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

Running title: Time-varying networks 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.

[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

Summary

Tracking animal movements over time can fundamentally determine the success of disease control interventions throughout targeting farms that are tightly connected. In commercial pig production, animals are transported between farms based on growth stages, thus it generates time-varying contact networks that may influence the dynamics of disease spread. Still, risk-based surveillance strategies are mostly based on static network. We reconstructed the static and temporal pig networks of one Brazilian state from 2017 to 2018, comprising 351,519 movements and 48 million transported pigs. The static networks failed to capture time-respecting movement pathways. Therefore, we propose a time-dependent network susceptible-infected (SI) model to simulate the temporal spread of an epidemic over our pig network globally through the temporal movement of infected animals among farms and locally with a stochastic compartmental model in each farm, configured to calculate the minimum number of farms needed to achieve effective disease control. In addition, we propagated disease on the pig temporal network to calculate the cumulative contacts as a proxy of epidemic sizes and evaluated the impact of network-based disease control strategies. The results show that targeting the first 1,000 farms ranked by degree would be sufficient to control disease spread. Our finding also suggested that assuming a worst-case scenario in which every movement could transmit disease, pursuing farms by degree would limit the transmission to 29 farms, which is lower than the number of infected farms for random surveillance, with epidemic sizes of 2,593 farms. Overall, the proposed modeling framework provides a parsimonious solution for targeted disease surveillance when temporal movement data is available. Finally, the top 1,000 farms ranked by degree could benefit from enhanced

biosecurity plans and improved surveillance, which constitute important next steps in strategizing targeted disease control interventions.

Key words: 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 approach, which are dominated by the use of static network metrics to identify vulnerable farms. In a contact network, each farm (node) can play a role in the dynamics of disease spread, and some can be classified as vulnerable because they periodically receive infected animals (a high “in” degree); therefore, the identification of these farms is more important in scenarios of the absence or low prevalence of disease (Qi et al., 2019). Such locations may serve as sentinels. On the other hand, farms that are more likely to spread disease throughout their contact network could be targeted, by which restricting or monitoring outgoing movements could effectively reduce disease spread (Cárdenas et al., 2018; Payen et al., 2019). 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); however, methodologies have not yet evolved as expected. Most published approaches make use of static networks to describe animal movement and subsequently make inferences about outbreaks and epidemics (Büttner et al., 2013, 2018; Marquetoux et al., 2016; Motta et al., 2017; Alarcón et al., 2019; Kinsley et al., 2019). However, the temporal anomalies and seasonality of movements can only be identified if movement paths are aggregated to smaller time windows (Cárdenas et al., 2018; Augusta et al., 2019; Sterchi et al., 2019), which may not be sufficient to make inferences about disease dynamics within the contact networks. Disease transmission is not restricted to the historical record of movement (Firestone et al., 2019; Qi et al., 2019; Sterchi et al., 2019); namely, when disease transmission actually occurs by the

movement of infected animals is likely to be an event in time that is dependent on when animals are sent and, more importantly, when they are received at the final destination, and this rationale has been largely overlooked (Chaters et al., 2019; Sterchi et al., 2019). Nevertheless, static networks have been used to measure the effect of targeted farm removal, on the network fragmentation by monitoring giant strongly or weakly connected components, which would create small islands restricting the overall connectivity among farms (Motta et al., 2017; Mekonnen et al., 2019). Other studies have proposed the use of the basic reproduction number (R_0) and have measured the contribution of node removal in disease transmission (Marquetoux et al., 2016; Alarcón et al., 2019; Passafaro et al., 2019), still based on static views of full networks. 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 methodologies (Pellis et al., 2015).

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, compartmental models can be 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). 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 networks while accounting for the temporal order of the movements. Our model formulation allowed the calculation of the minimum number of farms needed to reduce disease spread and approximate the impact of network-based disease control strategies (e.g., farm isolation, movement restriction, enhanced biosecurity) on the expected epidemic sizes. Finally, we applied the proposed model to the time-varying pig network, ultimately to provide a practical background for the identification of targeted farms, 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 of one Brazilian state 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 1 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, or 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. Finally, farms were classified as commercial if they had active contracts with integrated swine companies and

as noncommercial otherwise. From the total number of movement active pig farms 11,849, a subset of farms 9,500 had registered geographic coordinates, therefore were used for the simulation modeling subsections.

Complete and monthly networks reconstruction and analysis

Two directed networks were reconstructed. First, a static network with directed "edges" represented by pig shipments between two "nodes", where nodes corresponded to pig farms. The static network, movements from January 2017 to December 2018 were analyzed by the traditionally method of aggregating movements into one snapshot. Second, networks were constructed based on a temporal resolution of 30 day windows (Lentz et al., 2016). For both complete and monthly network, centrality metrics were calculated (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).

Temporal variability of the network structure

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 (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). This ratio is known as the causal fidelity "c", where:

$$c = \frac{p(P_n)}{p(P_n)} = \frac{Number\ of\ paths\ in\ the\ temporal\ network}{Number\ of\ paths\ in\ the\ static\ network}. \quad (1)$$

The number of paths is the number of nonzero elements in p or P. 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 (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).

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

For the node loyalty, we use the same Jaccard Index,

$$node\ loyalty\ {}_i^{t-1,t} = \frac{|V^{t-1} \cap V^t|}{|V^{t-1} \cup V^t|} \quad (3)$$

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; Schulz et al., 2017).

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

We created a stochastic susceptible-infectious (SI) epidemic model to calculate the minimum number of farms needed to effectively reduce the number of new cases within the contact

network. This model framework integrates infection dynamics in each subpopulation as continuous-time Markov chains using the Gillespie stochastic simulation algorithm (Widgren et al., 2019). Transitions from $S \rightarrow I$ was in a two-stage model with a one-way transition depending on $\frac{\beta S_i I_i}{S_i + I_i}$ with β as the transmission rate. The completely stochastic simulation can be summarized as follows: the empirical movement data from 2017 until 2018 was used to simulate disease spread over a time-varying network; here, we assume a herd prevalence of 10% and a within-farm prevalence of 0.1%, which could transmit between and within farms. For the within-farm transmission rate, we use a set of β values of 0.01, 0.05, 0.1 and 0.2, which can also be considered the product of the contact rates and the transmission probability between animals into the farms. Another assumption was that the contact rates among pigs were homogenous. For the between-farm transmission, we considered the observed number of pigs that moved between farms and the population size at each farm. As initial condition, model simulation started with 950 infected farms (10% prevalence from a total population of 9,500 farms) at time “0”. Here, we proposed two realistic strategies to seed infected nodes at the time “0”. First, pig farms were selected at random from all farms with at least one movement from 2017 to 2018. For the second strategy, infected farms were chosen proportionally to the number of farms in each production system (N=17). This approach allows a more realistic scenario in which disease can emerge at any location of the study area (see Figure 1). The simulated control intervention was based only on the sequential removal of farms from the time “0” based on the static network 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 ten times, from which simulations were run and the median incidence was derived for each run. For a sensitivity analysis, we ran simulations with a diverse set of β parameters (see supplementary Figure S2). In addition, we ran simulations for commercial and noncommercial farms separately with the same parameters described above (see supplementary figures S4 and S5).

Cumulative contacts as a proxy of epidemic sizes

The modeling setup described by (Payen et al., 2019) was adapted to identify the best network-based metric to be used in the identification of farms to undergo target surveillance. This approach is based on a 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 model started from each seed farm in the network at a given time “0”, with an infection that was active for one day. The hypothetical disease spread followed the chronological order of movements over 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, which are represented by averages and ± 95% CI, and we also calculated the frequencies of the

spread cascades sizes for each seed node in the network (n = 9,450) 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, PageRank, and closeness and then removed the top 10, 250, 500, 750 and 1,000 farms at day “0” of the simulation while recording the spread cascade sizes for the full two years of movement data. For comparison with usual surveillance practices, we selected the same number of farms at day “0” 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 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 farms were described.

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, 351,519 movements and more than 48 million pigs transported. The majority, 66%, were identified as noncommercial farms, while the number of farms per commercial system varied from 10 to 465 from a total of 17 production systems. Among those farms included 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. Finally, among the noncommercial farms, we identified 2,101 (17.73%) as small pig holders (backyard farms or for subsistence) and 102 (0.86%) slaughterhouses. Most commercial and noncommercial pig farms were located at the northern and central east of the state (see Figure 1). While we have described movements to slaughterhouses, they were not accounted in any network analysis thereafter (see Figure 2).

Figure 1. Geographical location of commercial and noncommercial pig farms

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 finisher farms and 4.3% of movements to the nurseries, 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. Depiction of pig movements among all farm types from January 2017 to December 2018. The arrow size indicates the percentage of movements, and the color is defined by the origin of the movements. The size of the circles represents the total number of farms.

Monthly network analysis

From the two years of movement data, we reconstructed the monthly static networks. The number of farms (nodes), movements (edges) and animals varied substantially with a steady increase from July 2017 until October of the same year (see 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. Regarding the giant network components, from a general view using the static networks, the giant weakly connected component (GWCC) was formed by 7,563 farms, and the giant strong connected component (GSCC) had 863 farms; these sizes corresponded to 80.03% and 9.13% of the total number of farms in the network. In addition, 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.

Figure 3. Monthly variations in the network metrics of pig movements from January 2017 through December 2018.

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. 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 (see supplementary Figure S1). 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. The concept of time does not per se exist in these static networks; thus, the use of traversal network models here would reduce the accuracy toward overestimating disease outbreaks, which would likely mislead the selection of farms to undergo network-based surveillance (Lentz et al., 2016). In addition, we calculated a 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 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 1.95 new cases per 100 farms when β of 0.2 was used. Since this study may be used 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 (personal communications with Dr. Lopes, Chair of the Animal Movement and Surveillance Department of the state of Rio Grande do Sul). Based on local capacities given that the average number of new cases was reduced to as low as 7.88 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. 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 and noncommercial farms. Both have very similar results which reinforced the importance of non-commercial farms in the role of spreading diseases into commercial pig farms and vice versa (Figure 4, also see supplementary figure S2, S4 and S5).

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 divided between commercial and noncommercial farms. The simulations assumed a farm prevalence of 0.1%.

Finally, based on deterministic runs (Payen et al., 2019), epidemic sizes were significantly smaller even if 500 farms were removed from the full network. The average spread cascade immediately decreased to below 40 after only 250 farms were removed, which was independent of network metrics, except by random removals (Figure 5). In the 1,000-node removal scenario, there were two very tight removal strategies: degree and betweenness. The smallest outbreak size of 29 pig farms was calculated when the first 1,000 farms with the highest degree were removed (Figure 6). Even though the cascades spread of both surveillance scenarios was similar, the degree was significantly lower than betweenness (Figure 6, also see supplementary table 2). As expected, random removals resulted in a much larger epidemic sizes, reaching up to 2,593 farms (Figure 6, also see supplementary figure S3).

Figure 5. Epidemic size by node removal. The y-axis shows the cumulative size of the spread cascades from January 2017 through December 2018 for five scenarios. On day "0", 10, 250, 500, 750 or 1,000 farms were removed from the simulation, while the temporal network metrics were calculated for all remaining farms. The lines is the average values and shaded ± 95% CIs.

Figure 6. Final spread cascades sizes by each target-network surveillance strategy. In light blue, the estimated spread cascade, which had a maximum value of 29 farms while targeting farms at random, resulted in a cascade of 2,593 farms (green).

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

The geographic locations of the 1,000 target farms across the study area are shown in Figure 7. Most vulnerable farms were commercial (73.9%), with one production system contribution with 138 farms. From the comprehensive list of biosecurity and infrastructure characteristics, 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.

Figure 7. The geographic locations of the top 1,000 farms ranked by logarithm of degree.

Discussion

Static networks have been widely used in the identification of farms with many contacts, often referred to as hubs. The removal of such highly connected nodes from networks has been one of the most prevalent approaches for guiding target activities such as enhancing surveillance; overall, removing these nodes has had some success in reducing disease transmission (Rautureau et al., 2012; Büttner et al., 2016; Passafaro et al., 2019). However, static network suffer from a number of drawbacks that often lead to overestimate the size of disease outbreaks (Rautureau et al., 2012; Büttner et al., 2016; Passafaro et al., 2019). Static networks very often cannot represent what is truly a transient event (Dubé et al., 2008; Fielding et al., 2019), such as when a farm receives a shipment, forming an edge between farms, whereas as soon as animals are unloaded, the edge no longer exists. Our findings emphasize that if static networks were to be used here, the size of disease outbreaks would be substantially overestimated. To address this issue, we developed models that can account for the temporal order of movements and provide a more realistic estimate of expected epidemic sizes. Our model formulation allows for the calculation of the minimum number of farms that need to be removed to reduce disease spread and approximate the impact of network-based target disease control strategies (e.g., farm isolation, movement restriction, enhancement of biosecurity) on the expected epidemic sizes.

The volume and types of movements of this study well represent the expectations of a modern swine industry in which farms are specialized and integrated (Augusta et al., 2019; Passafaro et al., 2019). As expected, the majority of the movements were from finisher farms to slaughterhouses and from nurseries to finishers (Lee et al., 2017; Alarcón et al., 2019; Augusta et al., 2019; Machado et al., 2019). We also identified shipments between commercial and

noncommercial farms (see supplementary table S1 for more details). These movements may represent important concern regarding foreign animal diseases. While we assume that most integrated pig systems in developed countries would not receive pig shipment from noncommercial farms, information about movement from external sources has not been reported widely in the literature (Sterchi et al., 2019). However, a more recent study in Iowa described the presence of such pig flows that were not considered in their analysis (Passafaro et al., 2019). Therefore, there is a need to capture movements between commercial and noncommercial pig farms and vice-versa. Gathering this information becomes more important as the pig industry around the world prepares for the introduction of ASF, which will require tracking animal movements among all pig farms (Brown and Bevins, 2018; Jurado et al., 2018).

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). 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.

The number of active pig farms is seasonal and skewed with a variation of plus or minus 300 farms over the two-year period. A similar trend was observed in the number of animals and overall monthly shipments. In contrast to our observations, the number of active pig farms varied largely compared with other pig populations in Germany (Büttner et al., 2016), France (Rautureau et al., 2012) and Canada (Thakur et al., 2016), even though it is difficult to compare

distinct networks (Miele et al., 2019). Some factors that have contributed to the variations in our study may be associated with hog prices, which tends to be more volatile than in other countries; thus, producers may choose to place more animals in a favorable economic scenario. In addition, the monthly network diameter almost doubled in the middle of 2018, which seems to be a highly abnormal pattern in the network. A possible explanation for this may be related to the global configuration of the network because the nodes were connected in a way that increased the length of the shortest paths between them, which was accompanied by an increase in the GWCC. Consequently, during this period, we observed an increase in the number of nodes and connections; therefore, a given node would require more steps to reach another farm, within the network which could alone reduce the speed of disease transmission (Vidondo and Voelkl, 2018). 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 (Schulz et al., 2017; Marquetoux et al., 2016).

Previous studies have considered static network views to make inferences about disease spread or to calculate outbreak sizes (Büttner et al., 2013; Lee et al., 2017; Salines et al., 2017). However, these followed the assumption that movement aggregation would not overestimate or introduce edge biases (Vidondo and Voelkl, 2018). It has been suggested that to some extent, static networks provide useful information about disease related risks (Mohr et al., 2018). However, most static network studies lacked basic statistical support for their decisions for data aggregation (Büttner et al., 2013; Lee et al., 2017; Salines et al., 2017), some studies have rather

mention that other studies also used similar time windows, which would support their decisions to data aggregation (Büttner et al., 2013; Lee et al., 2017; Salines et al., 2017). Contact network aggregation has been a practice, even when the temporal sequences of the movements were available (Amaku et al., 2015; Cárdenas et al., 2018). In addition, restricting movements from and to highly connected farms reduced the connectivity between network components (GWCC and GSCC) in cattle (Motta et al., 2017; Vidondo and Voelkl, 2018) and swine networks (Guinat et al., 2016; Kinsley et al., 2019; Sterchi et al., 2019), which, to some extent, may contain disease from spreading throughout the contact network. On the other hand, nodal static network measures of monthly networks performed poorly in predicting outbreak risk (Vidondo and Voelkl, 2018), which may reiterate the limitation of static network in explaining the spread of diseases over time-varying networks.

The causal fidelity test is used to 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 (Lentz et al., 2013; Büttner et al., 2016). In this study, we found that July 2017 had the best time-respecting movement representation; the value was far lower than the causal fidelity reported in the literature, for example, two different studies in pigs reported values of 92% and 72% for monthly networks (Büttner et al., 2016) and (Lentz et al., 2013), respectively. However, a study of Swiss pig transport data demonstrated that only a small fraction of 0.34% of the farms was connected within one month (Sterchi et al., 2019). The low casual fidelity we identified may be associated with how producers or companies do business, as a producer can easily start and stop contracting with production systems because of compensation, price of feed, etc. These heavily compromise

the use of static network metrics when the objective is to identify and direct active surveillance plans towards highly connected farms. The use of static networks tends to artificially connect a larger number of farms, which will consequently bias surveillance strategies to less relevant farms and compromise resource allocation.

Our results show that different network-based intervention schemes successfully reduced the spread of disease independently from the local β transmission probability rates at the farm. 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 quarantined. Finally, as anticipated random removal had little impact in controlling disease. A recent study 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. Two other studies attempted to account for time-dependent disease spread while aiming to reduce R_0. One study used noncompartmental 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 ASF spread was simulated and found that degree ranking was the best strategy to contain the disease (Ferdousi et al., 2019). In summary, degree was shown to be the best strategy in reducing disease burden, 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 noncommercial farms with high betweenness may bridge several

commercial firms; therefore, more details about these unexplored pathways should be investigated in the future.

Based on the identified minimum number of farms of 1,000 that 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 pig farms involved per outbreak (Figure 6). 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 clossenes and PageRank 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 clossennes and PageRank values; therefore, the impact on the propagation is expected to be the one resulting from random removals.

Our results have showed an uneven proportion of commercial and noncommercial pig farms within the first 1,000 farms with the highest degree. This illustrates the interplay between the two populations, where infection can arrive at either and propagate in both directions. 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 and breeding farms, 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 farms, the identification of relevant biosecurity gaps at those farms is invaluable, especially under the current preparedness for the introduction of foreign animal diseases such as ASF. One of the best options is the implementation of enhanced biosecurity plans, such the Secure Pork Supply (SPS) Plan, 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).

Finally, more comprehensive studies coupling animal movements with local and environmental routes of transmission while accounting for farms biosecurity and infrastructure are needed to further explore the mechanisms of pig disease propagation, for which a complete multiscale mechanistic model is necessary (Qi et al., 2019).

Considerations

The use of static networks to target key farms to control the disease from spreading should be interpreted with caution due to several caveats associated with data aggregation, as shown in this study 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 period. Therefore, we argue that the causal fidelity of the temporal network 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). Recent studies did not account for this issue (Büttner et al., 2013, 2018; Marquetoux et al., 2016; Motta et al., 2017; Alarcón et al., 2019), or considered the temporal network pathway accessibility of each farm. In summary, these studies used static networks to disassemble networks into small islands, which possibly overestimates the size of outbreaks systematically, and therefore, the results should be interpreted with caution.

A likely limitation of this study was how farms were classified as commercial or noncommercial. Farms without information about production systems were classified as non-commercial. According to the state veterinarians (SEAPI-RS, 2018), all farms are required by law to inform yearly whether they are raising pigs for any commercial system, which makes our assumption fair. However, this could be in some extend associated with the inflated amount of movement between commercial and non-commercial (see supplementary table S1).

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. The model may also help develop an idea of the amount of personnel and material resources that would need to be allocated to control the epidemic, which is key for preparedness for future events (Casal et al., 2019).

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 realized temporal movement pathways. In this scenario, the use of static networks to target vulnerable or high-risk farms by network metrics would likely overestimate the role of those farms in disease transmission and limit the accuracy needed to optimize surveillance. Our proposed modeling framework provides a parsimonious solution to this problem; 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 priority pig farms that had remarkably limited biosecurity. This fact 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 SPS plan. Finally, the introduction of risk-based approaches may optimize the costs of routine surveillance and can be used in preparation for the introduction of FAD into the local pig industry.

Acknowledgements

This work was supported by the Fundo de Desenvolvimento e Defesa Sanitária Animal (FUNDESA-RS) and by the NC State University, College of Veterinary Medicine, Global Health funds.

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.

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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)
PageRank	Measure of the Google PageRank, a link analysis algorithm that produces a ranking importance of all the farms from 0 to 1.	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 path between any two pairs of nodes in the network.	Freeman (1978)
Giant weakly connected	The proportion of nodes that are connected in the largest component when directionality of movement is ignored.	Wasserman and Faust

component (GWCC)		(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 commercial and non-commercial pig farms

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.

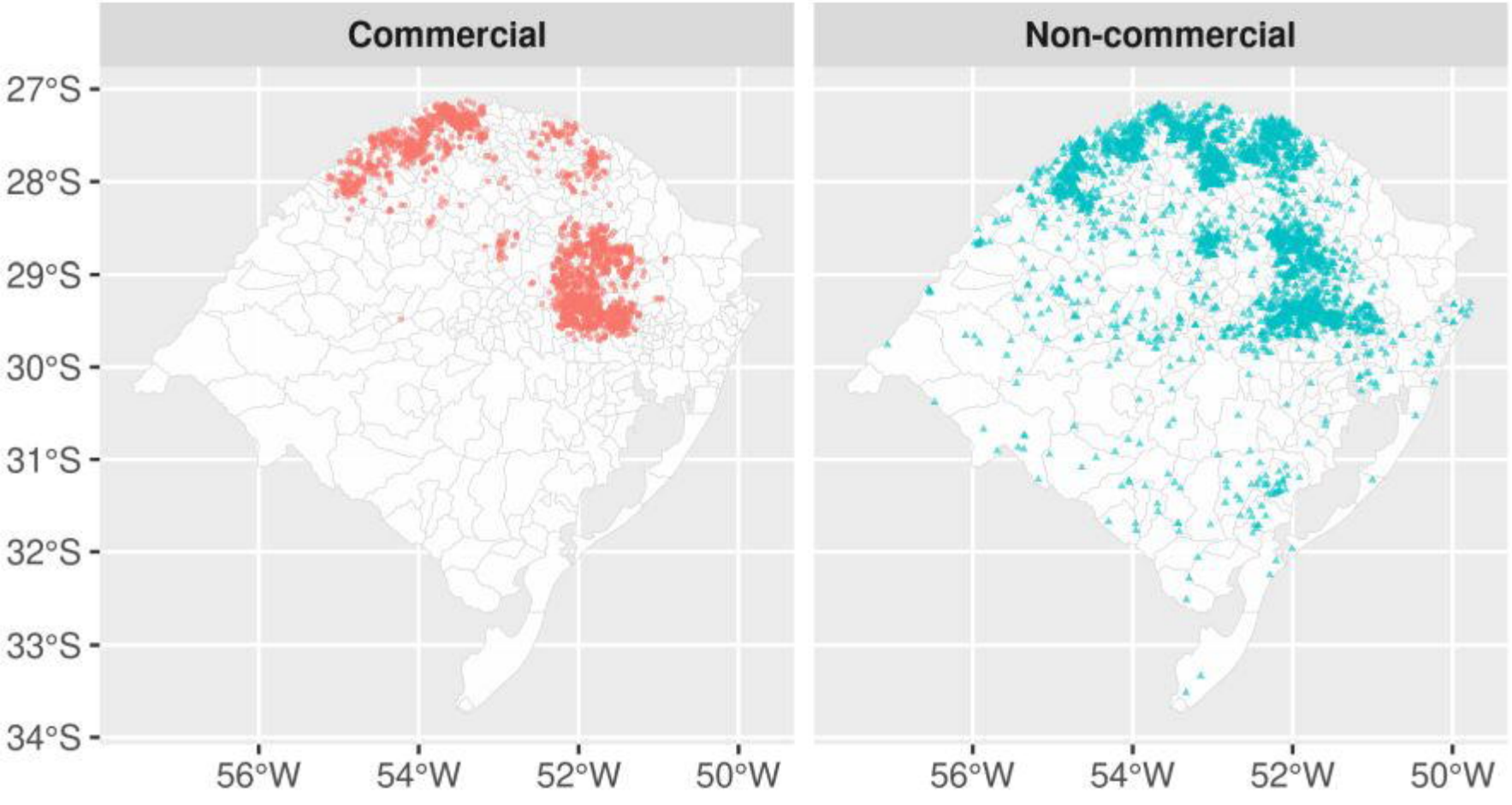
Figure 3. Description of the monthly variation of the network metrics of the pig movements from January 2017 until December 2018.

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 divided between commercial and noncommercial farms. The simulations assumed a farm prevalence of 0.1%.and non-commercial farms. The simulations assumed within farm prevalence of 0.1%.

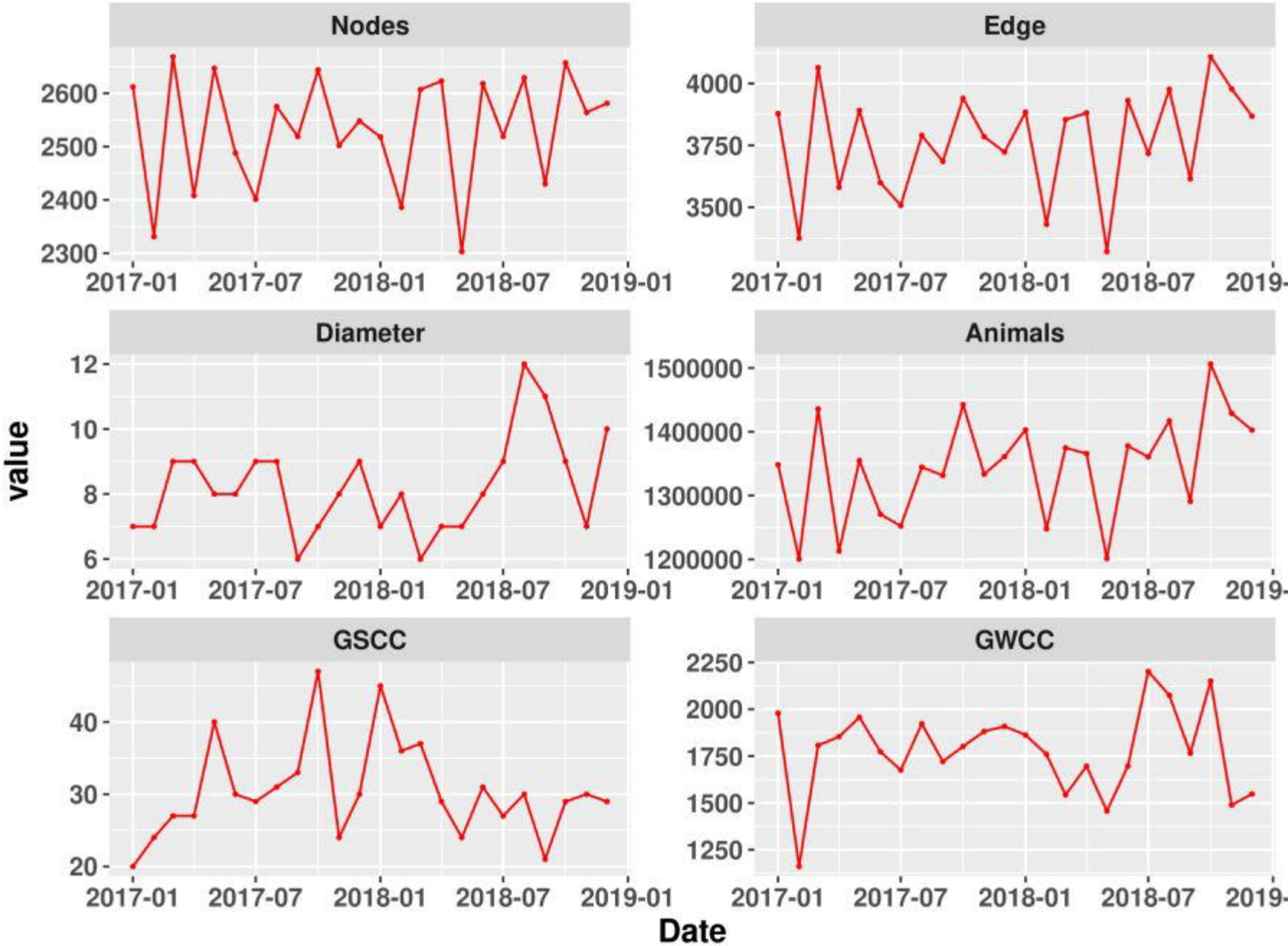
Figure 5. Epidemic size by node removal. Y-axis show the cumulative size of the spread cascades from January 2017 until December 2018 for five scenarios. From 10, 250, 500, 750 to 1,000 farms were removed on day “0” of the simulation while temporal network metrics were calculated for all remaining farms. Line are the average values and shade 95% CI.

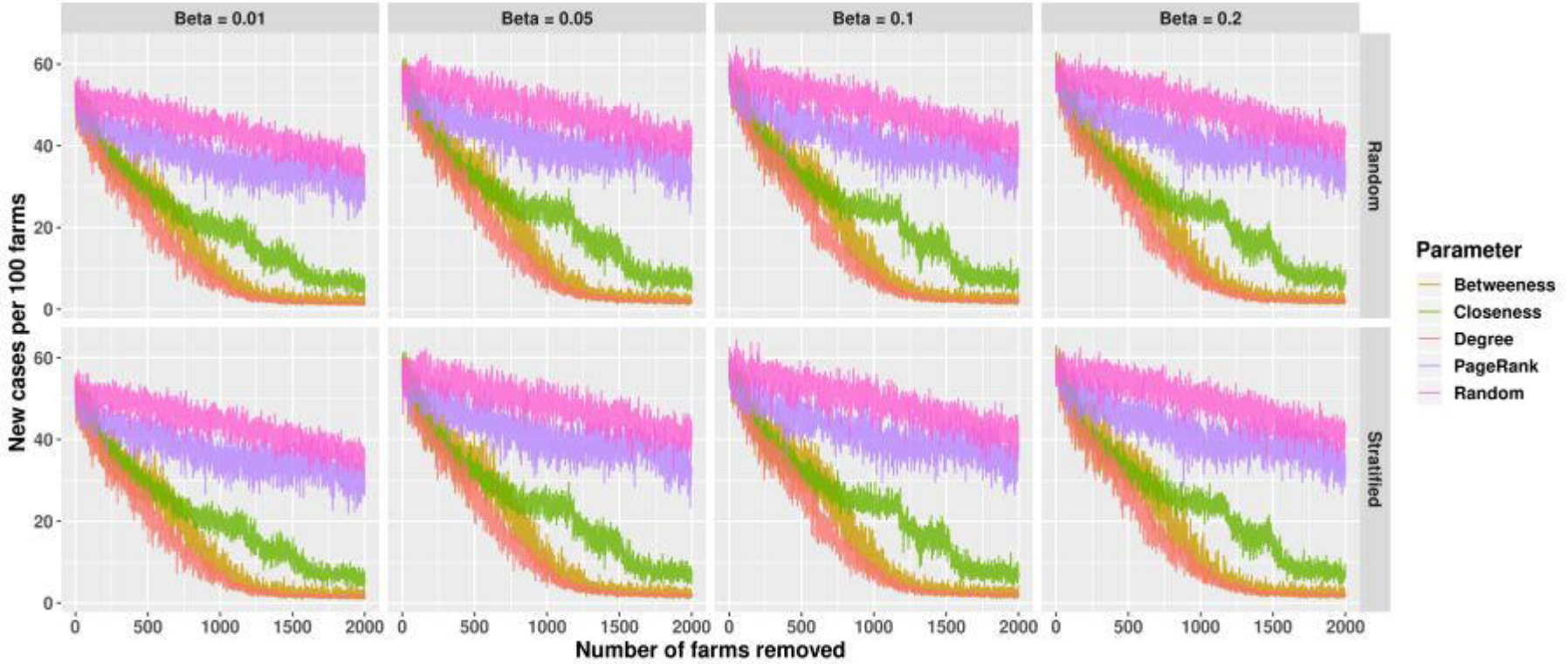
Figure 6. Final spread cascade sizes by each target-network surveillance strategy. In light-blue the estimate spread cascade which had maximum value of 29 farms while targeting farms at random resulted in cascade of 2,593 farms (green).

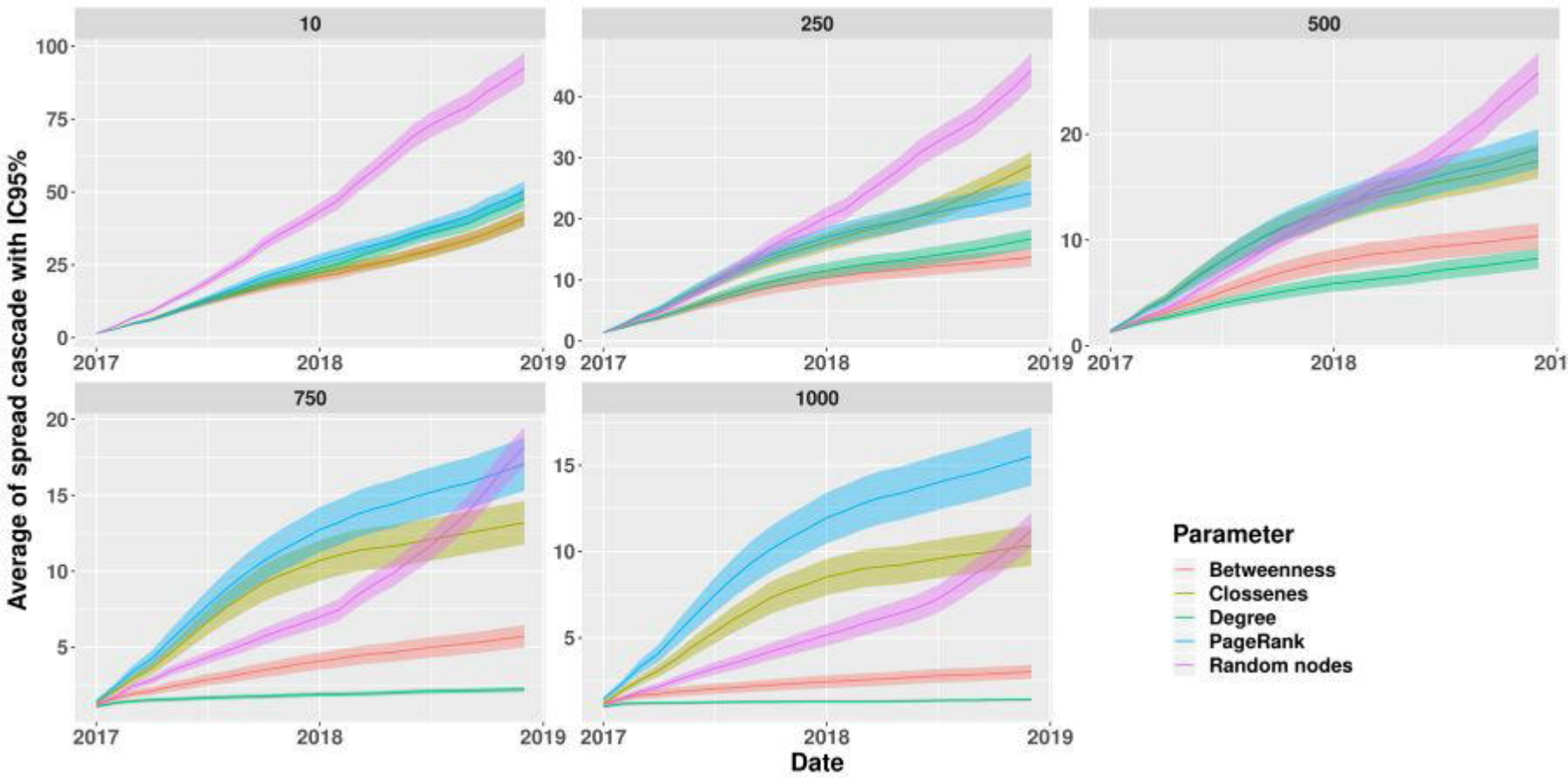
Figure 7. The geographic locations of the top 1,000 farms ranked by logarithm of degree.

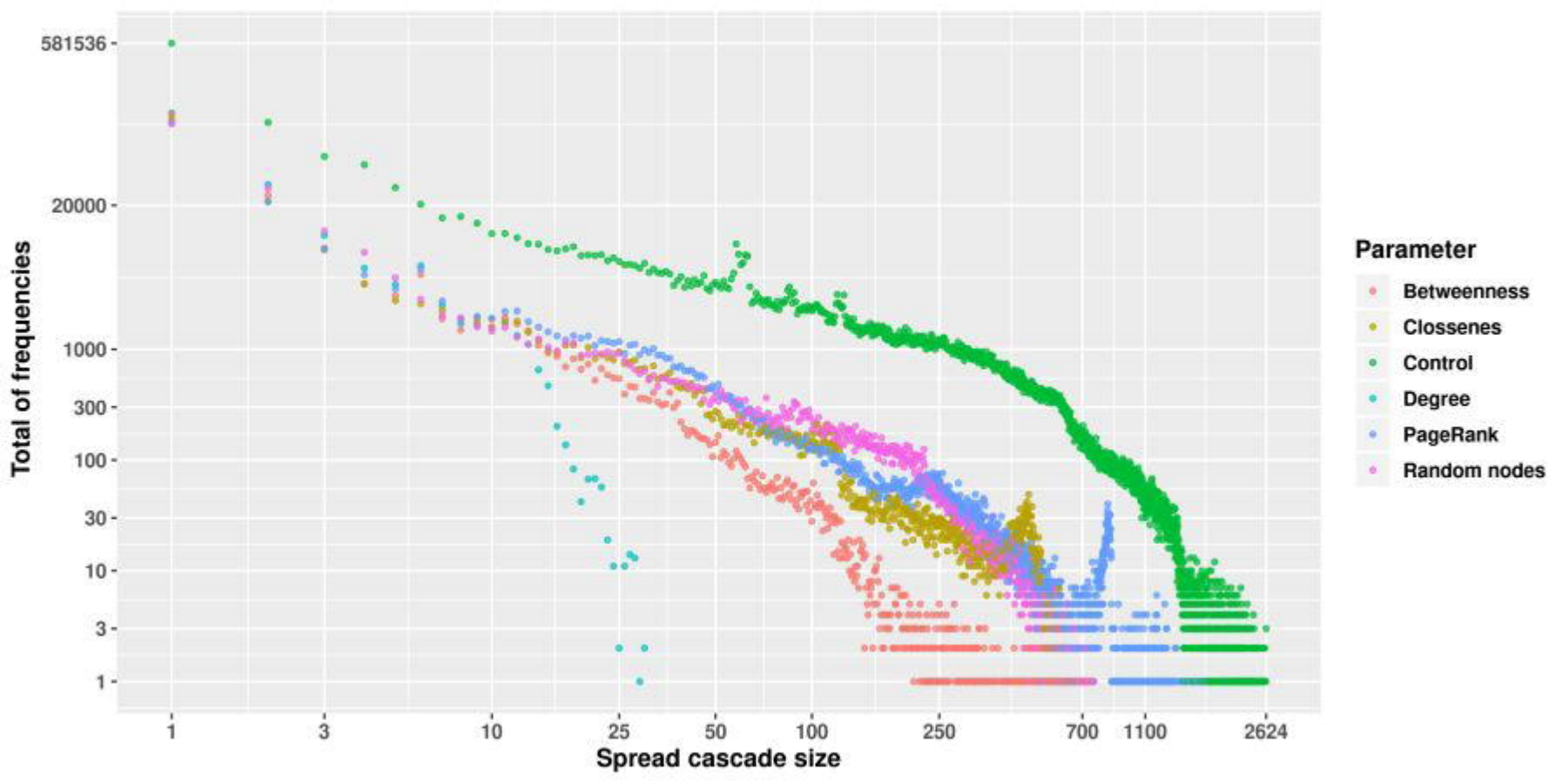

Commercial
Non-commercial
27°S
28°S
29°S
30°S
31°S
32°S
33°S
34°S
56°W
54°W
52°W
50°W
56°W
54°W
52°W
50°W

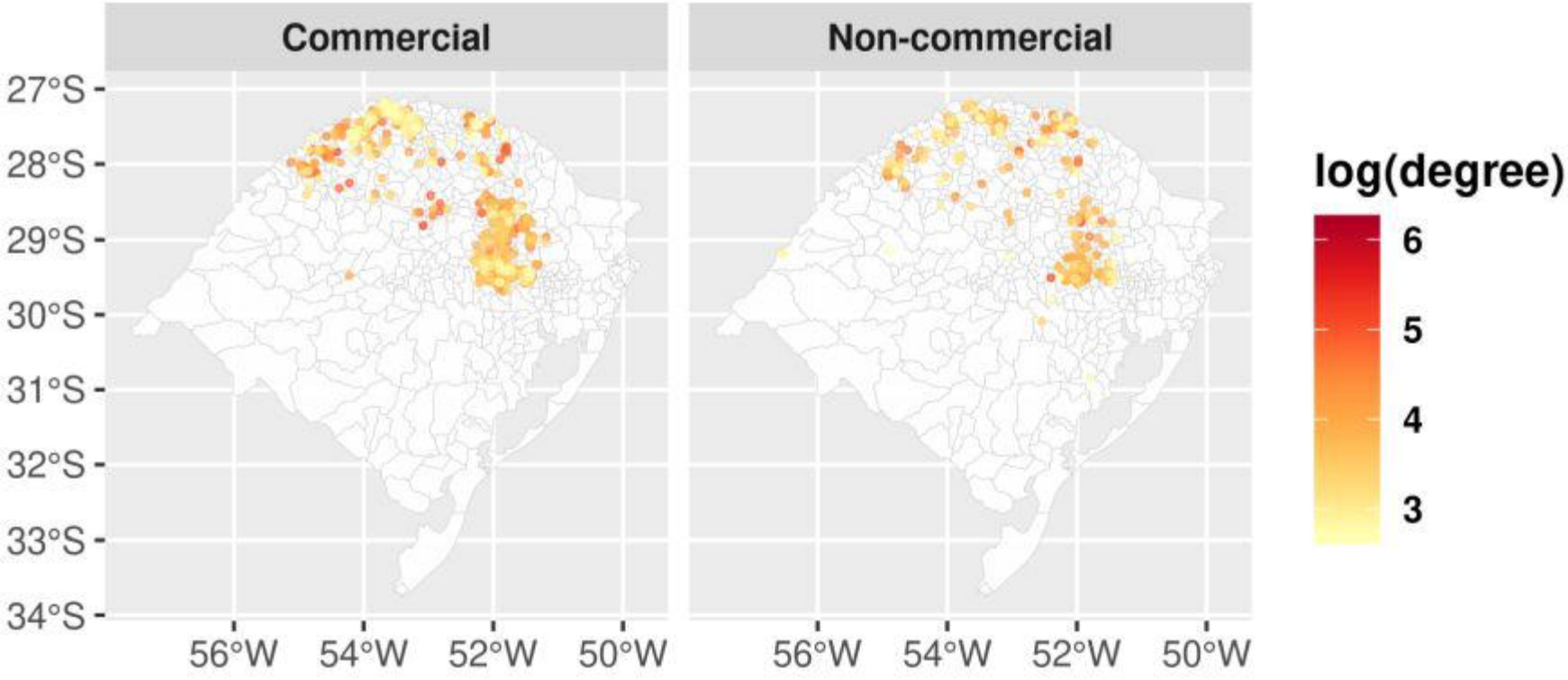
Finishers
6555
1.41
51.89
0.18
0.74
4.3
433
0.25
Breeding-farms
2.34
102
Slaughterhouses
4.65
13.3
1816
Nursery
2.2
1.0
0.24
0.41
0.26
0.87
0.42
0.66
3.54
2.81
0.15
0.86
122
CSBF
1.1
0.15
470
Wean-to-finisher
0.59
0.8
2.04
2101
0.12
Subsistence
1.0
250
Others


Nodes
Edge
Diameter
Animals
GSCC
GWCC
value
Date
2600
2500
2400
2300
4000
3750
3500
12
10
8
6
1500000
1400000
1300000
1200000
40
30
20
2250
2000
1750
1500
1250
2017-01
2017-07
2018-01
2018-07
2019-01
2019-


Beta = 0.01
Beta = 0.05
Beta = 0.1
Beta = 0.2
Random
Stratified
New cases per 100 farms
0
20
40
60
0
500
1000
1500
2000
Number of farms removed
Parameter
Betweeness
Closeness
Degree
PageRank
Random


10
250
500
750
1000
Average of spread cascade with IC95%
Date
2017
2018
2019
Parameter
Betweenness
Clossenes
Degree
PageRank
Random nodes


Total of frequencies
581536
20000
1000
300
100
30
10
3
1
1
3
10
25
50
100
250
700
1100
2624
Spread cascade size
Parameter
Betweenness
Clossenes
Control
Degree
PageRank
Random nodes


Commercial
Non-commercial
27°S
28°S
29°S
30°S
31°S
32°S
33°S
34°S
56°W
54°W
52°W
50°W
log(degree)
6
5
4
3