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

Running title: Time-varying network improve surveillance in pigs

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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 until 2018, comprising 351,519 movements and 48 million transported pigs. Here 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 between 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. Results show that targeting the first 1,000 farms ranked by degree would be enough 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, much lower if compared with random surveillance that resulted in epidemics 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 enhancing biosecurity plans and improved

surveillance, which constitute important next steps in strategizing targeted disease control intervention.

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

Introduction

The between farm animal movement had historically been associated with disease spread (Ortiz-Pelaez et al., 2006; Smith et al., 2013). Animal movement data allowed for the initial development of network-based approach, which is 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, some can be classified as vulnerable because periodically receive infected animals (high in-degree), therefore the identification of these farms is more important in a scenario of disease absence or at low prevalence (Qi et al., 2019), such locations may serve as sentinels. On the other hand, farms more likely to spread disease throughout their contact network could be targeted in 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 to undergo isolation or surveillance schemes have 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 of the published approaches make use of the static networks to describe animal movement and subsequently make inferences about outbreak 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 movements' temporal anomalies and seasonality 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 enough to make inferences about disease dynamics within the contact networks. The fact that disease transmission is not restricted to the historical record of movement (Firestone et al., 2019; Qi et al., 2019; Sterchi et al., 2019), when it actually occurs by the movement of

infected animals, it is likely to be an event in time, which is dependent on when animals are sent and more importantly when they are received at the final destination, this rationale has been strongly overlooked (Chaters et al., 2019; Sterchi et al., 2019). Still, static networks have been used to measure the effect of targeted farm removal, on the network fragmentation by monitoring giant strongly or weak 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 measure 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 have been a constant roadblock to the advancement of network epidemiology specially 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 the epidemics (Miller, 2017; P. Kim and Lee, 2018; Darbon et al., 2019). For example, compartmental models can be used to describe the epidemic spreading on temporal contact networks, which also 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 use two years of pig movement data of one Brazilian state to estimate the optimal number of farms to undergo target surveillance by tracking between-farm contacts pathways and infer epidemic sizes throughout disease propagation. First, we described the complete pig movements, then

challenged the use of static networks against dynamic networks. We proposed a stochastic compartmental model to simulate disease spread into the two years empirical networks while accounting for the temporal order of the movements. Our model formulation allowed for 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, enhancement of 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 between 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 fence, presence of cleaning and disinfection station, see table 1 for the full list), geolocation and farms' population capacity. Each pig shipment had: 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. Also, farms declared as inactive (no pigs were 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 had active contracts with integrated swine companies and as non-commercial 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", pig farm. For the static network, movements from January 2017 to December 2018 were analyzed as traditionally done by aggregating movements into one snapshot. Second, networks were constructed based on a temporal resolution of 30 days 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 are interested in potential disease spread among living animals, transports to slaughter were excluded from the network analysis, but are kept for descriptive purposes (see Fig 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). In order to quantify the amounts of such static error, the

number of paths in the static view can be compared to the number of paths in the time-series network (Lentz et al., 2013, 2016). This ratio is so called 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 non-zero elements in p or P, respectively. A causal fidelity of one means that temporal network is well represented by its static network, while networks with lower values would not represent well the temporal paths because most of the paths are not causal. Here we calculated the causal fidelity in timescales which are typically used to investigate animal movement data: monthly, 6 months and 1 year and for the full two years data (Lentz et al., 2016). We also calculated the edge loyalty (θ), which measure the fraction of preserved edges (θ) of a given premise between two consecutive years, $t-1$ and t. In order 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).

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

and 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}as set of farms that are active in the period $t-1$, on the other hand 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). Transition from $S \rightarrow I$ was in the two-stage model with one-way transition depend on $\frac{\beta S_i I_i}{S_i + I_i}$ with β 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 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 as the product of the contact rates and transmission probability between animals into the farms. Another assumption was that contact rates among pigs were homogenous. For the between farm transmission, we considered the observed number of pigs moved between farms and population size at each farm. As initial condition, model simulation started with 950 infected farms (10% of 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 proportional to the number of farms in each production system (N=17), this approach allows for 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. As a sensitivity analysis, we run simulations with a diverse set of β parameters (see supplementary Figure S2). Also, we run simulations for commercial and non-commercial farms separately with the same parameters described above (see supplementary Figure S4 and S5).

Cumulative contacts as a proxy of epidemic sizes

The modeling setup described by (Payen et al., 2019) was adapted to identify 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 will be a representation of the cumulative and consecutive contacts temporally between farms, 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 the movements over two years. In short, when there was a directed interaction, including the three dimensions 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. All together, we recorded the daily spread cascades which are represented by averages and ± 95% CI, 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 by: degree, betweenness, PageRank, 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. To compare 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 done by comparison of final spread cascade distributions using a non-parametric Kruskal-Wallis test followed Dunn's post hoc test, where the p-value below 5% were significant. Once the most efficient network-based surveillance strategy was defined the biosecurity, infrastructure and population of selected farms were described.

Software

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 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), brazilmaps 0.1.0 (Siqueira, 2019) packages. Spyder 3.3.3 software for Python version 3.7 and Adobe Illustrator CC 2018 software.

Results

Description of pig movements

The total number of active pig farms in the completed database included 11,849 farms, 351,519 movements and more than 48 million pigs transported. The majority 66% of the farms were identified as non-commercial, while the number of farms per commercial system varied from 10 to 465 from 17 production systems. This corresponded to 6,555 (55.32%) finisher, 1,816 (15.33%) nurseries, 470 (3.97%) wean-to-finisher, 433 (3.65%) breeding farms, 122 (1.03%) certified-swine-breeder-farm and 250 (2.11%) other farms which included, insemination stations, isolation units, finally from the non-commercial farms we identified 2,101 (17.73%) as small pig holders (backyard farms or for subsistence) and, finally slaughterhouses 102 (0.86%). Most commercial and non-commercial pig farms were located at the northern and central east of the state (see Figure 1). While we have described the movements to slaughterhouses they were not accounted for any network analysis thereafter (see Figure 2).

Figure 1. Geographical location of commercial and non-commercial pig farms

More than 51% of the movements were from finisher to slaughter, with a monthly median of 7,657 shipments. Second largest volume of movements from nursery to finisher with 13.51%, and monthly median of 1,992 transfers. Breeding-farms sent 4.65% to finisher farms and 4.3% to the nursery, with 673 monthly median movements. Finally, wean-to-finisher sent a small but significant amount of pigs to slaughter 3.5%, while certified-swine-breeder-farm to breeding-farm total 2.8%.

Figure 2. Description of pig movements between all farm types from January 2017 to December 2018. The arrow size shows the percentage of movements and the color is given of the origin of the movements. The size of the circles represented 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 more steady increase from July 2017 until October of the same year (see Figure 3). The network diameter revealed a positive increase trend of 33% from April 2018 until December 2018, and then decrease, this pattern was different compared with 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 correspond 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. Description of the monthly variation of the network metrics of the pig movements from January 2017 until December 2018.

Loyalty and causal fidelity

The node loyalty of 2018 compared to 2017 was 0.65 while edge loyalty was 0.19. This means that only 65% of the farms that traded pigs in 2017 were also 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 values 0.55 in July 2017 (see supplementary Figure S1). Regarding the causal fidelity, for the network evaluated in time periods of six months, for the first half of 2017 was 0.22 and the second half of 2018 showed 0.47, for the annual evaluation 2017 was 0.22 and 2018 was 0.18, and for the entire static network was 0.33. The causal fidelity has demonstrated that there is 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 overestimate disease outbreaks which likely would 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, this can be approximated by the inverse of "c" and represents the overall overestimation of disease outbreaks if static networks would be used. The first six months of 2017 had the worst results with overestimations at 4.54 and 1.81 for the network on July 2018.

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 1.95 maximum new cases per 100 farms when β of 0.2 was used. Since this study will be used to guide decisions on the field, we consulted with the local stakeholders before deciding about the final number of farms to be in the surveillance hot-list (personal communication Dr. Lopes chair of the animal movement and surveillance department in the state of Rio Grande do Sul). Based on the local capacities and 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 farms feasible to be targeted. Furthermore, we compared two infectious seed scenarios: a) infections started at random farms and b) stratified random infection were forced to start off proportionally by the number of commercial and non-commercial 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 the 950 pig farms (10% prevalence) were equally divided between commercial and non-commercial farms. The simulations assumed within farm prevalence of 0.1%.

Finally, based on the 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 decreased immediately below 40 after only 250 farms were removed independently 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 were 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. Y-axis shows 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 is the average values and shade ± 95% CI.

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

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

The geographic locations of the target 1,000 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). The farm capacity of about 1,100 pigs (IQR=162-9,925) pigs, where a medium number of piglets was 1,122 (IQR-16-7,229), breeding farms was 4 (IQR=1-18) boars and gilts population were 544 (IQR-11-3,044), more details about farms' biosecurity and infrastructure can be found on 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 as far as to guide target activities such as enhancing surveillance, overall it had some success in reducing disease transmission (Rautureau et al., 2012; Büttner et al., 2016; Passafaro et al., 2019). However, they suffer from a number of drawbacks that often led to overestimate the size of disease outbreaks (Rautureau et al., 2012; Büttner et al., 2016; Passafaro et al., 2019). The former occurs because static networks very often cannot represent what is truly a transient event (Dubé et al., 2008; Fielding et al., 2019), which is realized when a farm receives a shipment forming an edge between farms and as soon as animals are unloaded this edge does not longer exist. 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 have 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 needed 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 expectation 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 to slaughterhouses and 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 non-commercial farms (see

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

In this study, we did not examine feed-truck or other vehicle movements or sharing. The absence of such information has been highlighted elsewhere (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 have 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 was seasonal and skewed with a variation of plus or minus 300 farms over the two-year period; this 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 when compared to other pig populations in Germany (Büttner et al., 2016), France (Rautureau et al., 2012) and Canada (Thakur et al., 2016), even though it is hard to compare

distinct networks (Miele et al., 2019). Some factors that have contributed for the variations in our study may be associated with hog price, which tends to be more volatile than in other countries, 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 and this seems a high 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 for the second half of 2018, where new paths connected the GSCC with other minor components, and consequently increased the size of the GWCC that could have implications at disease transmission and persistence (Schulz et al., 2017; Marquetoux et al., 2016).

Previous studies have considered static network views to make inference 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 at some extent static networks would provide useful information about disease relative risks (Mohr et al., 2018). But, most static network studies lack 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). Besides that restricting movements from and to highly connected farms had 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 at some extent may contain disease from spreading throughout the contact network. On the other hand, when nodal static network measures of monthly networks were used to predict outbreak risk it performed poorly (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 windows inferences or metrics from static networks can be interpreted (Lentz et al., 2013; Büttner et al., 2016). For this study, we found that July of 2017 had the best time-respecting movement representation, that value was the lower causal fidelity reported in the literature, since two different studies in pigs found 92% and 72% for monthly networks (Büttner et al., 2016) and (Lentz et al., 2013), respectively. However, a study of the 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, a producer can easily start and stop contracting with production systems because of compensation, price of feed etc. These heavily compromises the

use of static network metrics when the objective it to identify and direct active surveillance plans towards highly connected farms. The use of static networks tends to artificially connect a higher number of farms, which will consequently bias surveillance strategies to less relevant farms and compromise resources 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 the betweenness which required ~ 1, 300 farms to be quarantined before number of new cases reduced, finally as anticipated random removal shown to have 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, suggested that epidemic sizes were sensitive to network activity (Farine and Whitehead, 2015; Lebl et al., 2016). Indeed, we explicitly consider node activity while disease spread was simulated. Another two studies attempted to account for time-dependent disease spread while aiming to reduce R_0. The first used a non-compartmental model approach and found that the number of farms needed to be removed by degree was up to 50% of all farms (Kinsley et al., 2019), while the second study, used a mechanistic and comparative approach in which ASF spread was simulated, they found that degree ranking was actually the best strategy to contain the disease (Ferdousi et al., 2019). In summary, degree shown to be the best strategy in reducing disease burden while betweenness had the second best performance. It is worth notice that betweenness is useful metrics when studying disease diffusion (Farine and Whitehead, 2015), mainly because it is a representation of the shortest path between nodes, here non-commercial farms with high betwenness 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 1,000, 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 propagation. One possible explanation may be because this network is not well connected, farms that remain to be removed may be too similar in respect their Clossennes and PageRank values, therefore the impact in the propagation is expected to be as the one resulted from random removals.

Our results have shown an unevenly proportion of commercial and non-commercial 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 into 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 that lack of biosecurity on highly connects 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 less risky practice when removing cull or dead pigs (Silva et al., 2019). Another relevant biosecurity point which has been described as risk for disease introduction was the number of farm entries, here we notice that the majority of the farms had only one main road, which potentially represent less risk for local disease transmission (Silva et al., 2019). A disproportion of these highly risky farms were nurseries and breeding farms, which has been often proposed as a desired group to be targeted for surveillance (Dorjee et al., 2013). Besides 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, carrying out a more comprehensive studies coupling animal movements, with local and environmental routes of transmission while accounting for farms' biosecurity and infrastructure is 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 between them throughout the whole study period. Therefore, we argue the causal fidelity of the temporal network should be presented before considering the use of the static network in the development of disease surveillance or control strategies (Lentz et al., 2016;

Payen et al., 2019). Recent studies did not account for such issue (Büttner et al., 2013, 2018; Marquetoux et al., 2016; Motta et al., 2017; Alarcón et al., 2019), nor considered the temporal network pathways 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, so results should be interpreted with caution.

A likely limitation of this study was how farms were classified as commercial or non-commercial. 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 if 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 is available. It also can approximate epidemic sizes and identify which network metrics should be preferred while selection target farms. In addition, it could be used as a decision tool for both the local official veterinary services and by the private sector that could evaluate their own animal movements to include a more risk-oriented surveillance strategy. The model may also help to get an idea of the amount of personnel and material resources that would need to be allocated to control the epidemic, and in preparation for future epidemics (Casal et al., 2019).

Conclusion

One third of all the 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 limited the accuracy needed to optimize surveillance. Our proposed modeling framework provides a parsimonious solution to this problem, it handles the temporal order of the 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. Results from the application of this approach, identified priority pig farms which had remarkable limited biosecurity. This fact imposes important vulnerability to pathogen introduction and spread, therefore, those farms could benefit from the implementation of enhancement biosecurity plans such what has been promoted and implemented in the US by the secure pork supply (SPS) Plan. Finally, the introduction of risk-based approaches may optimize costs of routine surveillance and be used in the preparation for the introduction of FAD into the local pig industry.

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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.

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

Parameter	Definition	References
Nodes	Pig farms.	Wasserman and Faust (1994)
Edge	Link between two nodes.	Wasserman and Faust (1994)
Degree (k)	Number of unique contacts from and to a farms. When direction was taken into account, the ingoing and outgoing contacts are separated: the out degree is the number of contacts originating from a specific farm, and the in degree is the number of contacts with direction to a specific premise.	Wasserman and Faust (1994)
PageRank	Measure 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 at incoming steps and otherwise 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 component (GWCC)	Proportion of the nodes that are connected in the largest component when directionality of movement is ignored.	Wasserman and Faust (1994)
Giant strongly connected component (GSCC)	Proportion of the 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
Present 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 load and unload outside farm's designated clean area	No=61.3% Yes=38.7%
Farm has own clothes (shower in)	No=77.7% Yes=22.3%
Feed bins internal 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	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.

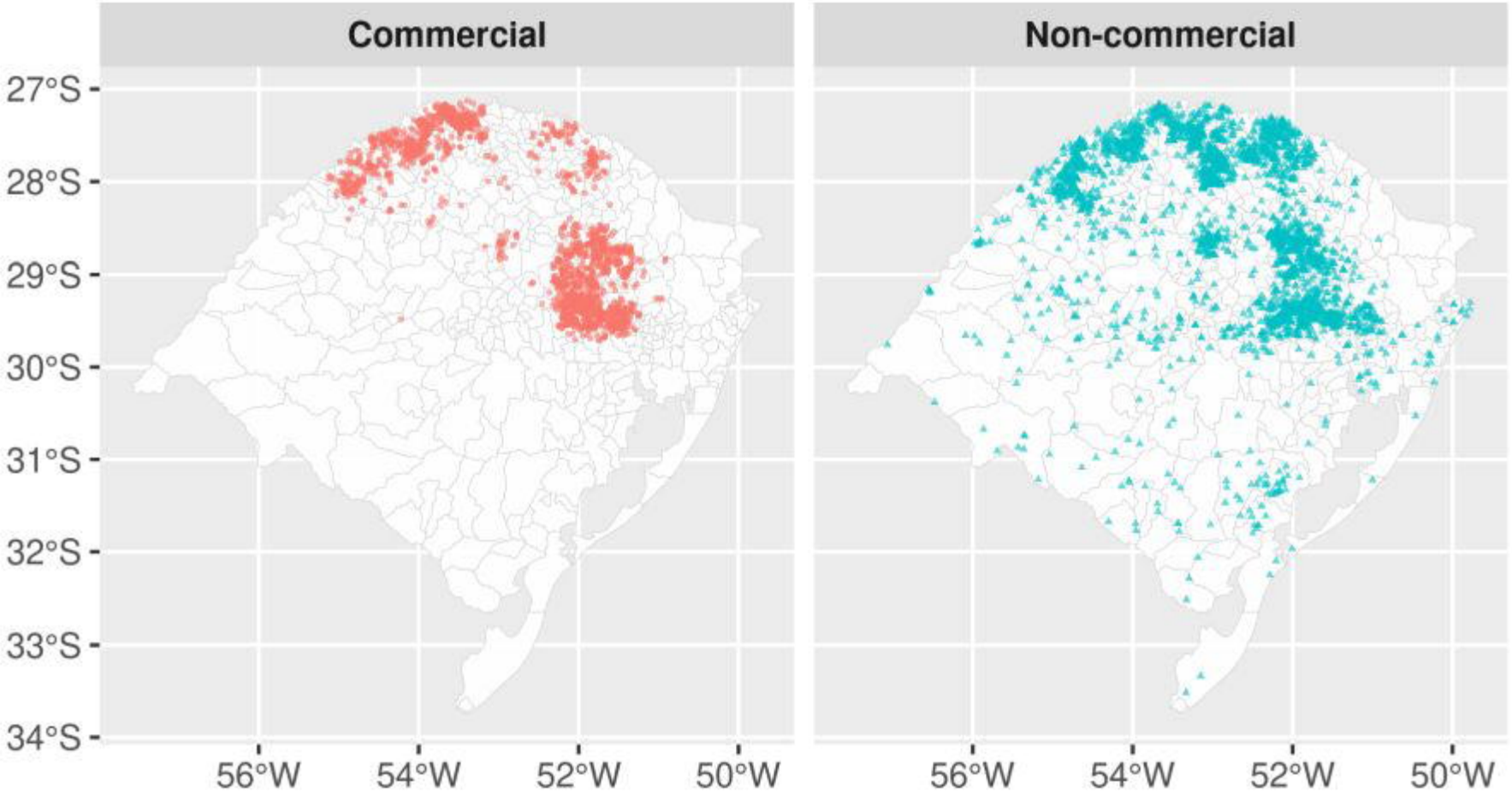
Figure 3. Description of the monthly variation of the network metrics of the pig movements from January 2017 until December 2018.

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 the 950 pig farms (10% prevalence) were equally divided between commercial and non-commercial farms. The simulations assumed within farm prevalence of 0.1%.

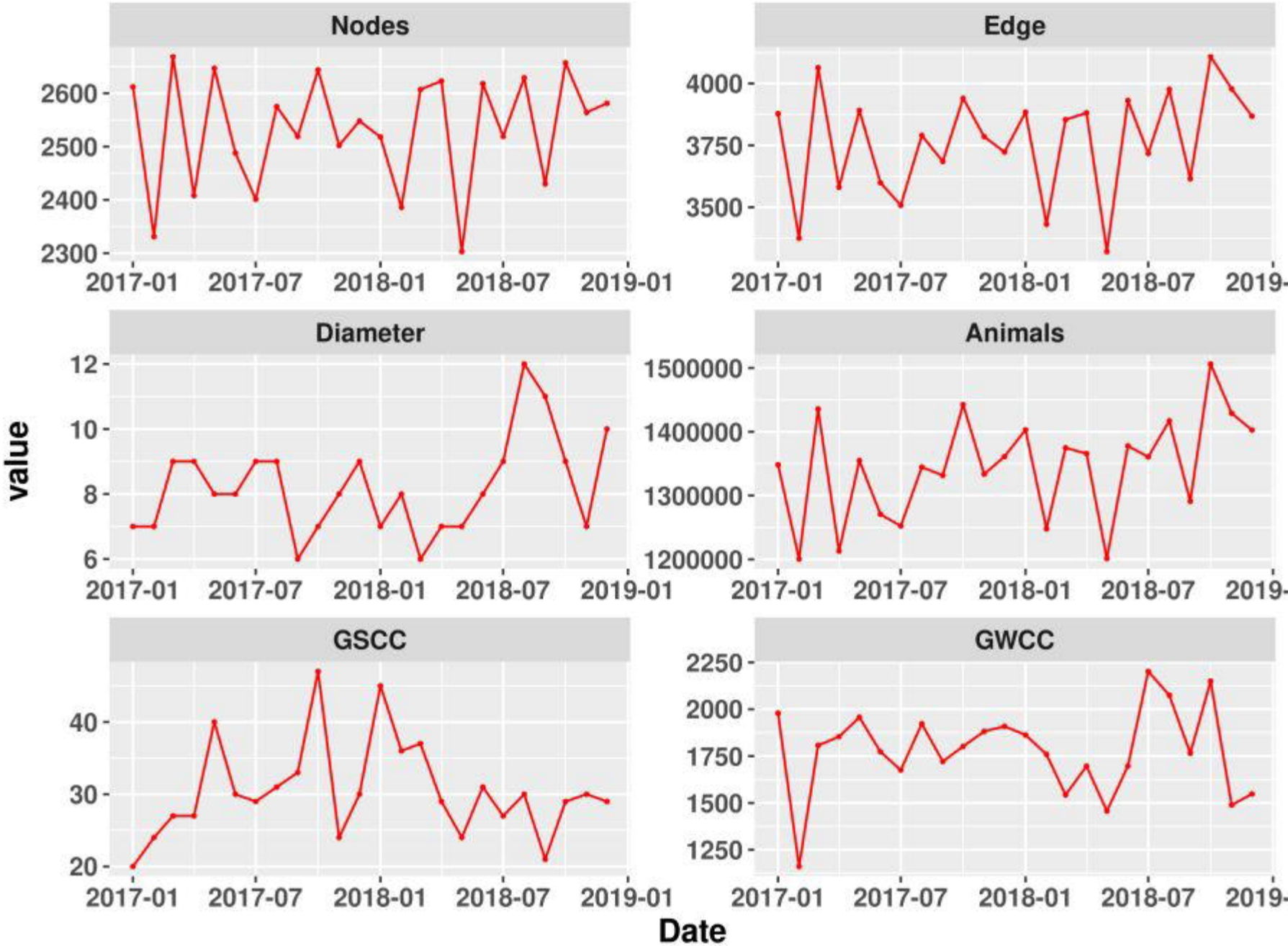
Figure 5. Epidemic size by node removal. Y-axis show the cumulative size of the spread cascades from January 2017 until December 2018 for five scenarios. From 10, 250, 500, 750 to 1,000 farms were removed on day=0 of the simulation while temporal network metrics were calculated for all remaining farms.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

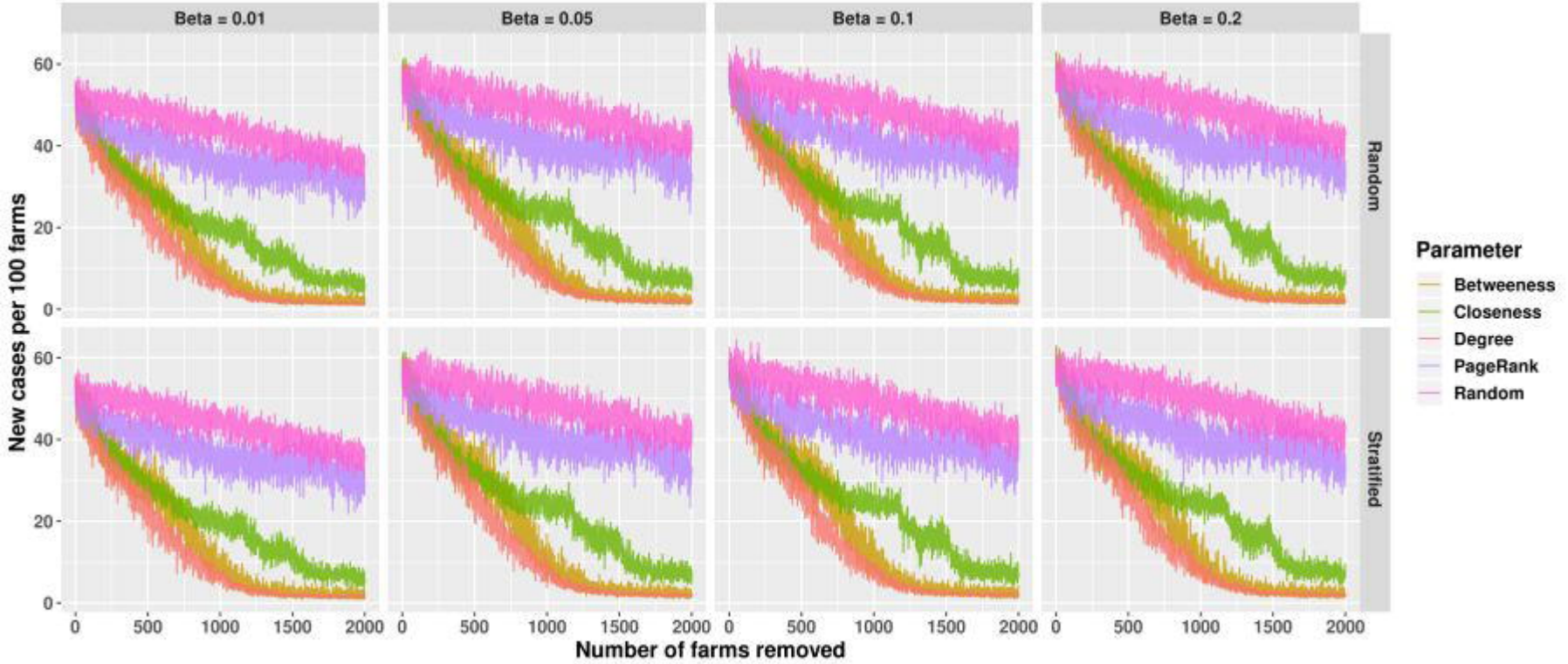
Figure 6. Final spread cascade sizes by each target-network surveillance strategy. In light-blue the estimate spread cascade which had maximum value of 29 farms while targeting farms at random resulted in cascade of 2,593 farms (green).

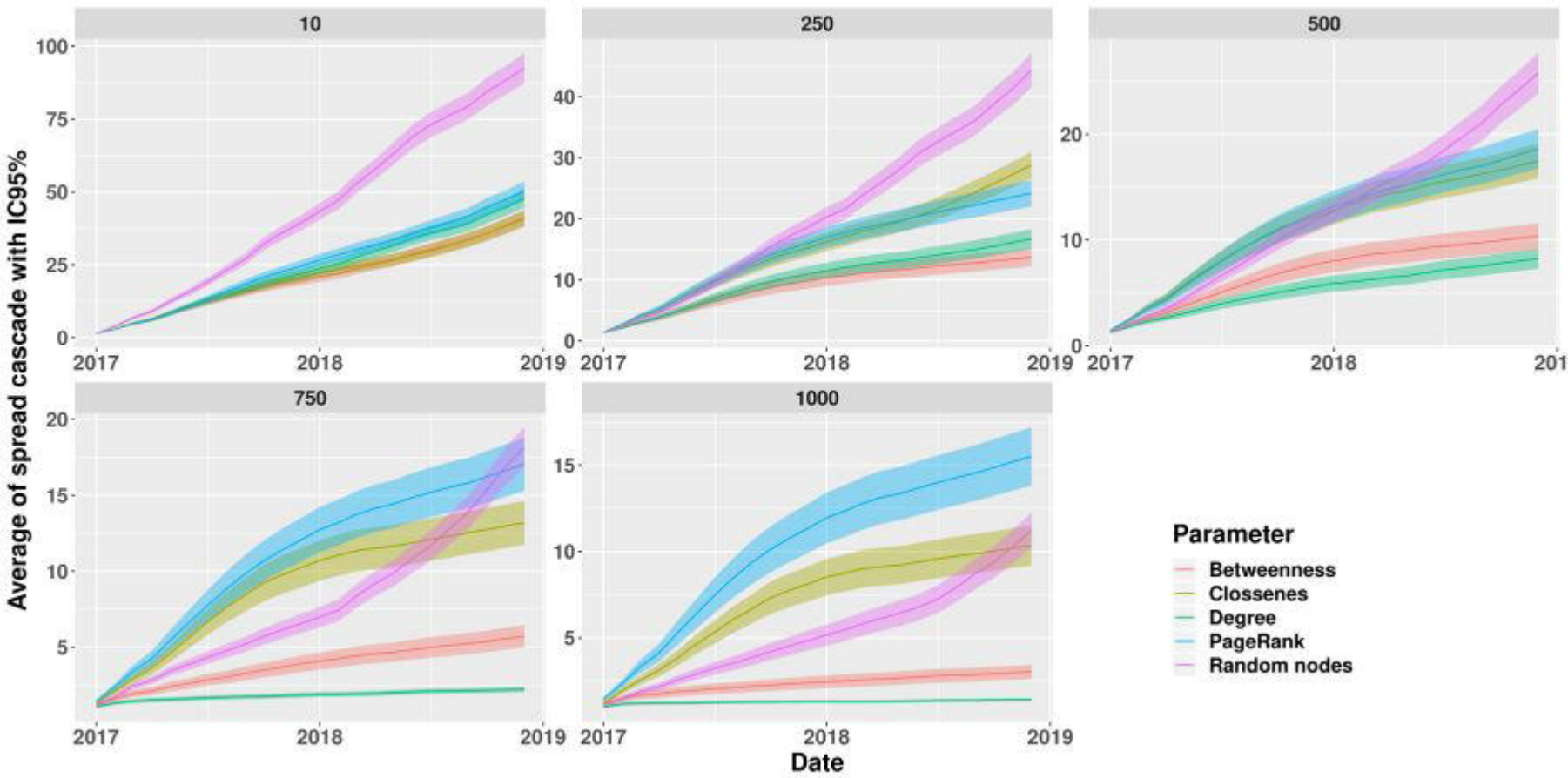
Figure 7. The geographic locations of the top 1,000 farms ranked by logarithm of degree.

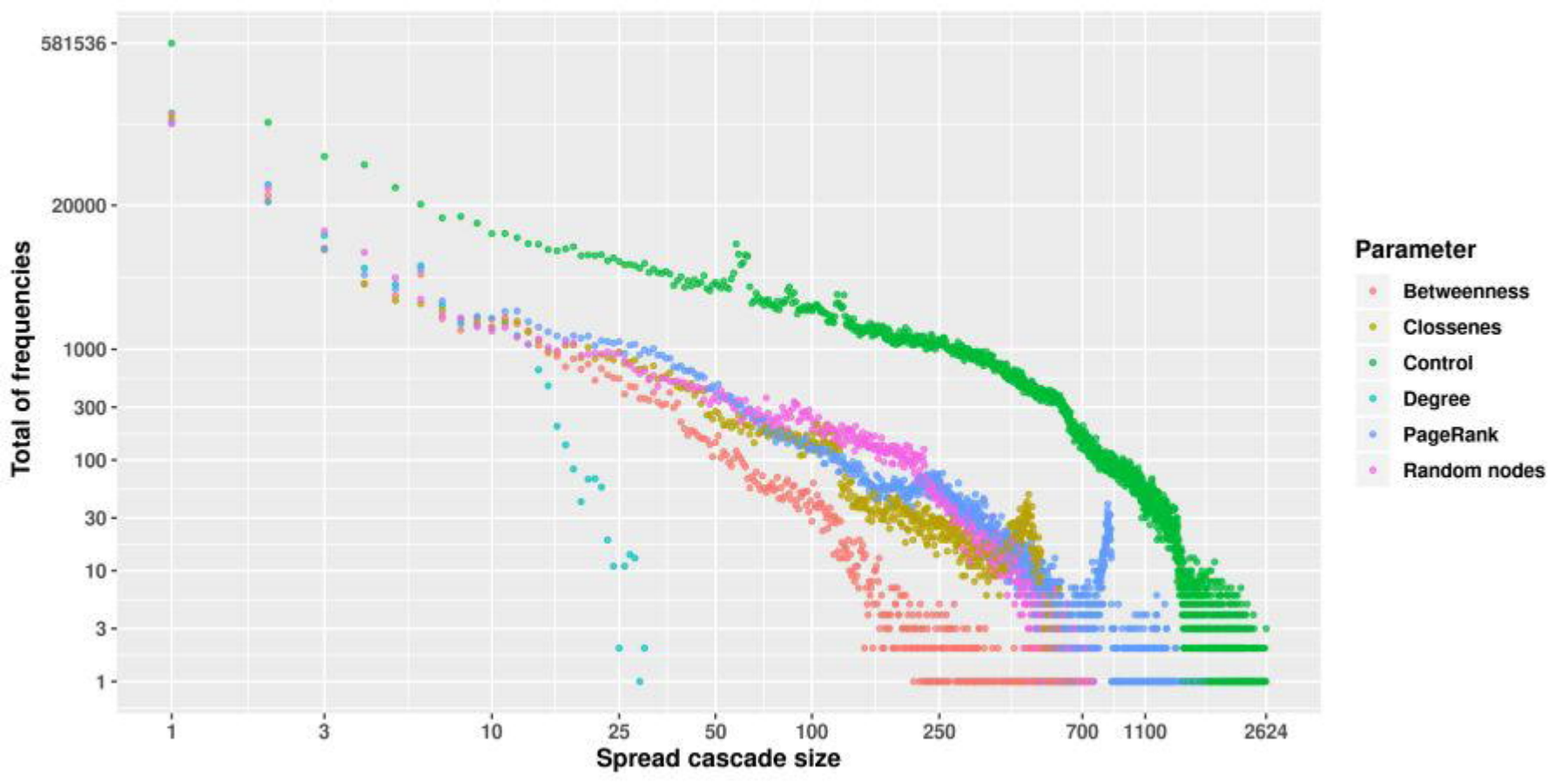

Commercial
Non-commercial
27°S
28°S
29°S
30°S
31°S
32°S
33°S
34°S
56°W
54°W
52°W
50°W
56°W
54°W
52°W
50°W

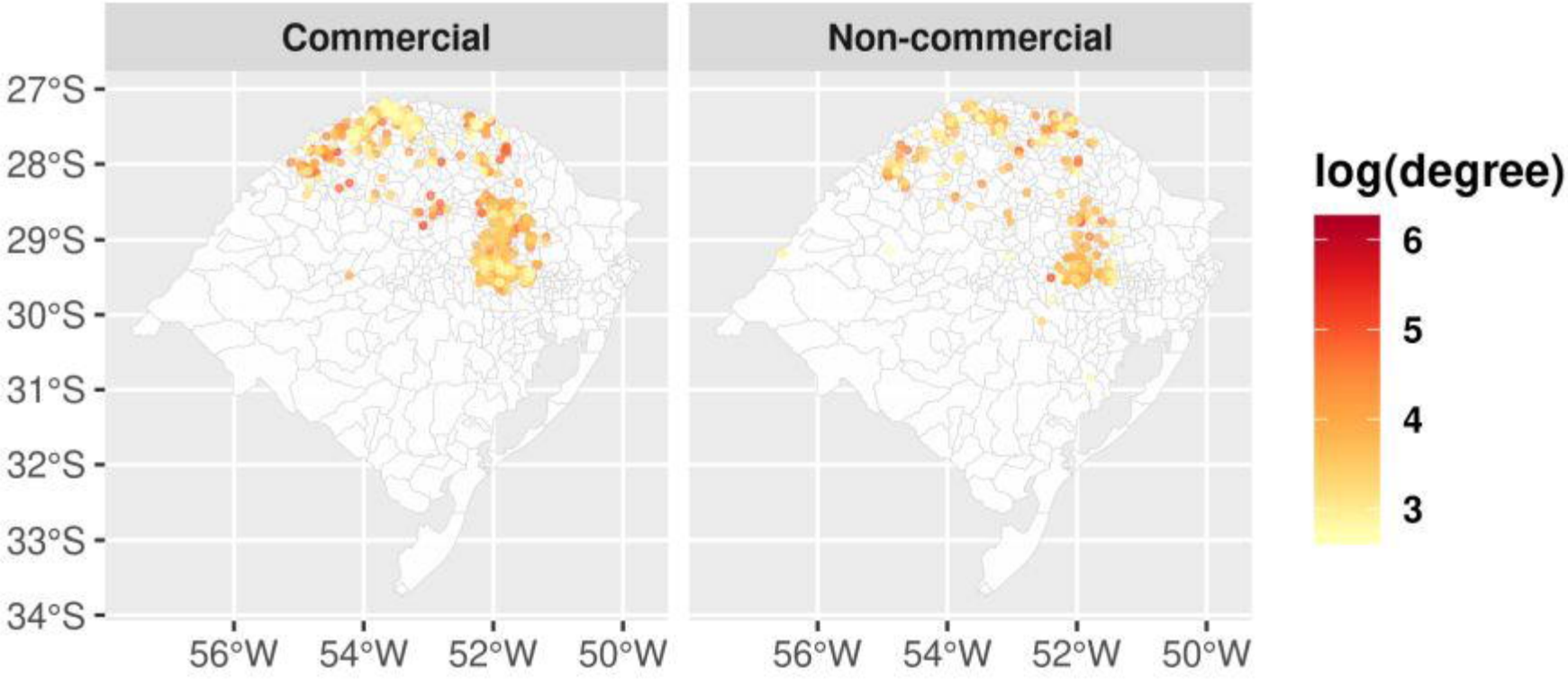
Finishers
6555
1.41
51.89
0.18
0.74
4.3
433
0.25
Breeding-farms
2.34
102
Slaughterhouses
4.65
13.3
1816
Nursery
2.2
1.0
0.24
0.41
0.26
0.87
0.42
0.66
3.54
2.81
0.15
0.86
122
CSBF
1.1
0.15
470
Wean-to-finisher
0.59
0.8
2.04
2101
0.12
Subsistence
1.0
250
Others


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