing geographic location were discarded.

Networks analysis: static and time-series networks

To analyze the stability of between-farm contacts over time, we reconstructed a directed static network. To apply a static network analysis, repeated between-farm contacts between two farms throughout the observation period, from January 2017 to December 2018, were aggregated to a single one. Here directed "edges" represented by pig shipments between two "nodes", where nodes corresponded to pig farms. Second, a temporal explicit directed network was constructed. To assess the temporal features of the network, static centrality metrics were calculated on monthly, six-months and yearly sub-networks (Lentz et al., 2016). For the static and the time-series networks, we calculated several centrality indicators for farms within the network: outdegree, indegree, page rank, closeness centrality, betweenness, giant weakly connected component (GWCC), and giant strongly connected component (GSCC) (Table 1) (Cárdenas et al., 2018) .As slaughterhouses constitute sinks and we were interested in potential disease spread among living animals, transports to slaughter were excluded from the network analysis, but are kept for descriptive purposes (see Figure 2 and supplement Table S1).

The variability of the network structure over time-series network aggregations

Static networks are considered an approximation of all movement paths for a defined period, e.g., animal movement between pig farms for one month (Büttner et al., 2013; Lentz et al., 2016). This can artificially create accessibility paths between nodes that are not always accessible by all "nodes" in a network, which can lead to an overestimation of the connectivity among the nodes (Holme and Saramäki, 2012; Lentz et al., 2016). To quantify the amounts of such static error, the number of paths in the static view can be compared with the number of paths in the time-series network (Lentz et al., 2013, 2016). A causal fidelity of one means that the temporal network is well represented by its static network, while networks with lower causal fidelity values would not represent the temporal paths well because most of the paths are not causal. Here, we calculated the causal fidelity on timescales that are typically used to investigate animal movement data: monthly, 6 months and 1 year and for the full two years of data that were used to reconstruct directed networks (Lentz et al., 2016). We also calculated the edge loyalty (θ), which measures the fraction of preserved edges (θ) of a given premise between two consecutive years, $t-1$ and t. To quantify $\theta_i^{t-1,t}$, we define Y_i^{t-1}as the set of edges from the premise i in the time $t-1$ and Y_i^t as the set of edges from the premise i at time t. Then, $\theta_i^{t-1,t}$is given by the Jaccard Index in equation 2 (Valdano et al., 2015; Schulz et al., 2017).

$$\theta_i^{t-1,t} = \frac{|Y_i^{t-1} \cap Y_i^t|}{|Y_i^{t-1} \cup Y_i^t|} \tag{2}$$

For the node loyalty (φ), we use the same Jaccard Index,

$$\varphi_i^{t-1,t} = \frac{|V^{t-1} \cap V^t|}{|V^{t-1} \cup V^t|} \tag{3}$$

where $V_i^{t-1}$is the set of farms that are active in period $t-1$, and V_i^t is the set of farms that moved at least one animal at time t (Valdano et al., 2015; J. Schulz et al., 2017).

The minimum number of farms needed for effective control disease spreading process over time-varying network

We developed a stochastic susceptible-infectious (SI) epidemic model to calculate the minimum number of farms needed to effectively reduce the number of new cases expected to spread through the contact network. The number of infections after the removal of farms ranked by network metrics betweenness, closeness, page rank and degree, random removals (similar to the current state of farm surveillance), and without farm removal were the main model outputs. In this work removal means effective target surveillance activities, which can include yearly visits for testing of viral circulation, for example. Ultimately, this is expected to approximate the impact of network-based target surveillance, which often include farm visits, sample collection, etc., to a feasible number of farms.

The epidemiological model structure and dynamics

A network based stochastic compartmental model with two compartments, susceptible (S) and infectious(I) representing different discrete health states, was used to model the within-farm transmission dynamics of a simulated disease assumed to spread only via pig movement. Transitions from S to I was a one-way transition depending on $S\overset{\beta}{\rightarrow}I$ with β as the transmission coefficient. Infected animals were assumed to be infectious until the end of simulations and were allocated in each farm modeled as metapopulations. We assumed homogenous mixing population within the farms, where all animals have identical transmission coefficients. For simplicity we have not considered the heterogeneities related to age, space or behavioral aspects of the populations. The model simulated disease spread at two levels (local and global), with the local level under the regular stochastic compartment model and formulated as a continuous-time Markov chain (CTMC). The Gillespie stochastic simulation algorithm (SSA) was applied to simulate the number of animals within each compartment through time using a transition rate from $S\overset{\beta}{\rightarrow}I$ as

$$\frac{dI}{dt} = \frac{\beta S_i I_i}{S_i + I_i} \qquad (1)$$

in a specific time t (Gillespie, 1977; Widgren et al., 2019). For the between-farm transmission (global-level) was realized over a directed temporal network on the daily movements between farms (origin, destination and number of animals) from January 1st 2017 to December 31st 2018. The number of incoming and outgoing animals was used to update the number of animals in a given node i at time t. The movements with destination to slaughterhouses were model as an "exit event", thus removed from the simulation systems. To assure the stability of the metapopulations the number of born alive declared to the local veterinary were used as the only "enter event" and only occurred in breeding farms and assumed to be susceptible. For model initialization we assume an initial herd prevalence of 10% and 0.1% of infected pigs in each farm, in which disease was allowed to be transmitted between and within farms. We use a set of β values of 0.01, 0.05, 0.1 and 0.2, as used for sensitivity analysis (supplementary Figure S3).

Model initialization followed two seed initial infected scenarios: scenario 1: from the 9,500 farms with least one movement from 2017 to 2018, 950 were selected randomly to serve as seed infection (where the disease was determinate to start spreading from). Scenario 2: from the 9,500 farms with least one movement from 2017 to 2018, 950 farms were sampled to serve as seed chosen proportionally to the number of farms in each production category, 40.4% commercial, 38.2%

independent, and 21.4% from the farm that did not report this information. This allowed the initial infection to be seeded within all types of pig operations. The comparison of both disease introduction approaches allowed us to test a more realistic scenario since disease can emerge at any location of the study area and in any pig operation (Figure 1). The simulated control intervention was based only on the sequential removal of farms from the time "0" based on the static network metrics described above. While farms were removed, the number of new cases per 100 susceptible farms was calculated. We chose an arbitrary number of 2,000 herds to be removed, and at the end of each simulation scenario the incidence of new cases I was calculated as follows:

$$I = \frac{Number\ of\ new\ infected\ herds\ in\ 2017-2018}{(Number\ of\ herds\ that\ traded\ with\ other\ herds\ in\ 2017-2018) - (Initial\ number\ of\ infected\ herds\ in\ 2017-2018\ that\ traded\ with\ other\ herds\ )}$$

Infection was seeded into all candidate farms randomly for 100 times, from which simulations were run and the median incidence was derived for each run The simulations were implemented in R package SimInf (Widgren et al., 2019).

To evaluate the predictability of our modeling approach, we reproduced the models described above over the 2019 temporal network. Briefly, we removed from 2019 network the 2000 farms identified in the model of 2018 network based on the most efficient network parameters, and ran the same model structure on the 2019 network, assuming that surveillance was done in all farms we calculated the remain expected number of infections in for 2019. In addition, based on the best network metric that reduced the incidence the most (model above), we ranked the farms to be priority in each year, 2017-2018 against 2019 to evaluate changes on ranking priority over time (Supplementary figure S4).

Cumulative contacts as a proxy of epidemic sizes

The modeling setup described by (Payen et al., 2019) was adapted to identify the network-based metric that can produce the smallest epidemic size distribution at the end of the two years of pig movements, and consequently allow the generation of a farm hot-list to use to target surveillance activities. This approach is based on the classic deterministic SI spreading model that follows movements temporality (Dubé et al., 2008; Nöremark et al., 2011; Konschake et al., 2013).

Thereafter, we will refer to this model as “spread cascade”, which is a temporal representation of the cumulative and consecutive contacts among farms, and therefore can be interpreted as the size of an epidemic (Payen et al., 2019). The hypothetical disease spread followed the chronological order of movements over the two years. In short, when there was a directed interaction, including the three dimensions of time *t*, infected farm *i* and susceptible farms *j*, disease has successfully been transmitted. These events were counted in favor of each farm *i* cascade and the triplet *t, i, j* and added to the temporal links of the stream; see (Payen et al., 2019) for more details of the methodology. Overall, we recorded the daily spread cascades for the two years of data, which are represented by weekly averages and ± 95% CI (see supplementary figure S4), and the accumulated spread cascades sizes for each seed node (9,500 farms) in the network at the end of the two years as a proxy for the worst-case scenario in epidemic propagation (Payen et al., 2019). We used the static network to initially rank all pig farms in descending order of degree, betweenness, page rank, and closeness and then removed the top 10, 250, 500, 750 and 1,000 farms before starting the model simulation while recording the spread cascade sizes. Since this study was designed to guide decisions in the field, we consulted with the local stakeholders before deciding on the final number of farms to be on the surveillance hot-list, which initially would be up to 1,000 farms (personal communications with Dr. Lopes, Chair of the Animal Movement and Surveillance Department of the state of Rio Grande do Sul). For comparison with usual surveillance practices, we selected the same number of farms randomly. The contribution on containing the epidemic spread by each network-based target surveillance strategy was evaluated by comparison of the final spread cascade distributions at December 2018 using a nonparametric Kruskal-Wallis test followed by Dunn's post hoc test, where the p-values below 5% were significant. Once the most efficient network-based surveillance strategy was defined, the biosecurity, infrastructure and population of the selected sentinel farms were described. The biosecurity and infrastructure is provided by field veterinarians or by pig producers directly to the local veterinary service.

Software

The software used for statistical analysis and graphics was R statistical software (versions 3.4.1, 5.1.3) (R Core Team) with R Studio editor using the igraph 1.2.4 (Csardi and Nepusz, 2006), tidyverse 1.2.1(Wickham, 2017), SimInf 6.3.0 (Widgren et al., 2019), sf 0.5-3 (Pebesma, 2018), and brazilmaps 0.1.0 (Siqueira, 2019) packages. Spyder 3.3.3 software for Python version 3.7 and Adobe Illustrator CC 2018 software were also used.

Results

Description of pig movements

The total number of active pig farms in the complete database included 11,849 farms, from which 9,500 had registered geographic coordinates and were considered in this analysis. The majority, 40.4%, were identified as commercial farms, 38.2% of independent pig producers, and 21.4% did not report pig operation type (Table S3 shows the description of the population for both pig operation classes). In the commercial farms there were 17 pig production systems, the number of farms within each system were from 10 to 465 farms. While we have described movements into the 102 registered slaughterhouses, they were not accounted for in any network analysis thereafter (Figure 2). Shipments from commercial to slaughterhouse totaled about 34% of the total movements, while 18% of the movements were from independent farms into slaughterhouses and 14% were between commercial farms. Importantly movements from independent pig producers and from farms that did not report pig operation types into commercial farms were, 3.35% and 1.97%, respectively. Among all farms with information about their production types 6,555 (55.32%) finisher farms, 1,816 (15.33%) nurseries, 470 (3.97%) wean-to-finisher farms, 433 (3.65%) breeding farms, 122 (1.03%) certified swine breeder farm and 250 (2.11%) other farms, which included insemination stations and isolation units, 2,101 (17.73%) as small pig holders (backyard farms or for subsistence).

Figure 1.

More than 51% of movements were from finisher farms to slaughterhouses, with a monthly median of 7,657 shipments. The second largest number of movements from nurseries to finisher farms was 13.51%, with a monthly median of 1,992 transfers. Breeding farms made up for 4.65% of the movements to nursery farms and 4.3% of movements to the finisher, with 673 monthly median movements. Finally, wean-to-finisher farms sent a small but significant amount of pigs to slaughter (3.5%), while certified swine breeder farms accounted for 2.8% of movements to slaughter (Figure 2).

Figure 2.

Monthly network analysis

From the two years of movement data, we reconstructed the monthly static networks. The number of farms, movements and animals varied substantially with a steady increase from July 2017 until October of the same year (Figure 3). The network diameter revealed a positive increasing trend of 33% from April 2018 through December 2018, December 2018, which decreased thereafter; this pattern was different from the monthly values from the previous year. The increase in the network diameter in 2018 increase the shortest paths between pairs of farms, thus likely to reduce the size of epidemics, because two GSCC would be less likely to be directed connected. The monthly analysis showed a positive trend of the GSCC in 2017 and a negative trend in 2018, and the GWCC had a more stable pattern with two consecutive peaks in July and October of 2018. In May 2017 GSCC peaked at 40 farms inflated with mostly commercial farms, and in November 2018 the GWCC had almost 600 farms in which most were also commercial (supplementary Figure S1 and Table S2 for the two years GSCC and GWCC).

Figure 3.

Loyalty and causal fidelity

The node loyalty of 2018 compared with 2017 was 0.65, while edge loyalty was 0.19. This means that only 65% of the farms that traded pigs in 2017 were preserved in 2018, and 19% of the edges were preserved between 2017 and 2018. In more details, for the six months loyalty the second half of 2018 was the highest at 75% and edge loyalty also increased to 19%, if compared with the lowest edge loyalty of the second half of 2017 at 17% and lower node loyalty for the first six month of 2017 at 68%. On the other hand, the monthly causal fidelity varied from 0.33 in July 2018 and reached the highest value of 0.55 in July 2017 (supplementary Figure S2). For the network that evaluated time periods of six months, the causal fidelity was 0.22 for the first half of 2017 and 0.47 for the second half of 2018, and the annual evaluation was in 2017, 0.18 in 2018, and 0.33 for the entire static network. The causal fidelity demonstrated a discrepancy between static and temporal network views. In addition, we calculated the causal error from the causal fidelity, which can be approximated by the inverse of “c” and represents the overall overestimation of disease outbreaks if static networks are used. The first six months of 2017 had the worst results, with overestimations at 4.54 and 1.81 for the July 2018 network.

Number of sentinel farms for targeted surveillance and epidemic sizes

The stochastic runs showed that the removal of 2,000 farms did not completely control the disease from spreading, but it was reduced markedly to a maximum of 1.88 new cases per 100 farms when β of 0.2 was used. Based on local capacities of the official veterinary service and that the average number of new cases was reduced to as low as 7.70 cases per 100 farms with a β of 0.2 when 1,000 farms were removed from the network, the former was set to be the maximum number of feasible farms to be targeted. In addition, to evaluate the impact of the deployment of the surveillance activates to the farms identified with the past network data (2018) on the number of infected farms for the following year (2019), assuming that all 2,000 farms were surveyed the number of new cases was 1.20 per 100 farms and if the 1,000 were targeted the maximum incidence would be reduced to 5.89 cases per 100 farms. Furthermore, we compared two infectious seed scenarios: a) infections started at random farms and b) stratified random infections forced to start in proportion to the number of commercial, independent, and not reported. Both have very similar results which reinforced the importance of independent farms in the role of spreading diseases into commercial pig farms and vice versa (Figure 4, supplementary Figure S3)

Figure 4.

After the removal of the first 1,000 farms with the highest degree which was the identified as the most effective in reducing the spread of the simulated disease, our model estimated that the maximum outbreak size would involve 29 farms secondarily infected (Figure 5). When compared with the removal of random nodes, which is a common practice where farms that are more convenient are visited, our model exercise estimated that the number of secondary infected farms could reach up to 2,593 farms (Figure 5, supplementary Table S4 and Figure S6). In addition, we compared the list of farms with the highest degree the 2018 with the 2019 network, we found that 68% of the top 1.000 in the 2018 network were the same in 2019, only a small portion of nodes 120 (9%) were different from the ones identified in 2018 see supplementary figure S4.

Figure 5.

Descriptive analysis of biosecurity, infrastructure and population profile of the targeted sentinel farms.

Most of the farms within the 1,000 target farms were commercial (55.6%) (Supplementary information Figure S7), with one production system contribution with 138 farms, and 29.7% were independent and 14.7% did not report business operation. From the comprehensive list of biosecurity and infrastructure characteristics of the commercial farms had a median of 2 barns (IQR-1-11), capacities for housing were approximately 1,100 pigs (IQR=162-9,925), the median number of piglets was 1,122 (IQR-16-7,229), breeding farms had 4 (IQR=1-18) boars, and the gilts population was 544 (IQR-11-3,044). More details about the farms' biosecurity and infrastructures can be found in Table 2.

Discussion

The use of static networks to identify farms for target activities, such as enhancing surveillance, should be utilized with caution due to several limitations associated with animal movement aggregation, as showed here and elsewhere (Lentz et al., 2016). An obvious issue here is to assume that the same pair of farms would trade with each other throughout the entire study periods. Therefore, we argue that at least one approach testing network stability, such as causal fidelity, should be presented before considering the use of the static networks in the development of disease surveillance or control strategies (Lentz et al., 2016; Payen et al., 2019). Our results suggested that the use of centrality metrics derivate from static networks would bias the selection of sentinel farms due to unstable networks, which also reflected in the overestimated number of expected outbreaks. Our modelling framework accounting for between-farm temporal contacts allowed to investigate disease spreading dynamics, calculate the number of farms needed to reduce expected epidemic sizes and to map sentinel farms. Comparing the two strategies to seed initial infected nodes, randomly and infection started from independent, commercial and farms lacking operation type, we find that the epidemic sizes and number of farms needed to be targeted to effectively control disease spread, were quite similar. This finding is more likely explained by the presence of contacts among all pig operation types (Table S1). Therefore, diseases are expected to spread from commercial to independent farms and vice versa. This clearly demonstrates the significance of identifying and further characterize the biosecurity infrastructure and practices of sentinel farms. Ultimately the identification of key biosecurity vulnerabilities can increase the local and national capacity to reduce the spread of endemic disease.

We found that static network was not represent the chronology fi the movements, thus did not provide a fair representation of the overall time-respecting movement pathways. A number of studies have considered static network views to make inferences about disease spread or to calculate outbreak sizes (Büttner et al., 2013; Salines et al., 2017) Mostly those studies did not fully considered the causal fidelity of the contacts, which is a recommended approach that can quantify the error of the static representation of a temporal network (Lentz et al., 2013). Thus, without such verification, it is difficult to decide if and at which time window inferences or metrics from static networks can be interpreted or used to summarize networks (Lentz et al., 2013; Büttner et al., 2016). It is risky to assume that aggregating contact movements into one snapshot would not overestimate or introduce edge biases (Vidondo and Voelkl, 2018). We found that the number of active pig farms was seasonal and skewed with variation of plus or minus 300 farms over the two-year period, a similar trend was observed in the volume of pigs traded. In our study, while the GWCC increased over the years, the GSCC suffered from relevant variations throughout the months, especially in the second half of 2018, where new paths connected the GSCC with other minor components and consequently increased the size of the GWCC, which could have implications for disease transmission and persistence (Marquetoux et al., 2016; J. Schulz et al., 2017). The sizes of GSCC and GWCC variation were mostly attributed to variation in the number of commercial farms activities. The size of GSCC and GWCC of the independent farms followed the same trends of the commercial farms for several months, therefore it pivotal that this farms are also considered in the proposed target surveillance strategies. Farms that did not report operation types represented the minority of the farms in both components, especially in April 2018 (supplementary Figure S1). In general, the use of static networks tends to artificially connect a larger number of farms, which could consequently bias surveillance strategies to less relevant farms and or compromise resource allocation.

Our results show that different network-based intervention schemes successfully reduced the spread of disease independently from the local β coefficient probability rates at the farm-level. We show that targeting farms by degree was the most effective intervention in reducing the number of new cases, followed by targeting farms by betweenness, which required ~ 1,300 farms to be targeted. As anticipated, random removal had little impact in controlling disease. Studies explored the contribution of existing trade duration on disease transmission probabilities and the impact on epidemic sizes, suggesting that epidemic sizes were sensitive to network activity (Farine and Whitehead, 2015; Lebl et al., 2016). Indeed, we explicitly considered node activity while disease spread was simulated. Other studies attempted to account for time-dependent disease spread while aiming to reduce R_0. One study used a non-compartmental model approach and found that the number of farms that needed to be removed by degree approached 50% of all farms (Kinsley et al., 2019). The second study used a mechanistic approach in which African swine fever (ASF) spread was simulated and found that degree ranking was the best strategy to contain the disease (Ferdousi et al., 2019). In summary, for most swine contact network studies, degree was shown to be the best strategy to select sentinel farms (identify target farms), while betweenness had the second-best performance. It is worth noting that betweenness is a useful metric when studying disease diffusion (Farine and Whitehead, 2015), mainly because it is a representation of the shortest path between nodes. Here independent farms with high betweenness may bridge several commercial farms; therefore, more details about these unexplored pathways should be investigated in the future. One limitation of our study is the fact that 21.4 % of the farms did provided information about type of pig operation, thus this group of farms could be formed by commercial or independent farms, and thus the real number of contacts among independent and commercial farms may not be precise. However, we provide a description of those farms in which we found that the median number of pigs was 415 (IQR 1-1441); median number of breeding female of 72 (IQR 1- 483), and median of 1 boar (IQR 0-4) (supplementary Table S3). By comparison with the local size of the commercial pig operations, these farms may be considered to be smaller operation which could include farms with limited biosecurity, thus, a follow-up study is needed to collect more information about these farms.

Based on the identified minimum 1,000 farms needed to be removed from the contact network, we simulated outbreak propagation with a deterministic SI model and identified the most efficient network-based metric capable of reducing the expected size of spread cascades. We showed that degree was the most significant intervention, with no more than 29 secondarily infected pig farms involved per outbreak (supplementary information Figure S7). In addition, our results demonstrated that targeting more than 500 farms by degree was efficient in reducing epidemic sizes. Random surveillance was unexpectedly better than closeness and page rank for most of the two years of propagation. One possible explanation may be that this network is not well connected, and farms that remain to be removed may be too similar with respect to their closeness and page rank values; therefore, the impact on the propagation is expected to be the one resulting from random removals. When we compared the list of targeted farms identified with in 2018 with the ones with the highest degree in 2019, the majority were the same farms. Thus the use of retrospective network to inform future surveillance activities is a reasonable approach. Indeed, to show the direct impact in the incidence of 2019, we ran the transmission model without the farms identified in 2018, ultimately the incidence at the end of the year was estimated to at 1.20 cases per 100 farms.

Our results showed that among the first 1,000 farms with the highest degree, more than half were commercial farms (55.6%) and 29.7% were independent pig farms. This illustrates the interplay between the two populations, where infection can arrive at either and propagate in both production sectors. Here, most farms of interest lacked important biosecurity features, such as cleaning and disinfection stations (Dee et al., 2006). A study in Argentina also highlighted the lack of biosecurity on highly connected farms (Alarcón et al., 2019). On the other hand, in our study, most farms did not utilize rendering, but preferred to compost dead animals. The former was previously described as an important risk factor for the spread of porcine reproductive and respiratory syndrome (PRRS) in the US (Velasova et al., 2012; Silva et al., 2019). In the same study, composting was found to be the less risky practice when removing cull or dead pigs (Silva et al., 2019). Another relevant biosecurity point that has been described as a risk for disease introduction is the number of farm entries; here, we noticed that the majority of the farms had only one main road, which potentially represents less risk for local disease transmission (Silva et al., 2019). A disproportionate number of these highly risky farms were nurseries (32.23%) and breeding farms (20.2%), which has often been proposed as a desired group to be targeted for surveillance (Dorjee et al., 2013). In addition to the identification of priority sentinel farms, the identification of relevant biosecurity gaps is invaluable, especially under the current risk of more global spread of foreign animal diseases such as ASF (Brown and Bevins, 2018; Jurado et al., 2018). One option would be the implementation of enhanced biosecurity plans, such as what has been proposed by the Secure Pork Supply (SPS) Plan in the US. The SPS plan was designed to provide business continuity in the event of a foreign animal disease outbreak as well as help protect operations from endemic diseases (Pudenz et al., 2019). In summary, to participate in the SPS Plan for Continuity of Business, each farm must: 1) Request a National Premises Identification Number (PremID) which include collecting the geolocation of the farm; 2) Prepare a biosecurity plan; 3) Create a premises map; 4) Write an enhanced site-specific biosecurity plan; 5) Monitor for symptoms of foreign animal diseases (FADs) including ASF; and 6) keep movement records of animals, people, equipment, and other items, therefore similar approach could be proposed to be initially implemented in the identified 1,000 sentinel farms.

In this study, we did not examine feed-truck or other vehicle movements or sharing. Such information is absent from the majority of the current literature (Lentz et al., 2016), but it has been included in some studies (Augusta et al., 2019; Sterchi et al., 2019). A more recent study suggested that sharing haulage vehicles has significant potential for spreading infectious diseases within the pig sector. The cleansing and disinfection process of haulage vehicles is therefore a critical control point for disease transmission risk mitigation (Porphyre et al., 2020). It is critical to acknowledge that the movement of feed trucks and short-distance transportation of breeding replacement animals or culled sows contributed to disease transmission (Silva et al., 2019). Indeed, before these additional contacts are not taken into consideration, our understanding of disease spread pathways will likely continue to be limited.

Finally, the modeling framework proposed here can be broadly used to calculate the minimum number of farms to be targeted for the control of disease spread when temporal contact data are available and to determine the network metrics that should be preferred for selection of target farms according to the approximation of epidemic sizes. In addition, the proposed framework could be used as a decision tool for both local official veterinary services and the private sector for evaluating animal movements and developing a more risk-oriented surveillance strategies. At production system level, it allows for the creation of a hot-list with farms to which the reinforcement of biosecurity would be key in the face of an outbreak. Future studies are also needed to explore the contribution of movements to slaughterhouses, especially when pig are redirected to other slaughterhouses (i.e., slaughter not able to slaughter all animals) or send back to the farm of origin, this is very common in the US (Russell et al., 2020). Another limitation was the number of farms missing geographic locations, since this analysis will be re-run be the local veterinary services yearly, once this farm location become available the results will be updated. In addition, a clear next step would be the modeling of the introduction and control strategies of a foreign animal disease, which combines between farm epidemiological dynamics to map the epidemic potential considering control strategies.

Conclusion

One-third of all pig farms traded with the same partners in the course of two years; consequently, the static networks did not offer reasonable information about the temporal movement pathways. Our proposed modeling framework provides a parsimonious solution; it handles the temporal order of movements, calculates the minimum number of farms needed to be targeted and approximates the expected epidemic size in a worst-case scenario where each movement can effectively transmit disease. The results from the application of this approach identified target farms for risk-based surveillance and disease mitigation efforts, with remarkably limited biosecurity. This finding imposes important vulnerability to pathogen introduction and spread; therefore, those farms could benefit from the implementation of enhanced biosecurity plans, such as what has been promoted and implemented in the US by Secure Pork Supply plan (https://www.securepork.org/). Finally, the introduction of risk-based approaches may optimize the costs of routine surveillance and during initial stages of a disease emergency; the lockdown or stamping of these farms could potentially reduce the final epidemic size.

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Authors' contributions

GM, FPNL, JV and AARM coordinated movement data collection. GM conceived paper ideas. GM, JAG and NCC participated in the design of the study. NCC and GM conducted data processing and cleaning. GM, JAG and NCC wrote and modified computer algorithms and conducted analysis. GM, JAG and NCC developed simulation models. GM and NCC wrote the manuscript and JA edited the manuscript. All authors discussed results and commented on the manuscript.

Conflict of interest

All authors confirm that there are no conflicts of interest to declare

Ethical statement

The authors confirm that the ethical policies of the journal, as noted on the journal's author guidelines page. Since this work did not involve animal sampling neither questioner data collection there was no need for ethics permits.

Data Availability Statement

The data that support the findings of this study are available from the regional veterinary office. Restrictions apply to the availability of these data, which were used under confidentiality agreements.

References

Alarcón, L. V, P. CIPRIOTTI, M. Monterubbianessi, C. Perfumo, E. Mateu, and A. Allepuz, 2019: Network analysis of pig movements in Argentina: identification of key farms in the spread of diseases and relationship with their biosecurity level. *Front. Vet. Sci.*DOI: 10.3389/conf.fvets.2019.05.00006.

Augusta, C., G.W. Taylor, and R. Deardon, 2019: Dynamic contact networks of swine movement in Manitoba, Canada: Characterization and implications for infectious disease spread. *Transbound. Emerg. Dis.*DOI: 10.1111/tbed.13220.

Bastard, J., M. Andraud, C. Chauvin, P. Glaser, L. Opatowski, and L. Temime, 2020: Dynamics of livestock-associated methicillin resistant Staphylococcus aureus in pig movement networks: Insight from mathematical modeling and French data. *Epidemics*DOI: 10.1016/j.epidem.2020.100389.

Brin, S., and L. Page, 1998: The anatomy of a large scale hypertextual Web search engine published version. *Comput. Networks ISDN Syst.*DOI: 10.1.1.109.4049.

Brown, V.R., and S.N. Bevins, 2018: A review of African swine fever and the potential for introduction into the United States and the possibility of subsequent establishment in feral swine and native ticks. *Front. Vet. Sci.*DOI: 10.3389/fvets.2018.00011.

Büttner, K., J. Krieter, A. Traulsen, and I. Traulsen, 2013: Static network analysis of a pork supply chain in Northern Germany-Characterisation of the potential spread of infectious diseases via animal movements. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2013.01.008.

Büttner, K., J. Salau, and J. Krieter, 2016: Quality assessment of static aggregation compared to the temporal approach based on a pig trade network in Northern Germany. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2016.05.005.

Cárdenas, N.C., J.O.A. Galvis, A.A. Farinati, J.H.H. Grisi-Filho, G.N. Diehl, and G. Machado, 2018: Burkholderia mallei: the dynamics of networks and disease transmission. *Transbound. Emerg. Dis.* **0**, DOI: 10.1111/tbed.13071.

Chaters, G.L., P.C.D. Johnson, S. Cleaveland, J. Crispell, W.A. De Glanville, T. Doherty, L. Matthews, S. Mohr, O.M. Nyasebwa, G. Rossi, L.C.M. Salvador, E. Swai, and R.R. Kao, 2019:

Analysing livestock network data for infectious disease control: An argument for routine data collection in emerging economies. *Philos. Trans. R. Soc. B Biol. Sci.*DOI: 10.1098/rstb.2018.0264.

Colman, E., P. Holme, H. Sayama, and C. Gershenson, 2019: Efficient sentinel surveillance strategies for preventing epidemics on networks. (Daniela Paolotti, Ed.)*PLOS Comput. Biol.* **15**, e1007517, DOI: 10.1371/journal.pcbi.1007517.

Csardi, G., and T. Nepusz, 2006: The igraph software package for complex network research. *InterJournal Complex Syst.*

Darbon, A., D. Colombi, E. Valdano, L. Savini, A. Giovannini, and V. Colizza, 2019: Disease persistence on temporal contact networks accounting for heterogeneous infectious periods. *R. Soc. Open Sci.*DOI: 10.1098/rsos.181404.

Dee, S.A., J. Deen, and C. Pijoan, 2006: Evaluation of an industry-based sanitation protocol for full-size transport vehicles contaminated with porcine reproductive and respiratory syndrome virus. *J. Swine Heal. Prod.*

Dorjee, S., C.W. Revie, Z. Poljak, W.B. McNab, and J. Sanchez, 2013: Network analysis of swine shipments in Ontario, Canada, to support disease spread modelling and risk-based disease management. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2013.06.008.

Dubé, C., C. Ribble, D. Kelton, and B. McNab, 2008: Comparing network analysis measures to determine potential epidemic size of highly contagious exotic diseases in fragmented monthly networks of dairy cattle movements in Ontario, Canada. *Transbound. Emerg. Dis.*DOI: 10.1111/j.1865-1682.2008.01053.x.

Engblom, S., R. Eriksson, and S. Widgren, 2020: Bayesian epidemiological modeling over high-resolution network data. *Epidemics*100399, DOI: 10.1016/j.epidem.2020.100399.

Farine, D.R., and H. Whitehead, 2015: Constructing, conducting and interpreting animal social network analysis. *J. Anim. Ecol.*DOI: 10.1111/1365-2656.12418.

Ferdousi, T., S.A. Moon, A. Self, and C. Scoglio, 2019: Generation of swine movement network and analysis of efficient mitigation strategies for African swine fever virus. DOI: 10.1371/journal.pone.0225785.

Firestone, S.M., Y. Hayama, R. Bradhurst, T. Yamamoto, T. Tsutsui, and M.A. Stevenson, 2019:

Reconstructing foot-and-mouth disease outbreaks: a methods comparison of transmission network models. *Sci. Rep.*DOI: 10.1038/s41598-019-41103-6.

Freeman, L.C., 1978: Centrality in social networks conceptual clarification. *Soc. Networks*DOI: 10.1016/0378-8733(78)90021-7.

Funk, S., A. Camacho, A.J. Kucharski, R.M. Eggo, and W.J. Edmunds, 2018: Real-time forecasting of infectious disease dynamics with a stochastic semi-mechanistic model. *Epidemics*DOI: 10.1016/j.epidem.2016.11.003.

Gillespie, D.T., 1977: Exact stochastic simulation of coupled chemical reactions. *J. Phys. Chem.* **81**, 2340–2361, DOI: 10.1021/j100540a008.

Guinat, C., A. Relun, B. Wall, A. Morris, L. Dixon, and D.U. Pfeiffer, 2016: Exploring pig trade patterns to inform the design of risk-based disease surveillance and control strategies. *Sci. Rep.*DOI: 10.1038/srep28429.

Holme, P., and J. Saramäki, 2012: Temporal networks. *Phys. Rep.*DOI: 10.1016/j.physrep.2012.03.001.

Jenness, S.M., S.M. Goodreau, and M. Morris, 2018: Epimodel: An R package for mathematical modeling of infectious disease over networks. *J. Stat. Softw.*DOI: 10.18637/jss.v084.i08.

Jurado, C., M. Martínez-Avilés, A.D. La Torre, M. Štukelj, H.C. de C. Ferreira, M. Cerioli, J.M. Sánchez-Vizcaíno, and S. Bellini, 2018: Relevant measures to prevent the spread of African Swine Fever in the European Union Domestic Pig Sector. *Front. Vet. Sci.*DOI: 10.3389/fvets.2018.00077.

Kim, M., D. Paini, and R. Jurdak, 2019: Modeling stochastic processes in disease spread across a heterogeneous social system. *Proc. Natl. Acad. Sci. U. S. A.*DOI: 10.1073/pnas.1801429116.

Kim, P., and C.H. Lee, 2018: Epidemic Spreading in Complex Networks with Resilient Nodes: Applications to FMD. *Complexity*DOI: 10.1155/2018/5024327.

Kinsley, A.C., A.M. Perez, M.E. Craft, and K.L. Vanderwaal, 2019: Characterization of swine movements in the United States and implications for disease control. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2019.01.001.

Konschake, M., H.H.K. Lentz, F.J. Conraths, P. Hövel, and T. Selhorst, 2013: On the Robustness of In- and Out-Components in a Temporal Network. *PLoS One*DOI:

10.1371/journal.pone.0055223.

Lanzas, C., K. Davies, S. Erwin, and D. Dawson, 2020: On modelling environmentally transmitted pathogens. *Interface Focus* **10**, 20190056, DOI: 10.1098/rsfs.2019.0056.

Lebl, K., H.H.K. Lentz, B. Pinior, and T. Selhorst, 2016: Impact of network activity on the spread of infectious diseases through the german pig trade network. *Front. Vet. Sci.*DOI: 10.3389/fvets.2016.00048.

Lentz, H.H.K., A. Koher, P. Hövel, J. Gethmann, C. Sauter-Louis, T. Selhorst, and F.J. Conraths, 2016: Disease spread through animal movements: A static and temporal network analysis of pig trade in Germany. *PLoS One*DOI: 10.1371/journal.pone.0155196.

Lentz, H.H.K., T. Selhorst, and I.M. Sokolov, 2013: Unfolding Accessibility Provides a Macroscopic Approach to Temporal Networks. *Phys. Rev. Lett.*DOI: 10.1103/PhysRevLett.110.118701.

Marquetoux, N., M.A. Stevenson, P. Wilson, A. Ridler, and C. Heuer, 2016: Using social network analysis to inform disease control interventions. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2016.01.022.

Martínez-López, B., A.M. Perez, and J.M. Sánchez-Vizcaíno, 2009: Combined application of social network and cluster detection analyses for temporal-spatial characterization of animal movements in Salamanca, Spain. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2009.05.007.

Miller, J.C., 2017: Mathematical models of SIR disease spread with sexual-network and other transmission mechanisms. *Infect. Dis. Model.*DOI: 10.1016/j.idm.2016.12.003.

Mohr, S., M. Deason, M. Churakov, T. Doherty, and R.R. Kao, 2018: Manipulation of contact network structure and the impact on foot-and-mouth disease transmission. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2018.05.006.

Nöremark, M., N. Håkansson, S.S. Lewerin, A. Lindberg, and A. Jonsson, 2011: Network analysis of cattle and pig movements in Sweden: Measures relevant for disease control and risk based surveillance. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2010.12.009.

Ortiz-Pelaez, A., D.U. Pfeiffer, R.J. Soares-Magalhães, and F.J. Guitian, 2006: Use of social network analysis to characterize the pattern of animal movements in the initial phases of the 2001 foot and mouth disease (FMD) epidemic in the UK. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2006.04.007.

Payen, A., L. Tabourier, and M. Latapy, 2019: Spreading dynamics in a cattle trade network: Size, speed, typical profile and consequences on epidemic control strategies. *PLoS One*DOI: 10.1371/journal.pone.0217972.

Pebesma, E., 2018: Sf: Simple Features for R. R package version 0.5-3. .

Pellis, L., F. Ball, S. Bansal, K. Eames, T. House, V. Isham, and P. Trapman, 2015: Eight challenges for network epidemic models. *Epidemics*DOI: 10.1016/j.epidem.2014.07.003.

Picault, S., Y.L. Huang, V. Sicard, S. Arnoux, G. Beaunée, and P. Ezanno, 2019: EMULSION: Transparent and flexible multiscale stochastic models in human, animal and plant epidemiology. *PLoS Comput. Biol.*DOI: 10.1371/journal.pcbi.1007342.

Porphyre, T., B.M. d. C. Bronsvoort, G.J. Gunn, and C. Correia-Gomes, 2020: Multilayer network analysis unravels haulage vehicles as a hidden threat to the British swine industry. *Transbound. Emerg. Dis.*DOI: 10.1111/tbed.13459.

Pudenz, C.C., L.L. Schulz, and G.T. Tonsor, 2019: Adoption of secure pork supply plan biosecurity by U.S. Swine producers. *Front. Vet. Sci.*DOI: 10.3389/fvets.2019.00146.

Qi, L., G. Beaunée, S. Arnoux, B.L. Dutta, A. Joly, E. Vergu, and P. Ezanno, 2019: Neighbourhood contacts and trade movements drive the regional spread of bovine viral diarrhoea virus (BVDV). *Vet. Res.*DOI: 10.1186/s13567-019-0647-x.

Russell, L.E., J. Polo, and D. Meeker, 2020 (16. February): The Canadian 2014 porcine epidemic diarrhoea virus outbreak: Important risk factors that were not considered in the epidemiological investigation could change the conclusions. *Transbound. Emerg. Dis.*tbed.13496, DOI: 10.1111/tbed.13496. Blackwell Publishing Ltd.

Sahneh, F.D., A. Vajdi, H. Shakeri, F. Fan, and C. Scoglio, 2017: GEMFsim: A stochastic simulator for the generalized epidemic modeling framework. *J. Comput. Sci.*DOI: 10.1016/j.jocs.2017.08.014.

Salines, M., M. Andraud, and N. Rose, 2017: Pig movements in France: Designing network models fitting the transmission route of pathogens. *PLoS One*DOI: 10.1371/journal.pone.0185858.

Schulz, J., A. Boklund, T.H.B. Halasa, N. Toft, and H.H.K. Lentz, 2017: Network analysis of pig movements: Loyalty patterns and contact chains of different holding types in Denmark. *PLoS One*DOI: 10.1371/journal.pone.0179915.

Schulz, K., F.J. Conraths, S. Blome, C. Staubach, and C. Sauter-Louis, 2019: African swine fever: Fast and furious or slow and steady? *Viruses*DOI: 10.3390/v11090866.

SEAPI-RS, 2018: SEAPI, Secretaria da Agricultura, Pecuária e arrigação [Online] Available at http://www.agricultura.rs.gov.br/inicial.

Silva, G.S., G. Machado, K.L. Baker, D.J. Holtkamp, and D.C.L. Linhares, 2019: Machine-learning algorithms to identify key biosecurity practices and factors associated with breeding herds reporting PRRS outbreak. *Prev. Vet. Med.*DOI: 10.1016/j.prevetmed.2019.104749.

Siqueira, P., 2019: brazilmaps: Brazilian Maps from Different Geographic Levels. .

Smith, R.P., A.J.C. Cook, and R.M. Christley, 2013: Descriptive and social network analysis of pig transport data recorded by quality assured pig farms in the UK. *Prev. Vet. Med.* **108**, 167–177, DOI: 10.1016/j.prevetmed.2012.08.011.

Smith, T.A., N. Chitnis, M. Penny, and M. Tanner, 2017: Malaria Modeling in the Era of Eradication. *Cold Spring Harb. Perspect. Med.* **7**, a025460, DOI: 10.1101/cshperspect.a025460.

Sterchi, M., C. Faverjon, C. Sarasua, M.E. Vargas, J. Berezowski, A. Bernstein, R. Grütter, and H. Nathues, 2019: The pig transport network in Switzerland: Structure, patterns, and implications for the transmission of infectious diseases between animal holdings. *PLoS One*DOI: 10.1371/journal.pone.0217974.

Valdano, E., C. Poletto, A. Giovannini, D. Palma, L. Savini, and V. Colizza, 2015: Predicting Epidemic Risk from Past Temporal Contact Data. *PLoS Comput. Biol.*DOI: 10.1371/journal.pcbi.1004152.

Velasova, M., P. Alarcon, S. Williamson, and B. Wieland, 2012: Risk factors for porcine reproductive and respiratory syndrome virus infection and resulting challenges for effective disease surveillance. *BMC Vet. Res.*DOI: 10.1186/1746-6148-8-184.

Vidondo, B., and B. Voelkl, 2018: Dynamic network measures reveal the impact of cattle markets and alpine summering on the risk of epidemic outbreaks in the Swiss cattle population. *BMC Vet. Res.*DOI: 10.1186/s12917-018-1406-3.

Wasserman, S., and K. Faust, 1994: Social Network Analysis: Methods and Applications : Cambridge University Press.

Wickham, H., 2017: Tidyverse: Easily install and load “tidyverse” packages. .

Widgren, S., P. Bauer, R. Eriksson, and S. Engblom, 2019: Siminf: An R package for data-driven stochastic disease spread simulations. *J. Stat. Softw.*DOI: 10.18637/jss.v091.i12.

Table 1. Description of network terminology and definition applied to pig movements.

Parameter	Definition	References
Nodes	A pig farms.	(Wasserman and Faust, 1994)
Edge	A link between two nodes.	Wasserman and Faust (1994)
Degree (k)	The number of unique contacts to and from a farm. When direction was taken into account, the ingoing and outgoing contacts were separated: the “out” degree is the number of contacts originating from a specific farm, and the “in” degree is the number of contacts directed toward a specific premise.	(Wasserman and Faust, 1994)
Page rank	Google PageRank measure, a link analysis algorithm that produces a ranking of importance for all nodes in a network with a range of values between zero and one. The PageRank calculation takes into account the degree of a given premises and the degree of its neighbors.	(Brin and Page, 1998)
Closeness centrality	Closeness centrality measures how many steps are required to access every other vertex from a given node. This measure can be directed as incoming steps or outgoing steps.	(Freeman, 1978)
Betweenness	The frequency at which a node is located on the shortest	(Freeman,

	path between any two pairs of nodes in the network.	1978)
Giant weakly connected component (GWCC)	The proportion of nodes that are connected in the largest component when directionality of movement is ignored.	Wasserman and Faust (1994)
Giant strongly connected component (GSCC)	The proportion of nodes that are connected in the largest component when directionality of movement is considered.	(Wasserman and Faust, 1994)

Table 2. Description of biosecurity and infrastructure of the targeted farms.

Variable	**Overall proportion**
Presence of isolation barn(s)	No=77.6% Yes=22.4%
Fence around the farm	No=54.7% Yes=45.3%
Cleaning and disinfection station(s)	No=72.7% Yes=27.3%
Vegetation barrier around the farm	No=86.7% Yes=13.3%
Single entry point	No=72.4% Yes=27.6%
Bird nets	No=59.6% Yes=40.4%
Pig loading and unloading outside the farm's designated clean area	No=61.3% Yes=38.7%
Special clothing dedicated for farm use (shower in)	No=77.7% Yes=22.3%
Feed bins inside the designated clean area while loading is external	No=60.3% Yes=39.7%
Vulnerability score *	
Low	0.21%
Medium	47.4%
High	17.8%
Not informed	34.8%
Veterinary care	
From commercial system	63.5%
Independent veterinary	4.5%

Absent	1.1%
Not informed	30.9%
Farm type	
Nursery	32.23%
Breeding farm	20.2%
Finisher farm	15.1%
Certified swine breeder farm	5.65%
Wean-to-finisher	1.49%
Not informed	25.33%
Water sources	
Pond	42.8%
Natural water fountain	22.2%
Public source	9.9%
Lake	1.5%
Water cistern	0.3%
Not informed	23.3%
Feed source	
From production system	68.7%
Own feed mill	7.8%
Not informed	23.5%
Destination of dead animals	
Compost	76.0%
Incinerator	0.23%
Bury	0.23%
Septic pit	0.24%
Not informed	23.3%
Manure destination	
Lagoon	28.9%
Septic pit	2.48%

Not informed	68.62%
Barn infrastructure	
Concrete or bricks	51.9%
Wood	1.29%
Mixed of wood and concrete	23.4%
Not informed	23.5%

*This measures the level of vulnerability the introduction of pathogen into certified-swine-breeder-farms, briefly is a combination of risks measurements form distance to farms to presence of biosecurity and infrastructure of the farm.

Figure Legend

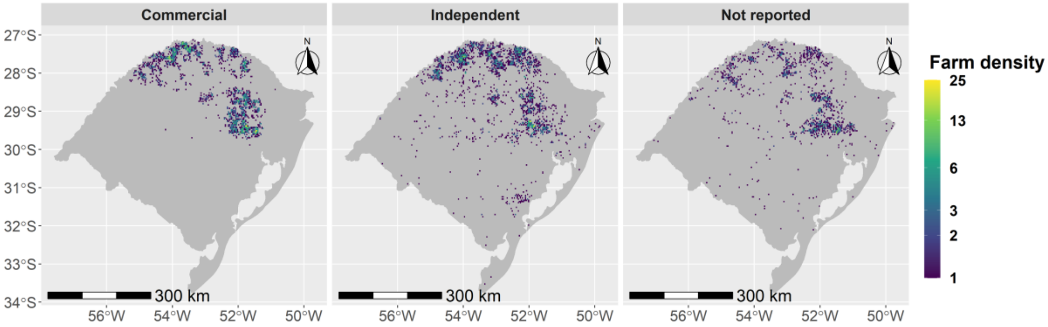
Figure 1. Geographical location of farm density by type of pig operation, commercial, independent, and not reported.

Figure 2. Description of pig movements between all farms types from January 2017 to December 2018. The arrows size shows the percentage of movements and the color is given by the origin of the movements. The size of the circles represented the total number of farms. * CSBF stands for Certified Swine Breeding Farm (in Portuguese Granja de Reprodutores Suínos Certificada, GRSC)

Figure 3. Description of the monthly variation of the network metrics of the pig movements from January 2017 until December 2018.

Figure 4. Simulated disease spread dynamics within the swine contact network. Simulations assumed two seed infection scenarios a) random, where 950 pig farms (10% prevalence) were infected at day “0”, and b) stratified, in which the proportion of the 950 pig farms (10% prevalence) was equally distributed by commercial, independent, and not reported farms operation types. The simulations assumed within farm prevalence of 0.1%.

Figure 5. The two years spread cascades sizes for each target-network surveillance strategy. In light blue, the estimated spread cascade, which had a maximum value of 29 farms while not targeting farms, resulted in a cascade of 2,624 farms (black).



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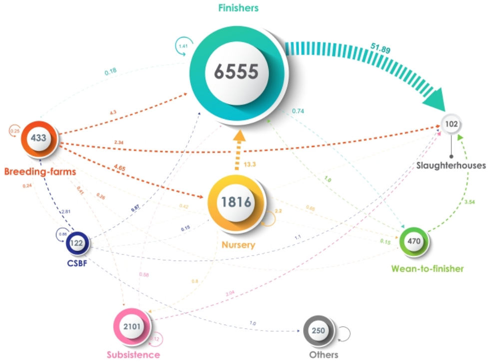

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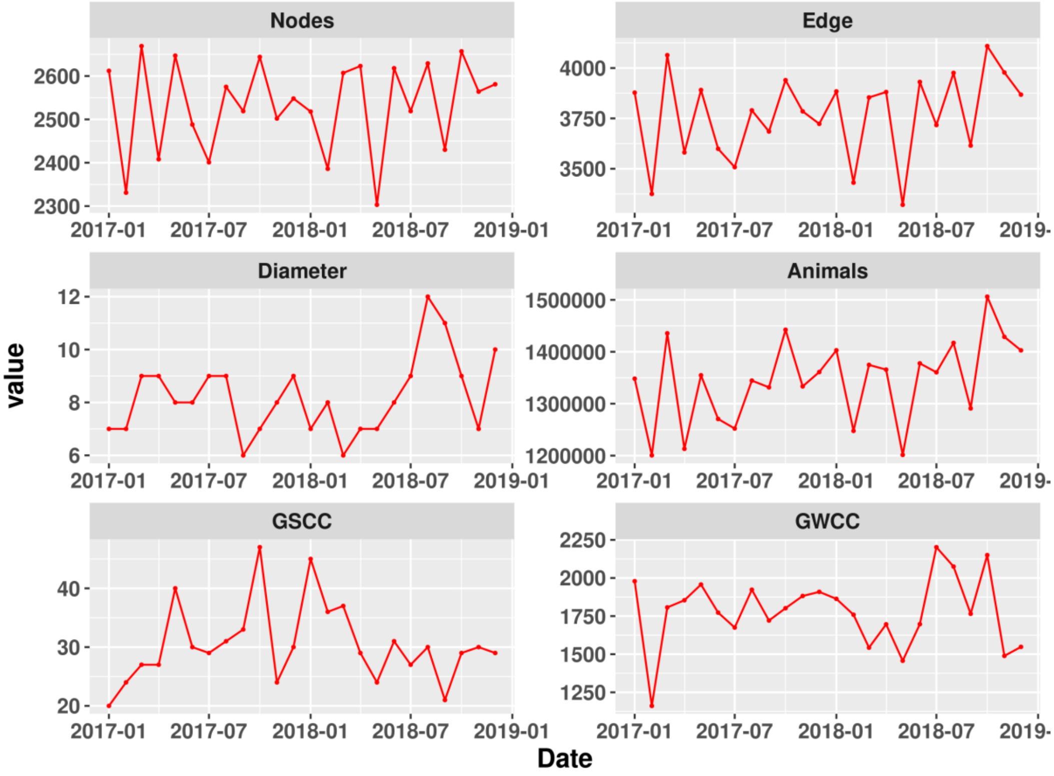

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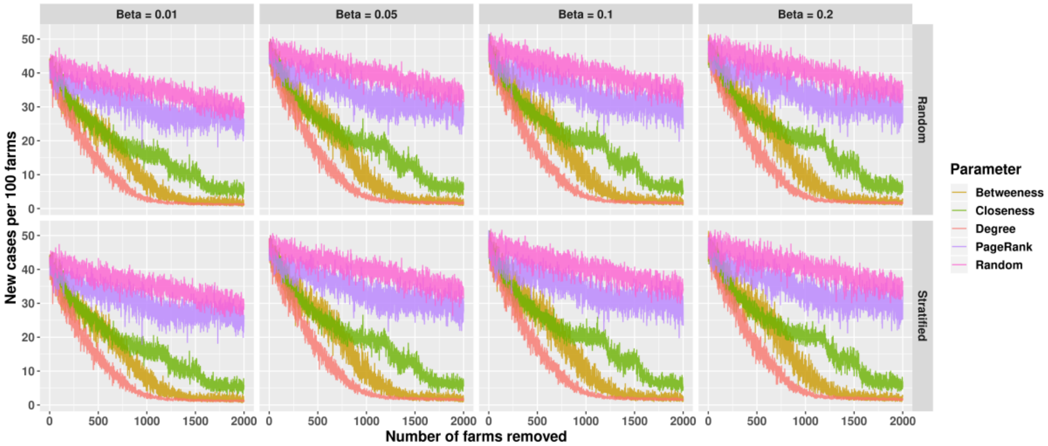

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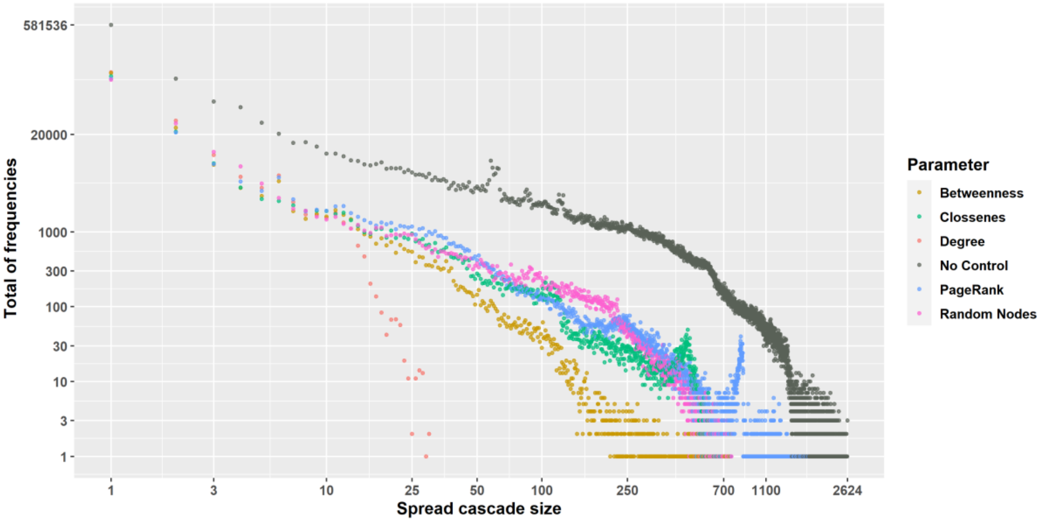

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