Preventive Veterinary Medicine 243 (2025) 106608

Contents lists available at ScienceDirect

Preventive Veterinary Medicine

journal homepage: www.elsevier.com/locate/prevetmed

Exploring structural changes in the Swedish cattle population and between-holding movements

Ivana R. Ewerlöf [a,b,*], Jenny Frössling [b], Madeleine Tråvén [c], Stefan Gunnarsson [a], Lena Stengärde [d], Emma Hurri [e], Stefan Widgren [b]

[a] Department of Applied Animal Science and Welfare, Swedish University of Agricultural Sciences (SLU), PO Box 234, Skara SE-532 23, Sweden
[b] Department of Epidemiology, Surveillance and Risk Assessment, Swedish Veterinary Agency (SVA), Uppsala SE-751 89, Sweden
[c] Department of Clinical Sciences, Swedish University of Agricultural Sciences (SLU), Uppsala SE-750 07, Sweden
[d] Växa Sverige, Färjestaden SE-386 90, Sweden
[e] Department of Animal Health and Antimicrobial Strategies, Swedish Veterinary Agency (SVA), Uppsala SE-751 89, Sweden

ARTICLE INFO

Keywords:
Network analysis
Location Change Pattern
Survival analysis
Disease prevention
Epidemiology
Sweden

ABSTRACT

Movements of livestock between holdings plays an important role in the spread of many infectious diseases, and network analysis can provide a greater understanding of potential spread dynamics. This study explored cattle movements between Swedish holdings from 2005 to 2022 to enhance the knowledge basis for epidemiological analyses.

In addition to classical network analysis, a novel method, Location Change Pattern (LCP), was used to analyse movements between holdings per individual. Furthermore, survival analysis was used to investigate animal- and herd level risk factors associated with moving cattle from a holding.

Although the number of cattle and holdings decreased, the number of movements increased substantially over the study period. Simultaneously, the network became more disassortative with an increased average path length, whilst indegree and in- and outgoing contact chains decreased. Combined, the results suggests that an epidemic spread in the cattle population may be slower and reach a smaller final size compared to 2005. Additionally, the clustering coefficient and reciprocity increased over time which might change the dynamics of disease spread. The increase in movements can be partly explained by an increased number of cattle being moved back and forth between holdings, particularly seen for female cattle. Male calves at holdings with a high proportion of female cattle had the greatest hazard of being moved, with an increased hazard at around 20 days of age.

In summary, significant changes over time were found in the cattle population and in the movement network, which must be accounted for when working with disease prevention.

1. Introduction

Infectious diseases are a major concern within the livestock sector as they can lead to substantial production losses with significant economic impact, an increased risk of the transmission of zoonotic diseases to humans, and various negative effects on animal welfare (Rushton, 2009). Livestock movements play a key role in the spread of many infectious diseases, e.g., foot and mouth disease and bovine tuberculosis (Fèvre et al., 2006). Therefore, analysing animal movements and contact structure between holdings can provide essential knowledge for the control and prevention of further spread of infectious agents. Social network analysis has become widely used in veterinary epidemiology to analyse livestock movements, wherein holdings represent the nodes in the network structure, and the animal movements between the holdings represent the edges or links between the nodes (Dubé et al., 2009; Martínez-López et al., 2009). These methods may facilitate contact tracing in an outbreak (Kiss et al., 2008), risk-based surveillance of holdings that have many in- or outgoing contacts (Stärk et al., 2006) as well as targeted preventive measures. Network analysis can also provide valuable insights about previous outbreaks (Ortiz-Pelaez et al., 2006),

* Corresponding author at: Department of Applied Animal Science and Welfare, Swedish University of Agricultural Sciences (SLU), PO Box 234, Skara SE-532 23, Sweden.
E-mail address: ivana.ewerlof@sva.se (I.R. Ewerlöf).

https://doi.org/10.1016/j.prevetmed.2025.106608
Received 12 February 2025; Received in revised form 28 May 2025; Accepted 25 June 2025
Available online 26 June 2025

and the size or behaviour of future epidemics (Dubé et al., 2008). For example, network metrics such as the giant strongly connected component (GSCC) or contact chains may be used to estimate the potential size of an outbreak (Kiss et al., 2006a; Dubé et al., 2011), and the clustering coefficient and average path length may give information about whether an epidemic would concentrate to certain clusters of nodes or rapidly reach a large part of the network (Watts and Strogatz, 1998; Eames and Keeling, 2003).

Properties of cattle movement networks may change over longer time periods. For instance, in the UK, various network metrics changed from the period 2004–2006 to 2015–2017 and a decrease in the total number of holdings was observed (Duncan et al., 2022). Similarly, in France, the number of holdings in the network decreased between the years 2005 and 2009 (Dutta et al., 2014). Movements may also be concentrated within or between certain regions in a country (Ensoy et al., 2014; Brown et al., 2019; Comper et al., 2023) which has also been previously reported in Sweden (Nöremark et al., 2009; Widgren and Frössling, 2010). Additionally, changes in network metrics over time may differ depending on the region (Ensoy et al., 2014). Properties of the nodes in the network may also depend on herd characteristics, such as herd size or production type (Bigras-Poulin et al., 2006), as well as historical network metrics and production indicators (Hidano and Gates, 2019). Hidano and Gates (2019) also demonstrated that animal characteristics can be associated with the animal's probability of being moved. Indeed, the varying temporal and spatial properties of the networks, as well as the influence of certain herd- and animal characteristics on the risk of between-holding movements, are important factors to consider when analysing risk of disease spread (Bajardi et al., 2012; Vernon and Keeling, 2012).

Throughout the last decades there have been structural changes within the Swedish agricultural sector, and for the cattle industry this has indicated a trend towards fewer holdings with larger herd sizes, as well as a simultaneous trend of a decreasing overall number of cattle (Hultén et al., 2022). The shift within the sector also includes changes in management practices and production orientation (Söderberg et al., 2015; Wästfelt and Eriksson, 2017). Despite the decreasing number of animals and holdings, a study based on Swedish cattle movements between the years 2005 and 2014 (Widgren et al., 2016) found an increase in the number of between-holding movements over time. The reasons behind the increase in Swedish cattle movements and the properties of holdings or animals that account for the movements, requires better understanding to design disease prevention strategies.

Thus, considering the dynamic properties of cattle networks, the importance of network characteristics for disease spread, and the structural changes within the Swedish agricultural sector, it is necessary to investigate both the development of the Swedish cattle movement network over time until present time, and implications for disease spread. This could be achieved through a new study on the Swedish cattle movement network, complementing and expanding on previous studies. Additionally, it could be investigated how different herd and animal characteristics, e.g., herd size, sex, and age, are associated with between-holding movements, as this has not yet been studied in depth for the Swedish cattle population.

Therefore, the aim of this study was to explore the temporal and spatial properties of the Swedish cattle movement network from 2005 to 2022, in regard to both herd and animal characteristics, to better understand the potential consequences for disease spread and to improve the knowledge basis for epidemiological analyses.

2. Material and methods

2.1. Background population

According to the Swedish Board of Agriculture (2022) there were approximately 1.5 million cattle in Sweden in June 2021, distributed on about 15,000 companies. The majority of cattle are situated in the southern regions of Sweden, and in June 2021 19 % of the companies were dairy farms, 66 % were beef producers with suckler cows, and 15 % were beef producers without cows. The average herd sizes were: 102 dairy cows and 232 cattle in total at dairy farms (40 % of the dairy farms had more than 199 cattle and 34 % had 100–199 cattle), 21 suckler cows and 65 cattle in total at beef producers with cows (82 % had less than 100 cattle in total), and 51 cattle for beef producers without cows (88 % had less than 100 cattle) (Swedish Board of Agriculture, 2022). The average lifespan for a Swedish dairy cow is around 5 years (Växa Sverige, 2022a), and for dairy and suckler cows combined it is around 6 years. Bull calves have an average lifespan of between approximately 18 months (beef breeds) and 19 months (dairy breeds) (Gård & Djurhälsan, 2023) In general, Swedish cattle production is intensive, with animals held indoors during the winter season. However, according to Swedish legislation (SFS 2019:66), cattle older than six months (excluding bulls) must have access to outdoor pasture during the summer season (sometime between April and October), with differences in period and duration (between 60 and 120 days, and 6–24 h per day) depending on age, production type, and region (SJVFS 2019:18). Sweden is officially free (in accordance with (EU) 2021/620) of certain listed diseases in the Animal Health law (EU) 2016/429 (category C, D, and E), such as bovine viral diarrhoea, brucellosis, enzootic bovine leucosis, infectious bovine rhinotracheitis, rabies, and tuberculosis (Swedish Veterinary Agency, 2023).

2.2. Data acquisition

All cattle births, deaths, slaughters, and movements between holdings must be reported by animal owners and abattoirs to the SBA, according to Swedish and European legislation. The records are stored in the central database for bovine animals (CDB) and contain unique identifiers of the holdings reporting and taking part in the event, type of event, date, and information about the animal, such as identifier, date of birth, and sex. Movements are reported both by the sending and the receiving holdings, with certain exceptions for holdings with the same owner. The SBA also keeps a register of all holdings, where a unique holding identifier corresponds to a unique geographical location where animals are kept, such as a pasture or buildings for housing cattle. However, the register does not contain any information regarding production type or whether the holding is a pasture. One owner can have multiple holdings with different identifiers, but holdings less than 500 m apart with the same owner are allowed to have the same identification (and are thus registered as one holding). During the majority of the study period, it was not mandatory to report the movements of animals between holdings with the same owner to the CDB, if they were situated in the same or adjacent municipalities (except for abattoirs and intermediaries for trading cattle) (more specifically between 2007 and 2016, SJVFS 2007:12 with amendments until 2016). However, these events were required to be noted in a separate journal on-farm. In 2016, changes in the legislation (SJVFS 2015:44) enabled owners to report these events directly to the CDB, instead of keeping the records in a separate journal. All reported events that occurred between 2005–01–01 and 2022–12–31 along with the register of holdings were obtained from the SBA during 2022–2023 for use in the present study.

2.3. Data preparation

Data preparation was conducted in R (R Core Team, 2022) using the R-package *data.table* (Barrett et al., 2023). Raw events from CDB (n = 39,741,453) were cleaned in the steps explained hereafter (and are illustrated in Fig. 1). If an animal had multiple birth events that were not consistent, all records for the animal were removed (n = 7659, 0.1 % of the animals). Events were classified as either a birth, death (any type, including slaughter), or movement, and stillbirths were removed (n = 428,873). At this stage, the data set contained 10,819,640 unique animals. For animals that were sent to slaughter, the death was set to

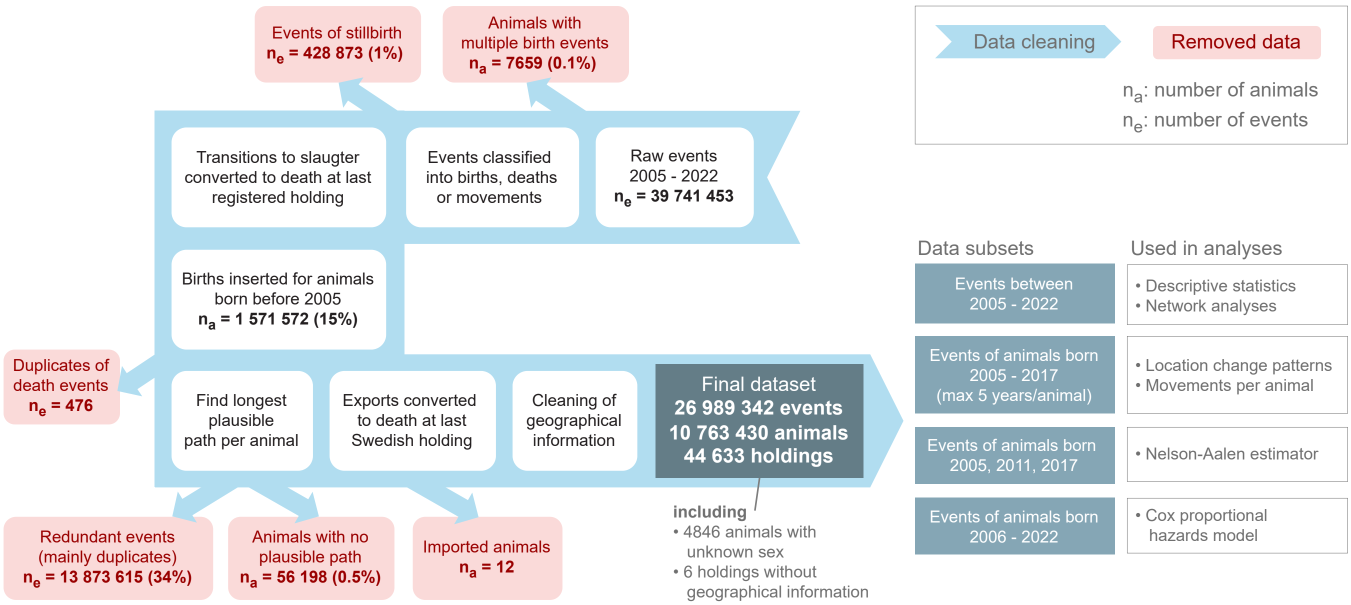

Fig. 1. Data cleaning process of Swedish cattle events from 2005–2022, and the data subsets used in different analyses.

occur at the last visited holding and not the abattoir. For animals that were born prior to the study period (n = 1571,572), a birth event was inserted at the day of birth of the animal (provided in the CDB), at the same holding as the animal's first registered event in the dataset. Duplicate reports of death were removed (i.e. reports made by the abattoir) (n = 476). In the next step of the cleaning, a new function *individual_events()* was added to the R-package *SimInf* (Widgren et al., 2019), which finds the longest plausible life history (path) for each animal and returns the corresponding events. In a plausible path, the birth, movements, and death occur in a chronological order with logical transitions between sending and receiving holdings. Sixty six percent of the events were included in these paths (thus 13,873,615 events, 34 %, were not used, of which the vast majority were duplicated reports). For certain animals (n = 56,198, 0.5 %) no logical order of events could be identified, and these animals were therefore excluded. The number of imports and exports of cattle to and from Sweden is limited. Throughout the last ten years, between 7 and 87 cattle were imported annually to Sweden and between 69 and 663 cattle were exported annually for intra-union trade, according to data from the Trade Control and Expert System of the European Commission (i.e. TRACES). Animals imported from abroad were excluded (n = 12) and animals exported were converted to "deaths" at the last registered Swedish holding. Between the years 2007 and 2013, some movements to and from transport vehicles were also required to be reported. However, given a list of vehicle identification numbers from the SBA, only reports from a few vehicles were found in the raw event dataset, and after the cleaning process only one vehicle remained. This vehicle, however, had many reported births and was active over a long period, and was resultingly assumed to not be a vehicle. Thus, it was re-categorised into a regular holding, and its 461 events were retained. Certain animals (4846 unique animals with 11, 599 events) had an unknown sex and were included in the final dataset but excluded from analyses that included sex. The final event dataset consisted of 26,989,342 events with 10,763,430 unique animals and 44, 633 unique holdings.

Out of the holdings in the event dataset, that also existed in the current holding register, 20 % (n = 8950) did not have any coordinates. Geographical information about these holdings was therefore collected through other sources. Firstly, previously retrieved holding registers from the SBA were used, which contained coordinates for 6340 additional holdings. Coordinates of three more holdings were fetched from an open geodata portal from The Swedish Land Survey Authority (2023). Additionally, 2378 holding coordinates, previously cleaned and used by Widgren et al. (2016), were added to the data. Of the holdings in the event dataset that were not in the current holding register at all (n = 102), some geographical information was found for almost all holdings: 90 from previously retrieved registers (58 with coordinates) and 6 with coordinates used by Widgren et al. (2016). Lastly, any geographical coordinates that were still missing were sampled randomly based on other available geographical information, within either the 5-digit postal code (n = 204), the parish area (n = 9), the municipality (n = 17), or the county (n = 1). For 6 holdings no geographical information could be found, and these holdings as well as the animals with events at these holdings, were excluded from analyses where geographical information was used (174 animals with 820 events). The final holding register consisted of 44,633 holdings, 6 of them without coordinates.

A holding was defined as active during a certain year if it held at least one animal at some time point within that year. The age of the individual animal at each event was calculated as the number of days since the birth event. Index change was calculated as the value of a variable for a certain year divided by the value in 2005, for the following variables: number of 'movements', 'animals', 'births', 'deaths', 'active holdings' and 'average number of animals per holding'. For all movements, the Euclidean distance between the coordinates of the holdings was calculated, with the function *st_distance* in the R-package *sf* (Pebesma, 2018). Sweden was divided into eight regions according to the Nomenclature of Territorial Units for Statistics (i.e. NUTS) on level 2, henceforth referred to as "regions". Movements per region were calculated as a sum of movements within, to, and from the region. Thus, movements within a region were only counted once, whilst a movement between two regions was counted to both the receiving and sending region.

2.4. Calculation of network metrics

In this study, weighted and directed networks were constructed in snapshots of yearly aggregation windows to avoid seasonal bias (Nöremark et al., 2009, 2011). Movements between two holdings were considered a directed edge (also called a link) with a weight of the total number of animals moved per year. Several network metrics were calculated (Table 1) for the yearly networks to describe the characteristics of the network, wherein some consider weights, direction, or temporal aspect of the movements. The R-package *EpicontactTrace*

Table 1
Network metrics calculated per year in the study of Swedish cattle movements, 2005–2022.

Network metric	Description
Per holding	
In- and outgoing animals	The number of ingoing or outgoing animals directly to or from a holding in the network
In- and outdegree	The number of holdings connected to a holding through direct links of at least one in- or outgoing animal (Wasserman and Faust, 1994)
In- and outgoing contact chain	The number of holdings directly and indirectly connected to a holding through chronological movements of animals during the studied time frame (Dubé et al., 2008; Nöremark et al., 2011).
Global	
Edge density	Ratio between the number of apparent edges in the network and the number of possible edges (Wasserman and Faust, 1994)
Clustering coefficient	The tendency for a holding's direct contacts to also have direct contact with each other (Wasserman and Faust, 1994). The "triangle-based" definition was used, which calculates the ratio of closed triplets to all triplets in the network.
Reciprocity	Probability that edges between two holdings are mutual (animals moved in both directions) (Wasserman and Faust, 1994)
Average path length	The average of the shortest path (number of steps) between all pairs of holdings (Watts and Strogatz, 1998)
Giant strongly connected component (GSCC)	The largest component in the network in which all holdings can reach each other through directed links (both indirect and direct) (Kao et al., 2006)
Degree assortativity	The degree correlation of the pairs of holdings that are directly connected (Newman, 2003)

(Nöremark and Widgren, 2014) was used to calculate the in- and outgoing contact chain on the 31st of December of each year, based on events during the prior 365 days. The R-package *igraph* (Csardi and Nepusz, 2006) was used to calculate all other metrics, by aggregating networks per calendar year.

The complementary cumulative distribution functions (CCDFs) were calculated yearly for the holding level network metrics, for active holdings with at least one in- or outgoing animal. The CCDFs describe the probability that a metric is greater than a certain value, and were plotted with logarithmic scales on both axes. Previously, trends over time in livestock movement networks have been evaluated with the non-parametric Mann-Kendall trend test (Mann, 1945) by Mweu et al. (2013). The Mann-Kendall test, with modifications for autocorrelated data (Hamed and Rao, 1998), was used in the present study to investigate if the global network metrics changed significantly over time. In addition, the test provides the Kendall's τ statistic (a value between -1 and 1), which shows the magnitude of the trend and whether it is positive or negative.

To enable comparison of the Swedish network with similar studies from other countries (e.g., Dubé et al., 2011; Mweu et al., 2013; Fielding et al., 2019), random networks were generated with the Erdös-Renyi model (Erdös and Renyi, 1959). Similar to Fielding et al. (2019), 10,000 random directed networks were generated based on the yearly network for 2022. The network metrics (clustering coefficient, reciprocity, average path length, GSCC, degree assortativity) were considered significantly higher than the random networks if at least 95 % of the random networks had a lower value for the corresponding measure. In addition, it was investigated whether the 2022 network could be considered a "small-world network" as defined by Dubé et al. (2011), to compare with the same studies. This definition of a small-world network includes an average path length similar to, or shorter, than the Erdös-Renyi random network and a clustering coefficient at least 20 times greater than in the random network.

2.5. Constructing location change patterns (LCP)

To enable a comparison of patterns of between-holding movements per animal and lifetime, a "path" was constructed for each individual. Each holding that an individual had been kept at was enumerated by the chronological order of registration, because the actual holding identifier that an individual visited was not of interest, only the enumeration. These paths are henceforth referred to as Location Change Patterns (LCPs) or simply "patterns". For example, all individuals that were kept in just one holding had an LCP equal to "1". Individuals registered in two different holdings could have an LCP equal to "1 → 2" or if they returned to the first holding, "1 → 2 → 1", etc. To compare LCPs during the same period for all animals, only events during the first 5 years per animal were included (or less if the animal lived for a shorter duration). This time frame was chosen as dairy and beef cows usually live 5–6 years and because 95 % of all movements (n = 6521,397) were conducted with animals up to 5 years old. Thus, only animals born 2005–2017 were included in this dataset, as the event dataset covered events up until five years ahead from 2017 (the same dataset was also used to calculate the number of movements per animal, Table 2). A relatively large proportion of the animals had LCPs where the birth holding reoccurred as every second holding, i.e. these individuals were never moved more than one step away from the birth node. These animals were therefore aggregated into one group, henceforth referred to as "home-comers", under the condition that they returned to the birth holding at least once. LCPs in this group were, for example, "1 → 2 → 1" or "1 → 2 → 1 → 3" and examples are illustrated in Fig. 2.

Pearson's chi-squared test was used to analyse if the number of animals who were never moved (LCP "1") significantly changed for animals born in 2017 compared to 2005, as this was the most common pattern and because these animals do not contribute to the risk of disease spread through moving to another holding. The test was then also performed for the home-comers. Moreover, it was a point of interest to uncover if the home-comers were regularly moved to holdings where animals from various holdings were gathered (i.e. holdings with an indegree greater than one), as that could imply a higher risk of disease spread. Therefore, the "intermittent holdings" (IHs) in the LCPs of home-comers, defined as holdings registered in-between the records at the first holding (not the last holding in the pattern) (Fig. 2), were further analysed. The in- and outdegree of the IHs were analysed descriptively for both 2005 and 2022 (only IHs active in each year respectively, not considering when, or how many times, during the study period the holding was registered as an IH) and compared with the remainder of holdings. The values of in- and outdegree were divided into three categories: zero, one, or greater than one, based on the skewed distributions of in- and outdegree.

Furthermore, the time spent at the first IH was calculated for all home-comers born in 2005 and 2017. Additional characteristics of the holdings that were involved in home-comers' movements were also investigated. The herd size and proportion of females were calculated for holdings that were either registered as a birth holding (BH) or only registered as an IH (not BH) and compared with all other holdings. For each holding, the average of the herd size and proportion of females in June 1st was calculated, where June 1st was selected to enable comparisons with published statistics from SBA (Swedish Board of Agriculture, 2022).

2.6. Survival analysis (Nelson-Aale estimator and Cox proportional hazards model)

Firstly, the Nelson-Aale estimator was used to estimate the expected number of movements per day in an animal's life (cumulative hazard functions), stratified by 'sex' and 'birth years' (years 2005, 2011, and 2017, evenly distributed during the same period that was used in the analysis of LCPs). Secondly, a multivariable Cox proportional hazards model was built to assess how the 'birth year' and 'sex' of the animal, as

Table 2
Movements per animal and distribution of number of movements in the Swedish cattle population (during the first five years of an animal's life), per sex and birth years 2005 and 2017, respectively.

Sex	Birth year	Movements per animal		Number of animals per number of movements (%)			
		Median	Mean	0	1	2	> 2
Female	2005	0	0.46	188,074 (71)	49,050 (19)	19,623 (7)	8351 (3)
Female	2017	0	0.75	162,129 (65)	40,905 (16)	27,196 (11)	20,068 (8)
Male	2005	1	0.65	113,528 (41)	151,018 (55)	9338 (3)	3007 (1)
Male	2017	1	0.80	88,524 (35)	139,105 (55)	19,594 (8)	7172 (3)

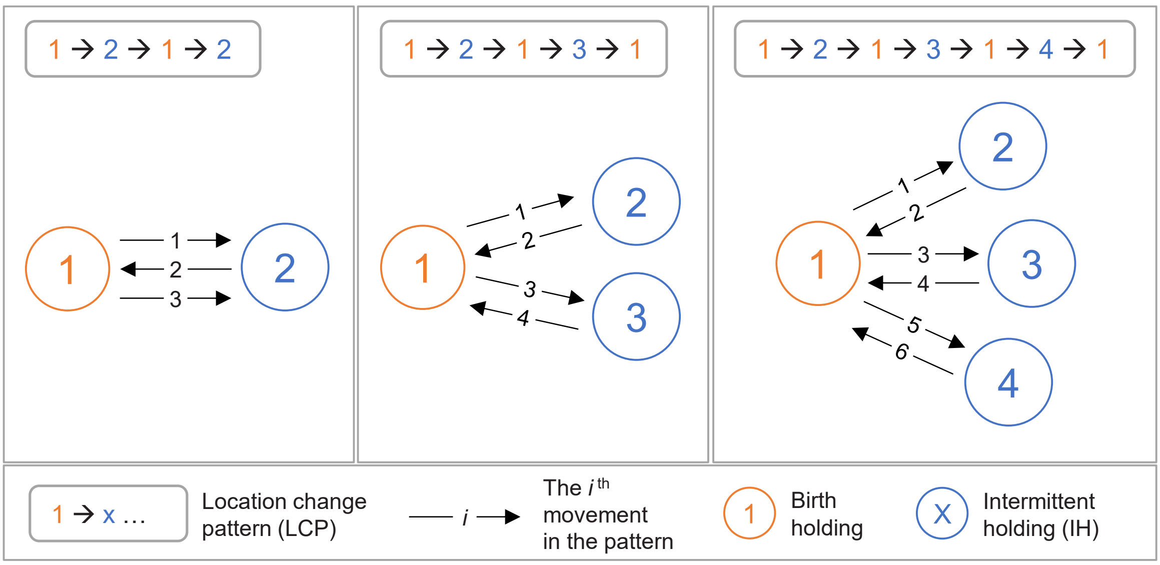

Fig. 2. Examples of Location Change Patterns (LCPs) of "home-comers", animals where every second registered holding was the birth holding, and who returned to the birth holding at least once.

well as the herd characteristics: 'herd size', 'proportion of females', 'in- & outgoing animals', and 'in- and outdegree', were associated with the risk of moving an animal. More specifically the outcome was defined as the time until which an animal was moved from one holding to another, i.e., 'time-to-movement'. In both survival analyses the data was structured as separate intervals for each period up to a movement, starting at the time of birth or the preceding movement, implying recurrent events for animals moved more than once. To adjust for recurrent events, the Nelson-Aale estimator was modified with a robust variance estimator while in the Cox proportional hazards model, the Prentice, Williams, and Peterson model was used including the total time from birth to each movement (i.e. PWP-TT), stratifying the data into groups based on the chronological number of each movement. Animals were censored either at time of death or at the end of the study period (2022–12–31). The herd level variables 'herd size' and 'proportion of females' were calculated at the start date of each time interval in the data, either at the holding where the animal was born or the holding to which the animal had previously been moved. Additionally, the number of 'in- and outgoing animals', as well as 'in- and outdegree', were calculated for the same holdings and time points, which considered events 365 days prior to each date. This time-window was chosen for consistency with the network analysis and to avoid effects of seasonal variation in movements, as observed by Nöremark et al. (2009). Resultingly, animals born during 2005 were excluded from the Cox proportional hazards model, as events 365 days prior to 2005 were not known.

A subset of 10,000 randomly chosen animals was initially used for the construction of the Cox proportional hazards model due to computational limitations. Martingale residuals were plotted against each continuous covariate to assess whether the assumption of linear relationships between each covariate and the log-hazard was approximately fulfilled. The variables 'birth year' and 'proportion of females' were kept as continuous following the assessment of linearity. 'Herd size', 'in- and outgoing animals', and 'in- and outdegree' were categorised due to non-linear relationships with the log-hazard, skewed distributions, and to make the model interpretation easier. Both 'herd size' and 'in- and outgoing animals' were categorised into three equally sized groups per covariate, while 'degree' was categorised into three groups with the values: zero, one, or greater than one, as these categories were considered to be of certain interest from a disease spread perspective. Univariable models were constructed for each covariate and the significant covariates were then added stepwise to the multivariable model (forward selection process). Akaike's information criteria (AIC) was used to compare the fit, where the covariate was kept if it decreased the AIC of the model. Previously, White et al. (2010) found significant interactions between enterprise type (dairy or suckler herds) and sex of the animal, regarding the hazard for Irish cattle to be moved from the birth herd. This was also assumed to be true for Swedish cattle, meaning that the effect of gender on the hazard to be moved was assumed to depend on the type of production. However, as production type was not known, the combination of herd size and proportion of females was used as a proxy for production type (Swedish Board of Agriculture, 2022). Thus, pairwise interactions of all combinations of the covariates 'herd size', 'proportion of females', and 'sex' were added stepwise to the model, again by using AIC to decide whether to include the interactions. Multicollinearity was assessed by calculating variance inflation factors (VIF), firstly for variables in the model without interactions and secondly when the interaction terms were added. The proportional hazards assumption was assessed visually using plots of scaled Shoenfeld residuals for each covariate. The overall fit of the final model was evaluated by plotting Cox-Snell residuals, as well as by assessing the concordance statistic and the pseudo R-square value proposed by Nagelkerke et al. (1984). In addition, bootstrapping was used to validate the model. Lastly, when the final model was constructed, it was rebuilt with all animals (born after 2005) and compared with the results when only using a subset of animals. The R-package *survival* (Therneau, 2022) was used to build the survival models, and the function *validate* from the R-package *rms* (Harrell, 2025) was used to validate the Cox proportional hazards model using bootstrap.

3. Results

3.1. Descriptive statistics of the Swedish cattle population and movements

Whilst the cattle population and number of active holdings decreased over time, the average number of animals per holding (holding size) and number of reported movements increased (Fig. 3). Reported movement distances had a positively skewed distribution, with a median distance of approximately 21 km (19 km for females and 21 km for males) in 2005 which decreased to 12 km in 2022 (8 km for females and 18 km for males).

There were regional differences in the development of reported movements over time, but similarities between the four regions that had most movements in 2022 (SE23, SE21, SE12 and SE22), with increases of around 50 % over the study period (Fig. 4). For all regions, the proportion of movements made by female cattle increased over time.

The mean number of movements per animal increased and it became more common for animals to be moved two or more times within their lifetime. For animals born in 2005 and 2017 it was most common for female cattle to never be moved and for male cattle to be moved once (Table 2).

3.2. Network metrics

The number of active holdings with no reports of ingoing animals were 14,780 out of 29,868 (49 %) in 2005, 10,042 out of 23,739 (42 %) in 2014, and 9067 out of 22,341 (41 %) in 2022. Active holdings with no reported outgoing animals were 14,123 (47 %) in 2005, 9431 (40 %) in 2014, and 8493 (38 %) in 2022. The number of in- and outgoing animals, degree, and contact chain all had positively skewed distributions (Fig. 5). Throughout the study period, the probability for a holding to have an indegree > 1 decreased (Fig. 5B). This pattern was also observed for in- and outgoing contact chains (Fig. 5 C and 5 F). In contrast, the probability increased for holdings to have more in- and outgoing animals (Fig. 5 A and 5D).

The number of holdings in the yearly networks as well as the number of edges (Table 3) significantly decreased over the study period ($\tau = -0.95$, $p < 0.001$ and $\tau = -0.90$, $p < 0.001$ respectively). Significant positive trends were observed for edge density ($\tau = 0.52$, $p = 0.035$), clustering coefficient ($\tau = 0.87$, $p < 0.001$), reciprocity ($\tau = 0.99$, $p < 0.001$), and average path length ($\tau = 0.63$, $p < 0.001$), whilst degree assortativity significantly decreased ($\tau = -0.71$, $p < 0.001$). The lowest percentage of holdings in the giant strongly connected component (GSCC) were found in years 2005 and 2018 (Table 3) but the metric showed no significant trend throughout the study period ($\tau = 0.16$,

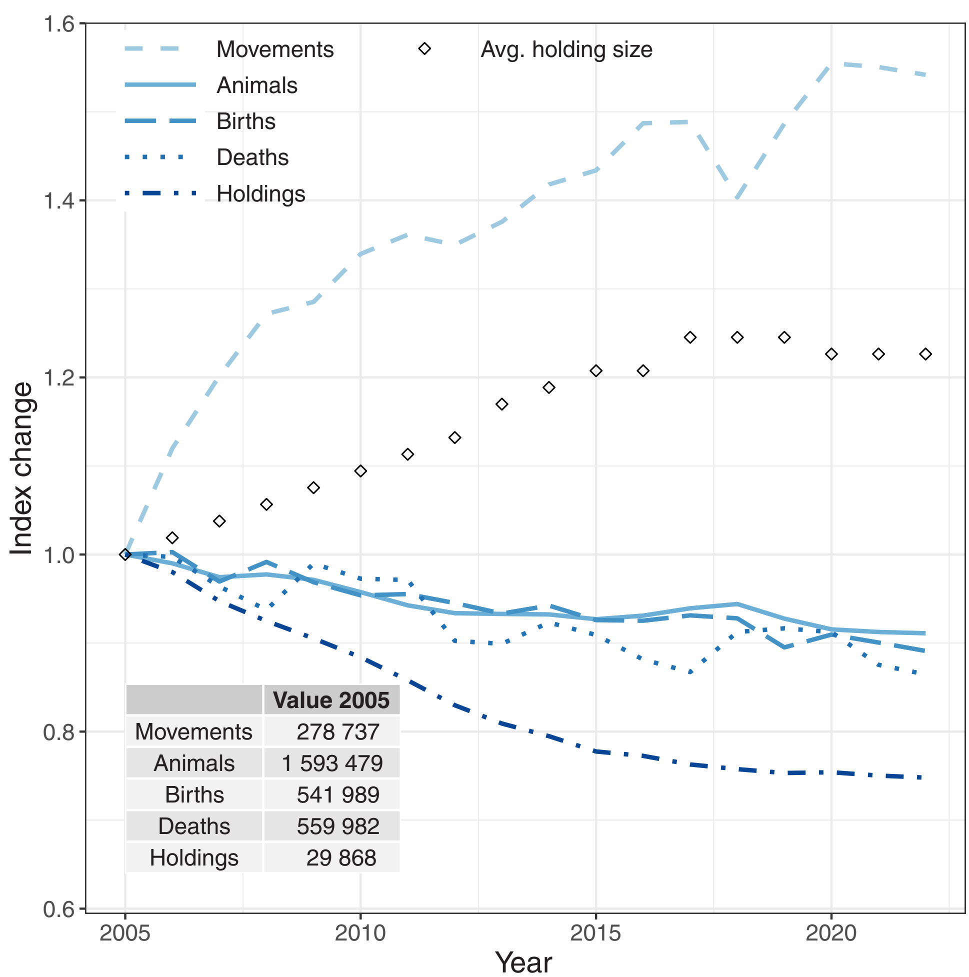

Fig. 3. Changes in reported movements, animals, births, deaths, active holdings, and average (avg.) holding size (number of animals per holding), between 2005 and 2022 in the Swedish cattle population. The figure shows the index change in yearly values, based on values in 2005 which are provided in the table inside the plot.

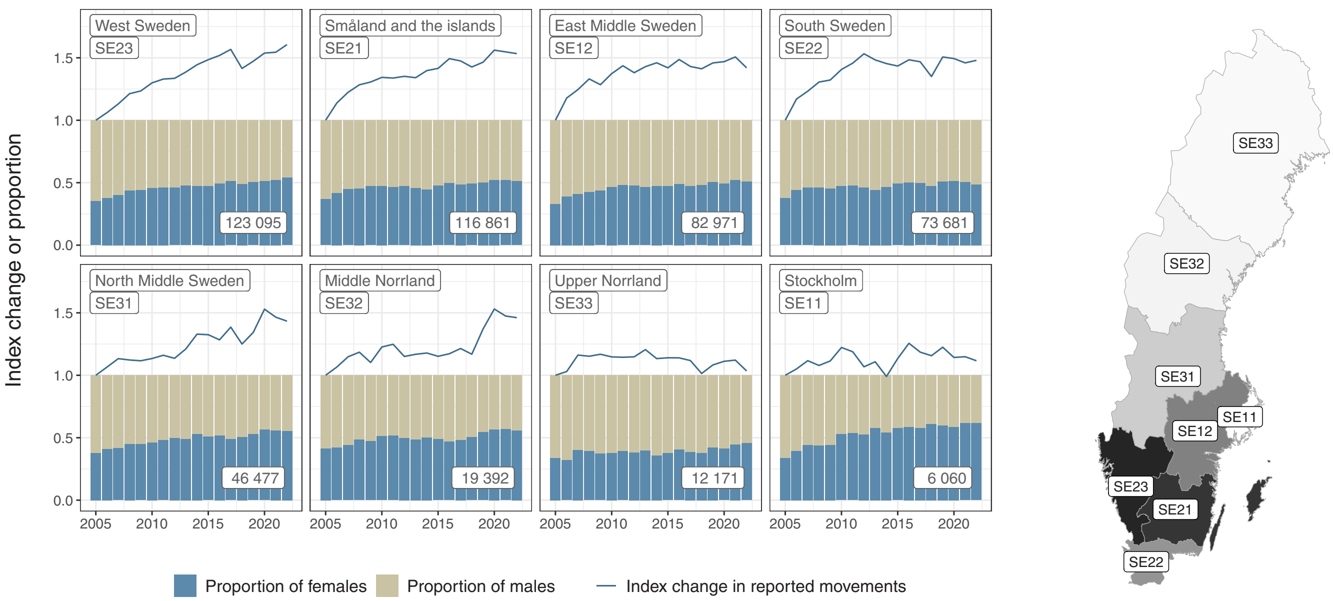

Fig. 4. Change in reported movements between 2005 and 2022 in the Swedish cattle population, divided by region (Nomenclature of Territorial Units for Statistics, NUTS, level 2). The figure shows the index change in yearly values, based on values in 2005. The total number of movements in 2022 (to, from, and within each region) is provided in the lower right corner in each subfigure and illustrated in the map where darker colour indicates a higher number of movements.

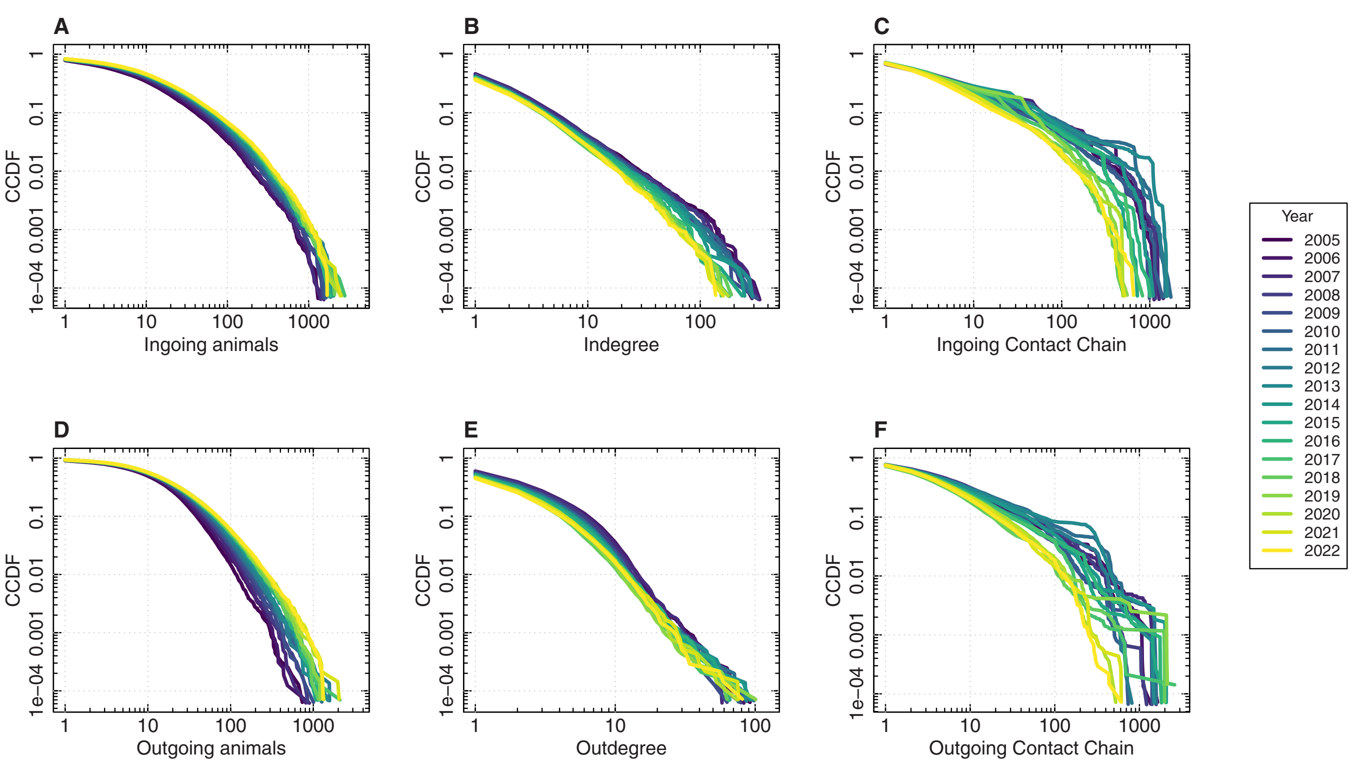

Fig. 5. The complementary cumulative distribution functions (CCDFs) for six holding-level network metrics (yearly aggregation windows) in the Swedish cattle movement network. Only holdings with at least one reported in- or outgoing animal are included. The y-axis shows the probability of having a value higher than the corresponding value on the x-axis. For example, the probability of having an indegree larger than one was approximately 0.5 in 2005 (for holdings with at least one ingoing animal).

$p = 0.054$). The observed network in 2022 significantly differed from the random networks for all investigated metrics. The clustering coefficient was approximately 84 times greater in the observed network in 2022 and the average path length was almost 8 times longer, compared to the random networks. In addition, the reciprocity was higher in the observed network while the percentage of holdings in GSCC and degree assortativity were lower, compared to the random networks (Table 3).

3.3. *Location change patterns (LCP)*

Table 4 shows the most common LCPs for all animals born between 2005 and 2017. For females LCP “1” was most common, followed by LCP

Table 3
Global metrics for yearly networks of Swedish cattle movements between holdings. Median values and interquartile ranges (IQR) of the metrics for 10,000 randomly generated networks (based on the 2022 network) are also provided.

Year	Number (%) of holdings[a]	Number of edges	Edge density [%]	Clustering coefficient [%]	Reciprocity [%]	Average path length [steps]	GSCC* [% of network]	Degree assortativity [-1, 1]
2005	22,630 (75.8)	48,108	0.0094	0.83	9.8	50.6	8.8	0.009
2006	22,510 (76.9)	49,846	0.0098	0.83	13.0	53.0	12.8	0.021
2007	21,986 (77.7)	49,091	0.0102	1.01	13.8	57.9	16.2	0.024
2008	21,284 (77.0)	46,121	0.0102	1.03	16.7	66.8	14.8	0.019
2009	20,961 (77.5)	42,975	0.0098	1.07	19.0	83.4	14.3	0.025
2010	20,404 (77.3)	42,209	0.0101	1.09	19.6	100.6	15.0	0.017
2011	19,805 (77.3)	40,721	0.0104	1.09	21.5	86.8	15.2	−0.001
2012	19,193 (77.4)	38,920	0.0106	1.11	22.4	69.6	16.0	−0.004
2013	18,755 (77.6)	37,695	0.0107	1.23	23.3	60.3	15.5	−0.003
2014	18,442 (77.7)	37,033	0.0109	1.36	23.9	73.4	14.5	0.007
2015	18,280 (78.7)	36,463	0.0109	1.52	25.8	85.9	15.2	0.019
2016	18,273 (79.2)	35,981	0.0108	1.64	28.9	80.7	17.6	−0.005
2017	17,961 (78.8)	34,149	0.0106	1.75	29.5	84.4	16.9	−0.017
2018	17,452 (77.1)	31,119	0.0102	1.50	31.8	120.4	9.3	−0.008
2019	17,469 (77.7)	32,179	0.0105	1.71	32.5	95.7	14.3	−0.018
2020	17,647 (78.4)	33,308	0.0107	1.75	32.2	102.7	16.1	−0.022
2021	17,452 (77.9)	32,724	0.0107	1.87	33.1	98.0	15.5	−0.019
2022	17,211 (77.0)	31,422	0.0106	1.67	34.6	117.1	13.9	−0.022
Median values (with IQR in parenthesis) from random directed networks with the same number of holdings and edge density as the 2022 network[b]								
				0.02[c] (0.02, 0.03)	0.01[c] (0.01, 0.01)	14.7[c] (14.6, 14.8)	55.0[c] (54.6, 55.5)	0.000[c] (−0.004, 0.004)

[a] The number (and percentage) of active holdings (holdings that kept at least one animal at some point during the year) that were also included in the yearly networks (having at least one ingoing or outgoing movement).
[b] 10,000 random directed networks were generated with the Erdös-Renyi model.
[c] Significantly higher or lower value compared to the 2022 network.
* Giant strongly connected component.

"1 → 2". In contrast, for males the most common patterns were LCP "1 → 2" and secondly LCP "1". However, in total, 1788 unique LCPs were identified, ranging from 217 unique patterns for animals born in 2005 to 611 unique patterns for animals born in 2017. Of all unique LCPs for the entire period, 893 were unique to a single individual.

Significantly fewer animals (irrespective of sex) born in 2017 were never moved (LCP "1") (50 %: 250,672 out of 504,717), compared to 2005 (56 %: 301,602 out of 541,989) (Chi-squared test, $p < 0.001$). The number of home-comers was significantly higher for animals born in 2017 (9 %: 44,245 out of 504,717) than 2005 (4 %: 21,101 out of 541,989) compared to animals with other LCPs (Chi-squared test, $p < 0.001$). Approximately 14 % ($n = 35{,}542$) of females and 3 % ($n = 8703$) of males born in 2017 were home-comers, and the corresponding values for birth year 2005 were 7 % ($n = 18{,}850$) and 1 % ($n = 2251$). The number of animals with other LCPs with more than one movement also increased (Tables 2 and 4). For home-comers, the median time spent at the first IH was 150 days (4.9 months) for females and 142 days (4.7 months) for males born in 2017. Corresponding values for animals born in 2005 were 154 days (females) and 142 days (males).

For holdings that were registered, at least once during the study period, as an IH in the LCPs of home-comers, it became more common to have an indegree or and outdegree of one and less common to have values greater than one, when comparing 2022 with 2005 (Table 5). Holdings that were registered as BHs ($n = 8259$, out of which 3510 had also been registered as IHs) were in general larger (on average 106 animals, IQR: 28–133) with higher proportion of females (on average 0.75, IQR: 0.68–0.86) compared to holdings that were only registered as IHs but not BHs ($n = 11{,}248$). The latter had an average size of 24 animals (IQR: 3–22) and an average proportion of females of 0.46 (IQR: 0.27–0.67). Holdings that were never registered as neither BH nor IH ($n = 25{,}126$) had an average size of 25 (IQR: 3–26) and an average proportion of females of 0.54 (IQR: 0.29–0.78).

3.4. Survival analysis

Male cattle had a greater hazard of being moved compared to females, particularly during their first year of life whereas females were most likely to be moved during approximately their first 2.5 years (Fig. 6B). For males born in 2017 the hazard of being moved at around 20 days of age was greater compared with animals born in earlier years of the study period (Fig. 6 A). Among males born in 2005, 2011, or 2017, the median age at censoring was 556 days (interquartile range, IQR: 452–699) and 3 % ($n = 26{,}407$) were over three years old at the time of censoring. The corresponding values for females was a median age of 1363 days (IQR: 791–1983) with 60 % ($n = 464{,}918$) being older than three years when censored.

During the process of building the multivariate Cox proportional hazards model, the assumption of proportional hazards was considered to hold for all covariates and interactions, therefore no adjustment was made. All investigated covariates were significant in the univariate models, and each covariate and examined interaction term improved the model AIC and were thus included. The VIFs of the variables, not including the interaction terms, were between 1.67 and 3.25, indicating low correlation among predictors. In the full model, the variables included in the interaction terms showed moderate to high correlation, as is expected. The model had a concordance of 0.81 and a R-squared value of 0.35, and when corrected after bootstrapping the R-squared value remained at 0.35, indicating that the model generalizes well to new data. Most of the Cox-Snell residuals followed the expected distribution and the deviating observations generally had longer time-to-movement. The final model (Table 6) included 8649,097 animals and a total of 14,874,485 observations with almost identical hazard ratios as the model with the subset of 10,000 animals. Additionally, the final model had a concordance of 0.81 and R-squared value of 0.34. The median value of time-to-movement (of the 6225,597 observations that were not censored) was 145 days (IQR: 73–255).

The hazard for male cattle to be moved was higher in a holding with a high proportion of females, compared to a holding with a low proportion of females, regardless of herd size category (Fig. 7). For female cattle, the hazard to be moved was greater in small holdings, compared to medium and large holdings. In addition, in a small holding, the hazard for females to be moved was greater when the proportion of females was

Table 4
Number of animals born per year in the Swedish cattle population, for the most common Location Change Patterns (LCPs) (during five years). The table is divided by sex.

Location Change Pattern (LCP)	Birth year													Total	Proportion of all animals
	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017		
Female cattle															
1	188,074	183,373	177,202	181,861	174,561	170,382	171,220	171,120	167,023	166,334	160,117	160,773	162,129	**2234,169**	0.331
1 → 2	49,050	49,701	45,057	44,490	42,585	42,295	41,350	39,329	38,385	39,246	40,406	40,035	40,905	**552,834**	0.082
1 → 2 → 1	13,858	16,238	17,049	18,872	19,724	20,766	22,110	22,487	22,963	22,918	21,951	21,664	21,753	**262,353**	0.039
1 → 2 → 3	5765	6152	6314	6329	6972	6666	6455	5819	5705	5928	6220	5943	5443	**79,711**	0.012
1 → 2 → 1 → 3 → 1	945	1313	1721	1899	2306	2750	2718	2973	2973	3144	3216	3401	3470	**32,829**	0.005
1 → 2 → 1 → 2 → 1	1316	1606	1780	2175	2211	2335	2545	2630	2665	2888	2887	2649	3172	**30,859**	0.005
1 → 2 → 3 → 2	1312	1496	1633	1907	2261	2195	2359	2301	2627	2640	2791	2313	2281	**28,116**	0.004
1 → 2 → 1 → 3	1337	1846	1985	2278	2200	1773	2162	2329	2206	2357	2399	2963	2273	**28,108**	0.004
Remaining LCPs	3441	4431	4942	5581	6175	6256	6293	6473	7199	8224	8645	8557	8872	**85,089**	0.013
Total (female)	**265,098**	**266,156**	**257,683**	**265,392**	**258,995**	**255,418**	**257,212**	**255,461**	**251,746**	**253,679**	**248,632**	**248,298**	**250,298**	**3334,068**	**0.494**
Male cattle															
1 → 2	151,018	152,569	150,243	151,665	144,718	144,118	146,072	141,595	141,793	142,389	138,841	136,335	139,105	**1880,461**	0.279
1	113,528	108,746	100,523	102,082	101,570	96,874	90,823	90,932	87,278	88,145	87,671	88,642	88,524	**1245,338**	0.185
1 → 2 → 3	7681	9639	9902	10,691	11,061	11,877	14,249	14,639	14,324	14,784	14,083	14,513	14,046	**161,489**	0.024
1 → 2 → 1	1657	2545	2718	3049	3317	3277	3560	3574	3861	4497	5163	5355	5548	**48,121**	0.007
1 → 2 → 3 → 2	1333	1504	1818	1889	1913	1953	2161	2585	2859	3168	2807	3087	2169	**29,246**	0.004
1 → 2 → 1 → 3	307	459	538	766	927	982	1078	1186	1123	1284	1461	1756	1858	**13,725**	0.002
Remaining LCPs	1367	1843	2017	1902	2513	2482	2606	2305	2846	2773	3178	3464	3145	**32,441**	0.005
Total (male)	**276,891**	**277,305**	**267,759**	**272,044**	**266,019**	**261,563**	**260,549**	**256,816**	**254,084**	**257,040**	**253,204**	**253,152**	**254,395**	**3410,821**	**0.506**
Total	**541,989**	**543,461**	**525,442**	**537,436**	**525,014**	**516,981**	**517,761**	**512,277**	**505,830**	**510,719**	**501,836**	**501,450**	**504,693**	**6744,889**	**1.000**

low, compared to a high proportion of females (Fig. 7). Furthermore, the hazard for an animal to be moved was approximately twice as great if the holding during the preceding year had 67–4005 ingoing animals compared to holdings with 0–3 ingoing animals (Table 6). Similarly, the hazard to be moved was more than three times higher at holdings with 52–2669 previously outgoing animals, compared to holdings with 0–8 outgoing animals (Table 6). At holdings with an outdegree of 1 or > 1 during previous year, the hazard was higher, compared to holdings with a previous outdegree of 0. In contrast, animals at holdings with an indegree > 1 during the preceding year had a lower hazard to be moved, compared to animals at holdings with an indegree of 0 or 1 (Table 6). Further, the hazard for animals to be moved increased with birth year, by approximately 1 % increase per year (Table 6).

4. Discussion

The results show that the number of cattle movements in Sweden increased throughout the last two decades, despite the decreasing cattle population and trend towards fewer but larger holdings. However, there were regional differences, where the increase in movements was most pronounced in southern Sweden, which coincides with where most of the herds are located (Nöremark et al., 2009). Interestingly, there are differences when comparing trends in movements between countries. For example, a decrease in movements was found in both France (Dutta et al., 2014) and the United Kingdom (Duncan et al., 2022), whereas, similar to the present study, a significant increase in cattle movements was observed in Denmark (Mweu et al., 2013). This is despite a similar shift towards fewer and larger farms in several countries, e.g., in Denmark (Barkema et al., 2015), Great Britain (Fielding et al., 2019), and Canada (Comper et al., 2023). The drivers for the structural changes are likely similar between countries, e.g., technological innovations, economic incentives to increase productivity, political decisions and regulations (e.g. through EU), consumer demands, demographic shifts, etc. (Breustedt and Glauben, 2007; Barkema et al., 2015; Hajdu et al., 2020). However, the effect of the structural changes on the movement network is likely related to country specific differences on how cattle are traded, for example, directly between holdings or via livestock markets (Fielding et al., 2019).

The trajectory of epidemics on a network is not solely explained by the number of movements, animals and holdings, but is also dependent on other network characteristics. The degree assortativity in the Swedish network increased over time, and the comparison between the observed and random network in 2022 indicated the existence of "hubs": i.e. holdings connected to many holdings that in turn have fewer contacts. Hubs may rapidly pass on a disease to connected holdings (Kiss et al., 2006b), but the risk of introducing or passing on pathogens is also often highly dependent on the number of direct connections to other holdings, measured by indegree and outdegree (Frössling et al., 2012; Gates and Woolhouse, 2015). The positively skewed distribution of indegree and outdegree revealed that there are still a few holdings within the Swedish network that, unlike the majority, have a great number of contacts, as previously shown by Nöremark et al. (2011). However, the proportion of holdings with a large indegree decreased over the study period. In addition, epidemics generally spread more slowly on disassortative networks than in random networks (Kiss et al., 2008). Targeting control measures towards hubs can also effectively reduce the size of the giant strongly connected component (GSCC) (Newman, 2002), a metric that has been used to estimate the potential size of an epidemic (Kiss et al., 2006a). The proportion of nodes in the GSCC in Sweden was low, both compared to the random networks generated in this study and compared with, e.g., yearly networks in Great Britain (ranging from 34.0 % to 57.5 % between the years 2001 and 2015) (Fielding et al., 2019). However, because the GSCC does not consider temporal aspects of the movements, contact chains have been suggested as a more suitable metric (Dubé et al., 2011; Nöremark et al., 2011). Subsequently, because the results suggest a decrease of both in- and outgoing contact chains in

Table 5
Number of active cattle holdings in Sweden for the years 2005 and 2022, per different values of in- and outdegree. The table is divided by two categories of holdings: first holdings that were registered, at least once between 2005 and 2022, as an intermittent holding (IH) in Location Change Patterns (LCP) of "home-comers", and secondly the remaining holdings.

	IHs in LCPs of home-comers				Other holdings *(never acting as IHs)*			
	2005		2022		2005		2022	
	n	%	n	%	n	%	n	%
total	**8265**	**100**	**7871**	**100**	**21,603**	**100**	**14,470**	**100**
indegree 0	3051	37	2063	26	11,729	54	7004	48
indegree 1	2483	30	3749	48	5630	26	4735	33
indegree > 1	2731	33	2059	26	4244	20	2731	19
outdegree 0	2888	35	2024	26	11,235	52	6469	45
outdegree 1	2056	25	3571	45	4283	20	4076	28
outdegree > 1	3321	40	2276	29	6085	28	3925	27

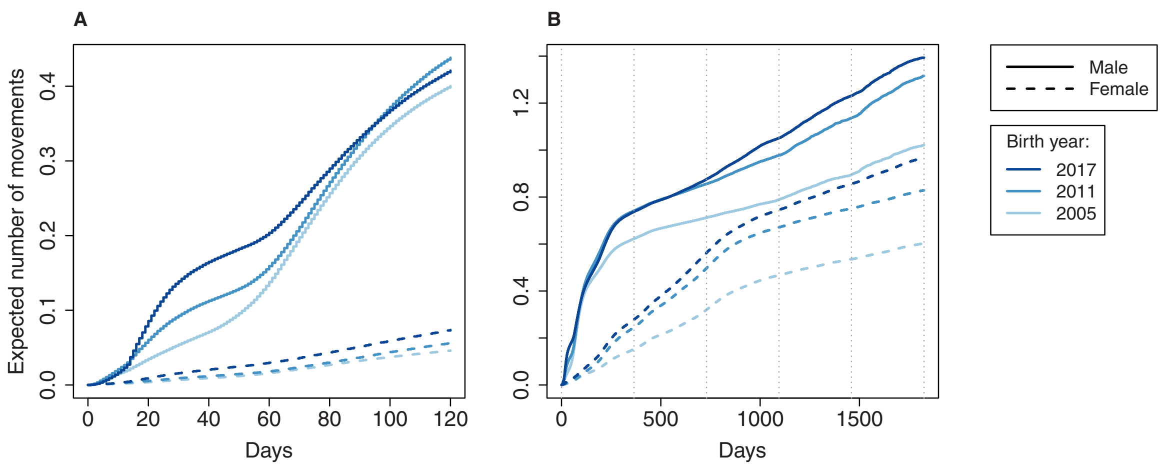

Fig. 6. Cumulative hazards (expected number of movements) at a certain age in days for Swedish cattle, based on Nelson-Aale estimates. A. The first 120 days of the animals' lives. B. Five years of animal life, with dotted vertical lines dividing the period by year. Three percent of the male cattle and 60 % of female cattle included in the figure were over three years of age at the time of censoring.

Sweden since 2005, the potential epidemic size of an outbreak may have decreased over time.

The Swedish network became significantly more clustered and denser over time. This is similar to the Danish cattle network (Mweu et al., 2013), whereas in Great Britain the density increased while clustering remained stable over time (Fielding et al., 2019). In addition, the average path length in the Swedish network increased over time and was in 2022 substantially larger than in random networks, implying that the criteria for a small-world network (Dubé et al., 2011) were not met, despite the large clustering coefficient. This is in contrast to several countries where the small-world network criteria is commonly met in cattle movement networks (Natale et al., 2009; Dubé et al., 2011; Mweu et al., 2013; Fielding et al., 2019). A small-work network might facilitate disease spread within clusters and between topologically distant clusters (Watts and Strogatz, 1998). However, the definition of the clustering coefficient used in the present study does not account for the directions or weights of the movements. Thus, it is important to be cautious when interpreting the influence of the clustering coefficient on disease dynamics in these networks. In addition, there are limitations in the comparison with Erdös-Renyi random networks, as these seldom resemble real-world networks (Koutrouli et al., 2020). Therefore, using other random network models with properties more similar to livestock movement networks, e.g., scale-free random networks (Barabási and Albert, 1999), could provide further insights of the properties of the cattle network.

Furthermore, many of the analysed network metrics are based on static networks, and hence do not account for dynamical and temporal properties of the network. This leads to limitations as pathogen transmission through livestock movements depends not only on chronological ("time-respecting") sequence of movements between holdings, but also the time intervals between those movements, and properties of a pathogen, e.g., infectious period (Holme and Saramäki, 2012; Enright and Kao, 2018). Consequently, interventions based on static network metrics may affect the course of an epidemic differently when comparing fast and slow transmitting pathogens, although targeted measures may be advised in both cases (Chaters et al., 2019). In addition to contact chains, which account for time-respecting paths, there are further extensions of network metrics that also account for properties of a pathogen. For instance, Frössling et al. (2014) suggested a method to identify holdings with a high risk of disease introduction, accounting for movement directions, temporal aspects of both the movements and pathogen, number of animals in each batch along with disease prevalence. Moreover, there are frameworks for disease spread models, such as SimInf (Widgren et al., 2019), which allows for a simulation of spread both within and between herds, using disease specific parameters and true movement data. For instance, a recent Swedish study (Rosendal et al., 2020) used SimInf to model the spread of *Mycobacterium avium* subsp. *paratuberculosis* (a slow-spreading pathogen with an incubation period that may range from 2 to 5 years) on the Swedish cattle movement network between 2005 and 2017. Based on this modelling it was shown that, in most of the simulations, the outbreak died out over the study period (starting with one single infected holding), and surveillance based on annual random sampling was in fact more sensitive than targeted sampling based on indegree. Through data driven disease spread modelling it is also possible to account for dynamic herd sizes and age- and sex structure, both for the animals within a herd and for the

Table 6
Results from a multivariable Cox proportional hazards model with the outcome "time-to-movement", for Swedish cattle (born 2006–2022). The final model included 8649,097 animals and 14,874,485 observations.

Variable	Level	Hazard ratio	Confidence interval, 95 %	p-value
Birth year (per year)		1.01	1.01, 1.01	< 0.001
Sex	Female	(Reference)		
	Male	0.05	0.05, 0.05	< 0.001
Herd size	Small (1−99)	(Reference)		
	Medium (100−257)	0.26	0.25, 0.26	< 0.001
	Large (258–4592)	0.07	0.07, 0.07	< 0.001
Proportion of females[a]		0.86	0.86, 0.86	< 0.001
Sex * Herd size	Female * Small	(Reference)		
	Male * Medium	1.93	1.92, 1.93	< 0.001
	Male * Large	2.83	2.81, 2.84	< 0.001
Sex * Proportion of females[a]	Female * Proportion of females[a]	(Reference)		
	Male * Proportion of females[a]	2.53	2.52, 2.54	< 0.001
Herd size * Proportion of females[a]	Small * Proportion of females[a]	(Reference)		
	Medium * Proportion of females[a]	1.13	1.13, 1.14	< 0.001
	Large * Proportion of females[a]	1.38	1.37, 1.38	< 0.001
No. of ingoing animals[b]	0 – 3	(Reference)		
	4 – 66	1.51	1.50, 1.51	< 0.001
	67 – 4005	2.10	2.10, 2.11	< 0.001
No. of outgoing animals[b]	0 – 8	(Reference)		
	9 – 51	1.93	1.92, 1.93	< 0.001
	52 – 2669	3.41	3.39, 3.42	< 0.001
Indegree[b]	0	(Reference)		
	1	0.99	0.99, 1.00	< 0.001
	> 1	0.65	0.65, 0.65	< 0.001
Outdegree[b]	0	(Reference)		
	1	1.59	1.58, 1.60	< 0.001
	> 1	1.51	1.50, 1.51	< 0.001

[a] Per 20 % increase in proportion of females
[b] 365 days prior

moved animals, as was incorporated in the model by Rosendal et al. (2020). This may improve epidemiological models and analyses further, as characteristics of animals may be associated with their susceptibility to infections as well as the risk of being moved between holdings.

The results from the survival analysis are in line with the report "A snapshot of the cattle sector in June 2021" (Swedish Board of Agriculture, 2022), showing that the majority of sales of cattle born in 2017 (registered to SBA) were male cattle sold from dairy holdings (holdings with a high proportion of female cattle and usually a larger herd size) to beef producers. Similarly, White et al. (2010) demonstrated that bull calves at dairy holdings in Ireland had a greater hazard of being moved, compared to other animals and other types of holdings. Additionally, the present study showed that it became more likely over time to move young calves, which may impact disease spread as young calves have naïve immune systems and may be more susceptible to infections. Young calves are also more likely to carry undetected infections, e.g., due to the lack of testing (Byrne et al., 2022). The results also show that holdings that have previously introduced cattle from multiple holdings are less likely to have outgoing movements. This might be explained by expanding holdings or beef producers purchasing calves for slaughter. In contrast, Hidano and Gates (2019) demonstrated that in New Zealand larger previous values of indegree led to a higher probability of selling cows, but their study population was limited to dairy herds which could explain this difference. Additionally, Hidano and Gates (2019) showed that dairy cows with a higher frequency of being sold in the past were more likely to be sold again. Similarly in France, variables reflecting past trading events were important when predicting sales of veal calves (Marsot et al., 2022), despite the difference in production systems and study populations between these two studies. Overall, this highlights the importance of both herd- and animal characteristics for between-holding movements. However, additional variables of potential relevance could have been included in the Cox proportional hazards model in the present study, such as past trading events per animal, breed, season, region, production parameters, or social factors, as well as accounting for dependencies between observations from the same herd. Thus, to obtain a deeper understanding of the risk factors associated with moving animals, the model could be extended in future studies.

Although male cattle in Sweden were often moved once in their lifetime and female cattle were typically never moved, there was an increase during the study period of home-comers, which is connected to the increased reciprocity in the network. As expected, most home-comers were female, as dairy and suckler cows live longer and thus move more times between pastures. From a disease spread perspective, a relevant aspect to consider is whether IHs have large in- and outdegrees.

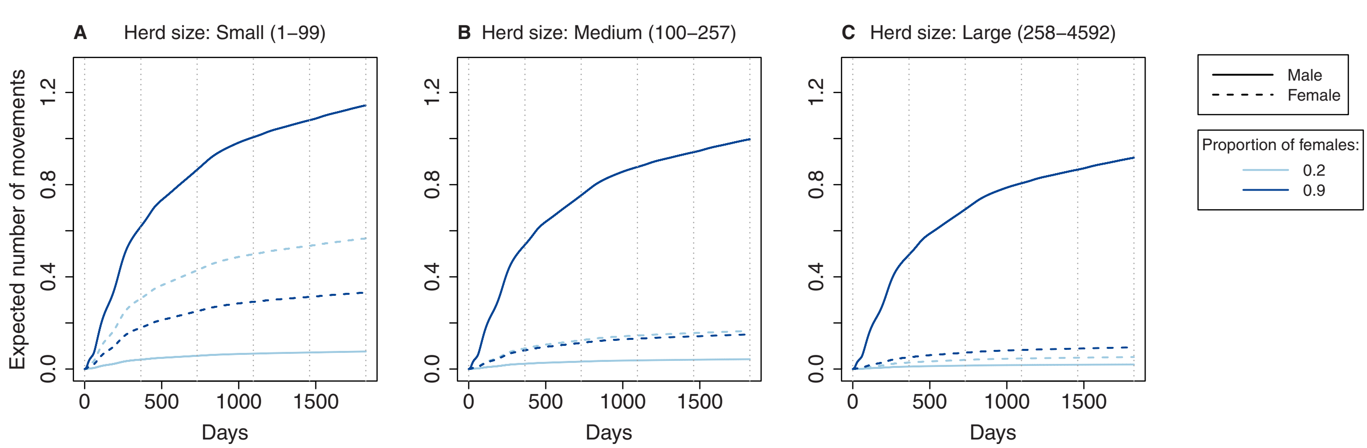

Fig. 7. Cumulative hazards (expected number of movements) at a certain age in days for Swedish cattle, derived from a multivariable Cox proportional hazards model with interaction effects between the covariates: 'sex', 'herd size', and 'proportion of females'. Each subfigure shows different categories of 'herd sizes', with the range of number of animals in parenthesis. In all figures, the covariate 'birth year' is 2022, and 'in- and outgoing animals' as well as 'in- and outdegree' are set as the lowest categories. The figures show up to five years of the animals' lives, with dotted vertical lines dividing the periods by year.

Interestingly, the proportion of IHs with an in- or outdegree > 1 decreased over the study period, and the proportions were in 2022 only slightly greater than for other holdings. Thus, IHs did not seem to mix animals from various herds to a large extent. Furthermore, the characteristics of the BHs were similar to the properties of dairy farms (Swedish Board of Agriculture, 2022), whilst in contrast, the IHs appeared to be non-dairy farms. In addition, the time that home-comers spent at the first IH suggests that these holdings might be pastures. However, it should be noted that movements between holdings and pastures owned by the same owner in proximity are excepted from the requirements to report to the central database for bovine animals (CDB), but are required to be documented in internal records (SJVFS 2007:12). Therefore, another plausible explanation for the increase in home-comers could be an increased tendency for agricultural companies to own various holdings and pastures further away from each other, between which movements are required to be reported to CDB. It may also have become more common with agreements of tenancy of holdings or pastures between different owners. It would be of interest to investigate this further, which would be facilitated if the holding types were available in CDB. The observed changes may also be partly explained by amended reporting requirements over time. More specifically, in 2016 it became acceptable to report movements between holdings in proximity with the same owner electronically to the CDB, instead of keeping internal records (SJVFS 2007:12 through amendment SJVFS 2015:44). In addition, the digital reporting systems have developed over time. Thus, the tendency to report movements between pastures and holdings owned by the same owner, as well as the interpretation of reporting requirements, may have varied over time and by region.

Overall, the structural changes within the Swedish cattle sector are a potential underlying cause for many changes in movement practices. Another example of this could be if the home-comers represent heifers moving from dairy to heifer hotels (contract rearing of dairy heifers), which is a probable consequence of the structural changes, i.e. a development towards both more specialised and efficient management practises (Grimstedt, 2019). Tratalos et al. (2020) likewise discuss an increase in heifer hotels in Ireland. However, the analysis of the IHs did not seem to suggest a significant increase in heifer hotels with a high indegree. In addition, given the proportion of females on the IHs, it appears that the majority of these holdings were not specialised heifer hotels. Furthermore, the structural changes have also caused small dairy farms to close and facilitated the formation of larger dairy farms (Swedish Board of Agriculture, 2022), which may have implied both an increase in movements as larger holdings purchase animals from closing farms, and possibly a decrease in indegree as there are fewer farms to purchase animals from. It is also possible that holdings have changed production orientation, e.g. from dairy to beef production, and thus by extension, their movement practices. Dairy farms may also have become more specialised on solely dairy production, which may have caused them to, e.g., sell more bull calves or to move more cows between different types of holdings within the company. If information regarding holding production types had been available, and if pastures were distinguished, such information could have been included in the analyses to provide a better understanding of the trends and plausible explanations.

Factors such as policy changes or movement restrictions that have been established for disease control purposes (Vernon and Keeling, 2012) have also likely had an impact on the movements of cattle over time. For instance, an eradication scheme for bovine viral diarrhoea virus was launched in Sweden in 1993 and continued until 2014, when the virus was considered eradicated (Swedish Veterinary Agency, 2024). The scheme gradually implemented regulations for movements between holdings (e.g., testing of animals before selling) and eventually became compulsory (Hult and Lindberg, 2005). Presumably, it increased the awareness regarding the risk of disease introduction through animal purchases and resulted in behavioural changes. Further, in 1999 a regulation about zoonoses (SFS 1999:660) came into force in Sweden. In practice, the regulation implies that in the case of salmonella detected at a holding, no economical compensation will be provided if the holding has purchased more than 150 individual cattle from more than five different holdings during the twelve months prior to disease detection. Furthermore, it is currently commonly advised that holdings make agreements for selling and purchasing animals, to limit the number of contacts in order to decrease the risk of disease introduction (Växa Sverige, 2022b).

The apparent decrease in movements and possible deviations in some of the network metrics during 2018 indicates that environmental factors may also influence between-holding movements and the network properties, as Sweden suffered an unusually dry summer that same year (Swedish Meteorological and Hydrological Institute, 2019). The drought primarily caused feed shortage of both forage and grain, which led to premature slaughters (Växa Sverige, 2022c). Furthermore, the drought and the warm summer in 2018 also led to decreased fertility and births due to heat stress in animals. Weather events such as this are more likely to occur in the future as a direct result of climate change, which may lead to changes in farming practises and to the livestock movement network, thereby affecting the risk of disease spread (Gale et al., 2009).

Although there are missing or inaccurate reports in the CDB, the degree of reporting coverage can be considered relatively high in Sweden (Nöremark et al., 2009; Widgren and Frössling, 2010). Additionally, data quality may have improved over time, as was observed in Sweden between 2006 and 2008 (Nöremark et al., 2011) and in the United Kingdom (Duncan et al., 2022). In the present study, 34 % of reported events were not used when determining the longest plausible path per animal, however, the vast majority of these events were matches (i.e. duplicates). All in all, the availability of detailed cattle event data over long time periods allows for sophisticated epidemiological analyses which may improve decision making for disease control.

Studies based on cattle event data could be further improved if production types of the holdings were known. Therefore, it may be advisable to include this information in the CDB, but classification of Swedish holdings into production types could also be the scope of future studies, for instance similar to that of Brock et al. (2021) in Ireland. In addition, future studies could aim to better understand the clusters of holdings in the Swedish cattle movement network, and disease dynamics with regards to clusters in directed and weighted networks, e.g. using extended definitions of the clustering coefficient accounting for direction and weights as proposed by Fagiolo (2007). Furthermore, accounting for temporal aspects of the network and properties of a certain pathogen, as well as other factors such as climate, local spread, etc., would also enhance the understanding of disease dynamics on the network. For instance, data driven disease spread modelling could be advised, which could also be used to analyse the impact of different control measures. In addition, results from the present study could be used as a basis for constructing or predicting “synthetical” movement networks, to simulate future disease spread in the cattle population (e.g. similar to Hoscheit et al. 2017 and Marsot et al. 2022).

5. Conclusions

This study revealed significant structural changes in the Swedish cattle population, and in the properties of the between-holding movement network from 2005 to 2022. The results indicate that the dynamics of disease spread on the network have altered over time, and that epidemics may spread slower and reach a smaller size, despite an increase in the number of movements. Furthermore, the Swedish livestock movement network differs from those in other countries, mainly since the Swedish network does not exhibit small-world properties.

Additionally, an increase of cattle being moved back and forth between holdings was observed, and male calves were more likely to be moved earlier in life, when comparing animals born in 2017 to those born in 2005. Moreover, the study identified several animal- and herd-level risk factors connected to the hazard for cattle to be moved, such as sex, herd size, proportion of females and previous movement practices of the holding.

On the whole, the results from this study are critical to consider when conducting epidemiological analyses that rely on cattle movements and network properties, to ensure accurate conclusions and effective disease mitigation strategies.

Funding

This work was supported by the Swedish Research Council FORMAS (grant number 2021-02279) (SW, IRE, JF, MT, SG, LS, EH) and co-funded by the European Union's Horizon Europe Project 101136346 EUPAHW (SW, IRE).

CRediT authorship contribution statement

Ivana R. Ewerlöf: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Jenny Frössling:** Writing – review & editing, Supervision, Methodology, Funding acquisition, Conceptualization. **Madeleine Tråvén:** Writing – review & editing, Supervision, Funding acquisition, Conceptualization. **Stefan Gunnarsson:** Writing – review & editing, Supervision, Funding acquisition, Conceptualization. **Lena Stengärde:** Writing – review & editing, Conceptualization. **Emma Hurri:** Writing – review & editing, Funding acquisition, Conceptualization. **Stefan Widgren:** Writing – review & editing, Visualization, Validation, Supervision, Software, Project administration, Methodology, Funding acquisition, Formal analysis, Data curation, Conceptualization.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

We would like to acknowledge both the farmers and SBA for providing the raw data used in this study, and to Ann-Christine Ring at SBA who provided valuable information about how the reporting requirements and how legislation changed over time. Thanks also to Thomas Rosendal who provided valuable support when conducting the survival analyses and Vivian Wei Huang for contributing to discussions about the study. We also acknowledge Claudia von Brömssen who gave input on possible statistical methods to use.

Data Availability

The data from the central database for bovine animals is confidential and cannot be shared by the authors. The Swedish Board of Agriculture owns the data, which has been shared with the Swedish Veterinary Agency through an agreement. Geographical data used in the study is publicly available from the Swedish Land Survey Authority.

References

Bajardi, P., Barrat, A., Savini, L., Colizza, V., 2012. Optimizing surveillance for livestock disease spreading through animal movements. J. R. Soc. Interface 9, 2814–2825. https://doi.org/10.1098/rsif.2012.0289.

Barabási, A.-L., Albert, R., 1999. Emergence of scaling in random networks. Science 286, 509–512. https://doi.org/10.1126/science.286.5439.509.

Barkema, H.W., von Keyserlingk, M.A.G., Kastelic, J.P., Lam, T.J.G.M., Luby, C., Roy, J.-P., LeBlanc, S.J., Keefe, G.P., Kelton, D.F., 2015. Invited review: changes in the dairy industry affecting dairy cattle health and welfare. J. Dairy Sci. 98, 7426–7445. https://doi.org/10.3168/jds.2015-9377.

Barrett, T., Dowle, M., Srinivasan, A., Gorecki, J., Chirico, M., Hocking, T., 2023. data.table: Extension of "data.frame." (R package version 1.14.8) [software]. ⟨https://CRAN.R-project.org/package=data.table⟩.

Bigras-Poulin, M., Thompson, R.A., Chriel, M., Mortensen, S., Greiner, M., 2006. Network analysis of danish cattle industry trade patterns as an evaluation of risk potential for disease spread. Prev. Vet. Med. 76, 11–39. https://doi.org/10.1016/j.prevetmed.2006.04.004.

Breustedt, G., Glauben, T., 2007. Driving forces behind exiting from farming in Western Europe. J. Agric. Econ. 58, 115–127. https://doi.org/10.1111/j.1477-9552.2007.00082.x.

Brock, J., Lange, M., Tratalos, J.A., More, S.J., Graham, D.A., Guelbenzu-Gonzalo, M., Thulke, H.-H., 2021. Combining expert knowledge and machine-learning to classify herd types in livestock systems. Sci. Rep. 11, 2989. https://doi.org/10.1038/s41598-021-82373-3.

Brown, E., Marshall, A.H., Mitchell, H.J., Byrne, A.W., 2019. Cattle movements in Northern Ireland form a robust network: implications for disease management. Prev. Vet. Med. 170, 104740. https://doi.org/10.1016/j.prevetmed.2019.104740.

Byrne, A.W., Barrett, D., Breslin, P., Fanning, J., Casey, M., Madden, J.M., Lesellier, S., Gormley, E., 2022. Bovine tuberculosis in youngstock cattle: a narrative review. Front. Vet. Sci. 9. https://doi.org/10.3389/fvets.2022.1000124.

Chaters, G.L., Johnson, P.C.D., Cleaveland, S., Crispell, J., de Glanville, W.A., Doherty, T., Matthews, L., Mohr, S., Nyasebwa, O.M., Rossi, G., Salvador, L.C.M., Swai, E., Kao, R.R., 2019. Analysing livestock network data for infectious disease control: an argument for routine data collection in emerging economies. Philos. Trans. R. Soc. B Biol. Sci. 374, 20180264. https://doi.org/10.1098/rstb.2018.0264.

Comper, J.R., Kelton, D., Hand, K.J., Poljak, Z., Greer, A.L., 2023. Descriptive network analysis and the influence of timescale on centrality and cohesion metrics from a system of between-herd dairy cow movements in Ontario, Canada. Prev. Vet. Med. 213, 105861. https://doi.org/10.1016/j.prevetmed.2023.105861.

Csardi, G., Nepusz, T., 2006. The igraph software package for complex network research. Inter. Complex Syst. 1695. ⟨https://igraph.org⟩.

Dubé, C., Ribble, C., Kelton, D., McNab, B., 2008. Comparing network analysis measures to determine potential epidemic size of highly contagious exotic diseases in fragmented monthly networks of dairy cattle movements in Ontario, Canada. Transbound. Emerg. Dis. 55, 382–392. https://doi.org/10.1111/j.1865-1682.2008.01053.x.

Dubé, C., Ribble, C., Kelton, D., McNab, B., 2009. A review of network analysis terminology and its application to foot-and-mouth disease modelling and policy development. Transbound. Emerg. Dis. 56, 73–85. https://doi.org/10.1111/j.1865-1682.2008.01064.x.

Dubé, C., Ribble, C., Kelton, D., McNab, B., 2011. Estimating potential epidemic size following introduction of a long-incubation disease in scale-free connected networks of milking-cow movements in Ontario, Canada. Prev. Vet. Med. 99, 102–111. https://doi.org/10.1016/j.prevetmed.2011.01.013.

Duncan, A.J., Reeves, A., Gunn, G.J., Humphry, R.W., 2022. Quantifying changes in the British cattle movement network. Prev. Vet. Med. 198, 105524. https://doi.org/10.1016/j.prevetmed.2021.105524.

Dutta, B.L., Ezanno, P., Vergu, E., 2014. Characteristics of the spatio-temporal network of cattle movements in France over a 5-year period. Prev. Vet. Med. 117, 79–94. https://doi.org/10.1016/j.prevetmed.2014.09.005.

Eames, K.T.D., Keeling, M.J., 2003. Contact tracing and disease control. Proc. R. Soc. Lond. B Biol. Sci. 270, 2565–2571. https://doi.org/10.1098/rspb.2003.2554.

Enright, J., Kao, R.R., 2018. Epidemics on dynamic networks. Epidemics 24, 88–97. https://doi.org/10.1016/j.epidem.2018.04.003.

Ensoy, C., Faes, C., Welby, S., Van der Stede, Y., Aerts, M., 2014. Exploring cattle movements in Belgium. Prev. Vet. Med. 116, 89–101. https://doi.org/10.1016/j.prevetmed.2014.05.003.

Erdös, R., Renyi, A., 1959. On random graphs. Publ. Math. 6, 290–297.

Fagiolo, G., 2007. Clustering in complex directed networks. Phys. Rev. E 76, 026107. https://doi.org/10.1103/PhysRevE.76.026107.

Fèvre, E.M., Bronsvoort, B.M., de, C., Hamilton, K.A., Cleaveland, S., 2006. Animal movements and the spread of infectious diseases. Trends Microbiol 14, 125–131. https://doi.org/10.1016/j.tim.2006.01.004.

Fielding, H.R., McKinley, T.J., Silk, M.J., Delahay, R.J., McDonald, R.A., 2019. Contact chains of cattle farms in Great Britain. R. Soc. Open Sci. 6, 180719. https://doi.org/10.1098/rsos.180719.

Frössling, J., Nusinovici, S., Nöremark, M., Widgren, S., Lindberg, A., 2014. A novel method to identify herds with an increased probability of disease introduction due to animal trade. Prev. Vet. Med., Special Issue: SVEPM 2014 - supporting decision making on animal health through advanced and multidisciplinary methodologies, 2014 Society of Veterinary Epidemiology and Preventive Medicine conference 117, 367–374. https://doi.org/10.1016/j.prevetmed.2014.07.013.

Frössling, J., Ohlson, A., Björkman, C., Håkansson, N., Nöremark, M., 2012. Application of network analysis parameters in risk-based surveillance – Examples based on cattle trade data and bovine infections in Sweden. Prev. Vet. Med., Special Issue: First International Conference on Animal Health Surveillance (ICAHS) 105, 202–208. https://doi.org/10.1016/j.prevetmed.2011.12.011.

Gale, P., Drew, T., Phipps, L.P., David, G., Wooldridge, M., 2009. The effect of climate change on the occurrence and prevalence of livestock diseases in Great Britain: a review. J. Appl. Microbiol 106, 1409–1423. https://doi.org/10.1111/j.1365-2672.2008.04036.x.

Gård & Djurhälsan, 2023. Lägre slaktvikt och ökad ålder vid slakt för många nötkreatur som slaktades under 2022 [WWW Document]. URL https://www.gardochdjurhalsan.se/nyheter/lagre-slaktvikt-och-okad-alder-vid-slakt/ (accessed 2025-01-22).

Gates, M.C., Woolhouse, M.E.J., 2015. Controlling infectious disease through the targeted manipulation of contact network structure. Epidemics Pap. Aris. Epidemics 4 (12), 11–19. https://doi.org/10.1016/j.epidem.2015.02.008.
Grimstedt, L., 2019. Viktigt att båda är nöjda. Husdjur -. Tidn. för Mjölkföretagare 6–7, 13–17.
Hajdu, F., Eriksson, C., Waldenström, C., Westholm, E., 2020. Sveriges förändrade lantbruk – Lantbrukarnas egna röster om förändringar sedan 1990-talet och strategier inför framtiden (No. 11), SLU Future Food Reports. Swedish University of Agricultural Sciences, Kalmar.
Hamed, K.H., Rao, A.R., 1998. A modified mann-kendall trend test for autocorrelated data. J. Hydrol. 204, 182–196. https://doi.org/10.1016/S0022-1694(97)00125-X.
Harrell, F.E., 2025. rms: Regression Modeling Strategies. (R package version 8.0-0) [software]. 〈〈https://cran.r-project.org/package=rms〉〉.
Hidano, A., Gates, M.C., 2019. Why sold, not culled? analysing farm and animal characteristics associated with livestock selling practices. Prev. Vet. Med. 166, 65–77. https://doi.org/10.1016/j.prevetmed.2019.03.005.
Holme, P., Saramäki, J., 2012. Temporal networks. Phys. Rep. 519, 97–125. https://doi.org/10.1016/j.physrep.2012.03.001.
Hoscheit, P., Geeraert, S., Beaunée, G., Monod, H., Gilligan, C.A., Filipe, J.A.N., Vergu, E., Moslonka-Lefebvre, M., 2017. Dynamical network models for cattle trade: towards economy-based epidemic risk assessment. J. Complex Netw. 5, 604–624. https://doi.org/10.1093/comnet/cnw026.
Hult, L., Lindberg, A., 2005. Experiences from BVDV control in Sweden. Prev. Vet. Med. 72, 143–148. https://doi.org/10.1016/j.prevetmed.2005.04.005.
Hultén, C., Sahlman, M., Comin, A., Ernholm, L., Frössling, J., Grant, M., Johansson, J., Lahti, E., Lundh, M., Malmsten, A., Ring, A.-C., Thelander, M., Wärnbring, R., Young, B., Ågren, E., 2022. Förstudie om åtgärder mot salmonella hos lantbrukets djur (No. ISSN 1654-7098), SVA:s rapportserie nr 77. Swedish Veterinary Agency (prev. National Veterinary Institute) (SVA), Uppsala, Sweden.
Kao, R.R., Danon, L., Green, D.M., Kiss, I.Z., 2006. Demographic structure and pathogen dynamics on the network of livestock movements in Great Britain. Proc. R. Soc. B Biol. Sci. 273, 1999–2007. https://doi.org/10.1098/rspb.2006.3505.
Kiss, I.Z., Green, D.M., Kao, R.R., 2006a. The network of sheep movements within Great Britain: network properties and their implications for infectious disease spread. J. R. Soc. Interface 3, 669–677. https://doi.org/10.1098/rsif.2006.0129.
Kiss, I.Z., Green, D.M., Kao, R.R., 2006b. Infectious disease control using contact tracing in random and scale-free networks. J. R. Soc. Interface 3, 55–62. https://doi.org/10.1098/rsif.2005.0079.
Kiss, I.Z., Green, D.M., Kao, R.R., 2008. The effect of network mixing patterns on epidemic dynamics and the efficacy of disease contact tracing. J. R. Soc. Interface 5, 791–799. https://doi.org/10.1098/rsif.2007.1272.
Koutrouli, M., Karatzas, E., Paez-Espino, D., Pavlopoulos, G.A., 2020. A guide to conquer the biological network era using graph theory. Front. Bioeng. Biotechnol. 8. https://doi.org/10.3389/fbioe.2020.00034.
Mann, H.B., 1945. Nonparametric tests against trend. Econometrica 13, 245–259. https://doi.org/10.2307/1907187.
Marsot, M., Canini, L., Janicot, S., Lambert, J., Vergu, E., Durand, B., 2022. Predicting veal-calf trading events in France. Prev. Vet. Med. 209, 105782. https://doi.org/10.1016/j.prevetmed.2022.105782.
Martínez-López, B., Perez, A.M., Sánchez-Vizcaíno, J.M., 2009. Social network analysis. review of general concepts and use in preventive veterinary medicine. Transbound. Emerg. Dis. 56, 109–120. https://doi.org/10.1111/j.1865-1682.2009.01073.x.
Mweu, M.M., Fournié, G., Halasa, T., Toft, N., Nielsen, S.S., 2013. Temporal characterisation of the network of danish cattle movements and its implication for disease control: 2000–2009. Prev. Vet. Med. 110, 379–387. https://doi.org/10.1016/j.prevetmed.2013.02.015.
Nagelkerke, N.J.D., Oosting, J., Hart, A.A.M., 1984. A simple test for goodness of fit of cox's proportional hazards model. Biometrics 40, 483–486. https://doi.org/10.2307/2531400.
Natale, F., Giovannini, A., Savini, L., Palma, D., Possenti, L., Fiore, G., Calistri, P., 2009. Network analysis of Italian cattle trade patterns and evaluation of risks for potential disease spread, 2008 Prev. Vet. Med. Spec. Sect. Schwabe Symp. 92, 341–350. https://doi.org/10.1016/j.prevetmed.2009.08.026.
Newman, M.E.J., 2002. Assortative mixing in networks. Phys. Rev. Lett. 89, 208701. https://doi.org/10.1103/PhysRevLett.89.208701.
Newman, M.E.J., 2003. Mixing patterns in networks. Phys. Rev. E 67, 026126. https://doi.org/10.1103/PhysRevE.67.026126.
Nöremark, M., Håkansson, N., Lewerin, S.S., Lindberg, A., Jonsson, A., 2011. Network analysis of cattle and pig movements in Sweden: measures relevant for disease control and risk based surveillance. Prev. Vet. Med. 99, 78–90. https://doi.org/10.1016/j.prevetmed.2010.12.009.
Nöremark, M., Håkansson, N., Lindström, T., Wennergren, U., Lewerin, S.S., 2009. Spatial and temporal investigations of reported movements, births and deaths of cattle and pigs in Sweden. Acta Vet. Scand. 51, 37. https://doi.org/10.1186/1751-0147-51-37.
Nöremark, M., Widgren, S., 2014. EpiContactTrace: an R-package for contact tracing during livestock disease outbreaks and for risk-based surveillance. BMC Vet. Res. 10, 71. https://doi.org/10.1186/1746-6148-10-71.
Ortiz-Pelaez, A., Pfeiffer, D.U., Soares-Magalhães, R.J., Guitian, F.J., 2006. Use of social network analysis to characterize the pattern of animal movements in the initial phases of the 2001 foot and mouth disease (FMD) epidemic in the UK. Prev. Vet. Med. 76, 40–55. https://doi.org/10.1016/j.prevetmed.2006.04.007.
Pebesma, E., 2018. Simple features for R: standardized support for spatial vector data. R. J. 10, 439–446. https://doi.org/10.32614/RJ-2018-009.
R Core Team, 2022. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria [software]. 〈https://www.R-project.org/〉.
Rosendal, T., Widgren, S., Ståhl, K., Frössling, J., 2020. Modelling spread and surveillance of *Mycobacterium avium* subsp. *paratuberculosis* in the Swedish cattle trade network. Prev. Vet. Med. 183, 105152. https://doi.org/10.1016/j.prevetmed.2020.105152.
Rushton, J., 2009. Wallingford. The economics of animal health and production. CABI.
Söderberg, T. , Brady, M. , Kumm, K.-I. , Hristov, J. , Wilhelmsson, F. , 2015. Jordbrukspolitik, inlåsning och strukturomvandling (No. ISRN SJV-R-15/12-SE). Swedish Board of Agriculture (SBA), Jönköping, Sweden.
Stärk, K.D., Regula, G., Hernandez, J., Knopf, L., Fuchs, K., Morris, R.S., Davies, P., 2006. Concepts for risk-based surveillance in the field of veterinary medicine and veterinary public health: review of current approaches. BMC Health Serv. Res. 6, 20. https://doi.org/10.1186/1472-6963-6-20.
Swedish Board of Agriculture, (SBA), 2022. Nötkreatussektorns uppbyggnad - En analys av struktur och slakt i nötkreatussektorn [WWW Document]. URL https://jordbruksverket.se/om-jordbruksverket/jordbruksverkets-officiella-statistik/jordbruksverkets-statistikrapporter/statistik/2022-02-01-notkreatussektorns-uppbyggnad–en-analys-av-struktur-och-slakt-i-notkreatussektorn (accessed 2023-12-1).
Swedish Land Survey Authority, 2023. Produktionsplatser för djurhållning. Geodata - Lantmäteriet. [WWW Document]. URL 〈https://www.geodata.se/geodataportalen/srv/swe/catalog.search;jsessionid=C3D20AF0E139DB2FCA6%20A2C6CF258DAC8#/search?resultType=swe-%20details&_schema=iso19139*&type=dataset%20or%20series&from=1&to=20&fast=index&_content_ty%20pe=json&sortBy=relevance&or=produktionsplats〉 (accessed 2023-02-14).
Swedish Meteorological and Hydrological Institute, (SMHI), 2019. Sommaren 2018 - en glimt av framtiden? (No. ISSN 1654-2258), KLIMATOLOGI Nr 52. SMHI, Norrköping, Sweden.
Swedish Veterinary Agency, (SVA), 2023. Surveillance of infectious diseases in animals and humans in Sweden 2022 (No. SVA:s rapportserie 89 1654-7098). swedish veterinary agency (prev. National Veterinary Institute) (SVA), Uppsala, Sweden.
Swedish Veterinary Agency, (SVA), 2024. BVD – bovin virusdiarré - SVA [WWW Document]. URL 〈https://www.sva.se/djurhaelsa/djursjukdomar-a-oe/sjukdomar/bvd/〉 (accessed 2025-06-27).
Therneau, T.M., 2022. A Package for Survival Analysis in R. (R package version 3.4-0) URL.〈https://CRAN.R-project.org/package=survival〉.
Tratalos, J.A., Madden, J.M., McGrath, G., Graham, D.A., Collins, Á.B., More, S.J., 2020. Spatial and network characteristics of irish cattle movements. Prev. Vet. Med. 183, 105095. https://doi.org/10.1016/j.prevetmed.2020.105095.
Växa Sverige , 2022a. Långlivade kor kan ge högre lönsamhet [WWW Document]. URL 〈https://www.vxa.se/nyheter/2022/langlivade-kor-kan-ge-hogre-lonsamhet/〉 (accessed 2025-01-08).
Växa Sverige , 2022b. Säkrare inköp med avtal [WWW Document]. URL 〈https://www.vxa.se/nyheter/2022/sakrare-inkop-med-avtal/〉 (accessed 2024-05-16).
Växa Sverige , 2022c. Rådgivning och åtgärder vid extrem torka - Lärdomar från sommaren 2018 [WWW Document]. URL 〈https://www.vxa.se/globalassets/dokumentsok/foder/radgivning-och-atgarder-vid-extrem-torka.pdf〉 (accessed 2024-04-17).
Vernon, M.C., Keeling, M.J., 2012. Impact of regulatory perturbations to disease spread through cattle movements in Great Britain. Prev. Vet. Med. 105, 110–117. https://doi.org/10.1016/j.prevetmed.2011.12.016.
Wasserman, S., Faust, K., 1994. Social network analysis: methods and applications, structural analysis in the social sciences. Cambridge University Press, Cambridge. https://doi.org/10.1017/CBO9780511815478.
Wästfelt, A. , Eriksson, C. , 2017. Det svenska lantbrukets omvandling 1990-2014. Exemplet Uppsala län (No. ISBN: 978-91-576-9509-3). Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden.
Watts, D.J., Strogatz, S.H., 1998. Collective dynamics of 'small-world' networks. Nature 393, 440–442. https://doi.org/10.1038/30918.
White, P., Frankena, K., O'Keeffe, J., More, S.J., Martin, S.W., 2010. Predictors of the first between-herd animal movement for cattle born in 2002 in Ireland. Prev. Vet. Med. Spec. Sect. Calvin. W. Schwabe Symp 2009 97, 264–269. https://doi.org/10.1016/j.prevetmed.2010.09.017.
Widgren, S., Bauer, P., Eriksson, R., Engblom, S., 2019. SimInf: an R Package for data-driven stochastic disease spread simulations. J. Stat. Softw. 91, 1–42. https://doi.org/10.18637/jss.v091.i12.
Widgren, S., Engblom, S., Bauer, P., Frössling, J., Emanuelson, U., Lindberg, A., 2016. Data-driven network modelling of disease transmission using complete population movement data: spread of VTEC O157 in Swedish cattle. Vet. Res. 47, 81. https://doi.org/10.1186/s13567-016-0366-5.
Widgren, S., Frössling, J., 2010. Spatio-temporal evaluation of cattle trade in Sweden: description of a grid network visualization technique. Geospatial Health 5, 119–130. https://doi.org/10.4081/gh.2010.192.